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(57) Abstract

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.

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NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS I

Cross-References to Related Applications

This application is a continuation-in-part of U.S. provisional patent application serial no. 60/068,755, filed December 23, 1997, and of U.S. provisional patent application serial no. 60/080,664, filed April 3, 1998, and of U.S. provisional patent application serial no. 60/105,234, filed October 21, 1998, each of which applications are incorporated herein by reference.

Field of the Invention

The present invention relates to novel polynucleotides, particularly to novel polynucleotides of human origin that are expressed in a selected cell type, are differentially expressed in one cell type relative to another cell type (*e.g.*, in cancerous cells, or in cells of a specific tissue origin) and/or share homology to polynucleotides encoding a gene product having an identified functional domain and/or activity.

Background of the Invention

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences

This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

Summary of the Invention

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides

and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, *e.g.*, these genes and proteins, including probes, antisense constructs, and antibodies.

Accordingly, in one embodiment, the present invention features a library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844. In related aspects, the invention features a library provided on a nucleic acid array, or in a computer-readable format.

In one embodiment, the library is comprises a differentially expressed polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379. In specific related embodiments, the library comprises: 1) a polynucleotide that is differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388; 2) a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374; or 3) a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

In another aspect, the invention features an isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof. In related aspects, the invention features recombinant host cells and vectors comprising the polynucleotides of the invention, as well as isolated polypeptides encoded by the polynucleotides of the invention and antibodies that specifically bind such polypeptides.

In one embodiment, the invention features an isolated polynucleotide comprising a sequence encoding a polypeptide of a protein family selected from the group consisting of: 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases,

GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins. In a specific related embodiment, the invention features a polynucleotide comprising a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379 , and 395.

In another embodiment, the invention features a polynucleotide comprising a sequence encoding a polypeptide having a functional domain selected from the group consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease domain. In a specific related embodiment, the invention features a polynucleotide comprising a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and 395.

In another aspect, the invention features a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, where the method comprises the step of detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400. Detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. In one embodiment, the detecting is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS:1-844.

In one embodiment of the method of the invention, the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123,

144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

In another embodiment of the method of the invention, the cell is a colon tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

In yet another embodiment of the method of the invention, the cell is a lung tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

Other aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Detailed Description of the Invention

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA and genes corresponding to these sequences, and to polypeptides and proteins encoded by these polynucleotides and genes.

Also included are polynucleotides that encode polypeptides and proteins encoded by the polynucleotides of the Sequence Listing. The various polynucleotides that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code, in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well-known in this art, and this information can be used for the construction of the polynucleotides within the scope of the invention.

Polynucleotides encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the polynucleotides and related cDNA and genes are also within the scope of the invention. The variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein. Once the amino acid change is selected, a polynucleotide encoding that variant is constructed according to the invention.

The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of

structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

I. Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOS:1-844; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

The invention features polynucleotides that are expressed in cells of human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-844 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS:1-844.

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by

hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-844) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice, canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides of at least one of SEQ ID NOS: 1-844. That is, when at least 15 contiguous nucleotides of one of the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. will hybridize with the same gene or mRNA if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% base pair mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% base pair mismatches, as well as a single base-pair mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-844, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats, canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.*, *J. Mol. Biol.* (1990) *215*:403-10.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3 and 5 non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3 and 5 untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5 and 3 end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3 and 5 , or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject differentially expressed polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nucleotides selected from the polynucleotide sequences as shown in SEQ ID NOS:1-844. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least twelve nucleotides selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-844.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-844. The probes are preferably at least about 12, 15, 16, 18, 20, 22, 24, or 25 nucleotide fragment of a corresponding contiguous sequence of SEQ ID NOS:1-844, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-844. More preferably,

probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule. They can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. They can be regulated by their own or by other regulatory sequences, as is known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques which are available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOS:1-844 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA and Full-Length Human Gene and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-844, or a portion thereof comprising at least 12, 15, 18, or 20 nucleotides, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook *et al., Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY). The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al., Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-844. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments

are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) is performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.,* 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length

cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO 95/04745 and Gruber *et al.*, U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) *15*:890-893; Edwards *et al.*, *Nuc. Acids Res.* (1991) *19*:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. The method uses lock-docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described in WO 96/40998.

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as

TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nucleotides (corresponding to at least 15 contiguous nucleotides of one of SEQ ID NOS: 1-844) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS: 1-844; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nucleotides of at least any one of SEQ ID NOS: 1-844, preferably the entire sequence of at least any one of SEQ ID NOS: 1-844, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS: 1-844 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS: 1-844.

II. Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotide (*e.g.*, a polynucleotide having a sequence of one of SEQ ID NOS:1-844), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product.

Constructs of polynucleotides having sequences of SEQ ID NOS:1-844 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, *e.g.*, Stemmer *et al., Gene (Amsterdam)* (1995) *164(1)*:49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) *370*:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (bla) can be assembled in a single reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) *275*:615; Goeddel *et al.*, *Nature* (1979) *281*:544; Goeddel *et al.*, *Nucleic Acids Res.* (1980) *8*:4057; EP 0 036,776; U.S. Patent No. 4,551,433; DeBoer *et al., Proc. Natl. Acad. Sci. (USA)* (1983) *80*:21-25; and Siebenlist *et al.*, *Cell* (1980) *20*:269.

Yeast. Expression systems in yeast include those described in Hinnen *et al., Proc. Natl. Acad. Sci. (USA)* (1978) *75*:1929; Ito *et al., J. Bacteriol.* (1983) *153*:163; Kurtz *et al., Mol. Cell. Biol.* (1986) *6*:142; Kunze *et al., J. Basic Microbiol.* (1985) *25*:141; Gleeson *et al., J. Gen. Microbiol.* (1986) *132*:3459; Roggenkamp *et al., Mol. Gen. Genet.* (1986) *202*:302; Das *et al., J. Bacteriol.* (1984) *158*:1165; De Louvencourt *et al., J. Bacteriol.* (1983) *154*:737; Van den Berg *et al., Bio/Technology* (1990) *8*:135; Kunze *et al., J. Basic Microbiol.* (1985) *25*:141; Cregg *et al., Mol. Cell. Biol.* (1985) *5*:3376; U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) *300*:706; Davidow *et al., Curr. Genet.* (1985) *10*:380; Gaillardin *et al., Curr. Genet.* (1985) *10*:49; Ballance *et al., Biochem. Biophys. Res. Commun.* (1983) *112*:284-289; Tilburn *et al., Gene* (1983) *26*:205-221; Yelton *et al., Proc. Natl. Acad. Sci. (USA)* (1984) *81*:1470-1474; Kelly and Hynes, *EMBO J.* (1985) *4*:475479; EP 0 244,234; and WO 91/00357.

Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051; Friesen *et al.*, "The Regulation of Baculovirus Gene Expression", in: *The Molecular Biology Of Baculoviruses* (1986) (W. Doerfler, ed.); EP 0 127,839; EP 0 155,476; and Vlak *et al., J. Gen. Virol.* (1988) *69*:765-776; Miller *et al., Ann. Rev. Microbiol.* (1988) *42*:177; Carbonell *et al., Gene* (1988) *73*:409; Maeda *et al., Nature* (1985) *315*:592-594; Lebacq-Verheyden *et al., Mol. Cell. Biol.* (1988) *8*:3129; Smith *et al., Proc. Natl. Acad. Sci. (USA)* (1985) *82*:8844; Miyajima *et al., Gene* (1987) *58*:273; and Martin *et al., DNA* (1988) *7*:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al., Bio/Technology* (1988) *6*:47-55, Miller *et al., Generic Engineering* (1986) *8*:277-279, and Maeda *et al., Nature* (1985) *315*:592-594.

Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al., EMBO J.* (1985) *4*:761, Gorman *et al., Proc. Natl. Acad. Sci. (USA)* (1982) *79*:6777, Boshart *et al., Cell* (1985) *41*:521 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) *58*:44, Barnes and Sato, *Anal. Biochem.* (1980) *102*:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

Polynucleotide molecules comprising a polynucleotide sequence provided herein propagated by placing the molecule in a vector. Viral and non-viral vectors are used,

including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

The polynucleotides set forth in SEQ ID NOS:1-844 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

III. Identification of Functional and Structural Motifs of Novel Genes

A. Screening Polynucleotide Sequences and Amino Acid Sequences Against Publicly Available Databases

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For example, sequences that show similarity with a chemokine sequence can exhibit chemokine activities. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides..

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world wide web at http://ww.ncbi.nlm.nih.gov/BLAST/. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is

utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) *70*: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

Results of individual and query sequence alignments can be divided into three categories, high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value.

The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1990) *87*:2264 and Karlin *et al., Proc. Natl. Acad. Sci.* (1993) *90*. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al., Nat. Genet.* (1994) *6*:119. Alignment programs such as BLAST program can calculate the p value.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More typically, the p value is no more than about 10^{-5}; more typically; no more than or equal to about 10^{-10}; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of

alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More typically, the p value is no more than about 10^{-5}; more usually; no more than or equal to about 10^{-10}; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Determining Activity from Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*,

polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) *24(14)*: 2730-2739. MSAs of some protein families and motifs are publicly available. For example, http://genome.wustl.edu/Pfam/ includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) *28*: 405-420. Other sources over the world wide web include the site at http://www.embl-heidelberg.de/argos/ali/ali.html; alternatively, a message can be sent to ALI@EMBL-HEIDELBERG.DE for the information. A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) *9(3)*:249-251. Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney *et al.*, *supra.* Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra.*

Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351 and Higgins *et al.*, *CABIOS* (1989) *5*:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng *et al.*, *infra.* In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. For example, most chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually,

at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

B. Screening Polynucleotide and Amino Acid Sequences Against Protein Profiles

The identify and function of the gene that correlates to a polynucleotide described herein can be determined by screening the polynucleotides or their corresponding amino acid sequences against profiles of protein families. Such profiles focus on common structural motifs among proteins of each family. Publicly available profiles are described above in Section IVA. Additional or alternative profiles are described below.

In comparing a novel polynucleotide with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) *48*:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) *2*:482. Exemplary protein profiles are provided below and in the examples.

Chemokines. Chemokines are a family of proteins that have been implicated in lymphocyte trafficking, inflammatory diseases, angiogenesis, hematopoiesis, and viral infection. See, for example, Rollins, *Blood* (1997) *90(3)*:909-928, and Wells *et al.*, *J. Leuk. Biol.* (1997) *61*:545-550. U.S. Patent No. 5,605,817 discloses DNA encoding a chemokine expressed in fetal spleen. U.S. Patent No. 5,656,724 discloses chemokine-like proteins and methods of use. U.S. Patent No. 5,602,008 discloses DNA encoding a chemokine expressed by liver.

Chemokine mutants are polypeptides having an amino acid sequence that possesses at least one amino acid substitution, addition, or deletion as compared to native chemokines. Fragments possess the same amino acid sequence of the native chemokines; mutants can lack the amino and/or carboxyl terminal sequences. Fusions are mutants, fragments, or native chemokines that also include amino and/or carboxyl terminal amino acid extensions.

The number or type of the amino acid changes is not critical, nor is the length or number of the amino acid deletions, or amino acid extensions that are incorporated in the chemokines as compared to the native chemokine amino acid sequences. A polynucleotide encoding one of these variant polypeptides will retain at least about 80% amino acid identity with at least one known chemokine. Preferably, these polypeptides will retain at least about 85% amino acid sequence identity, more preferably, at least about 90%; even more preferably, at least about 95%. In addition, the variants exhibit at least 80%; preferably about 90%; more preferably about 95% of at least one activity exhibited by a native chemokine, which includes immunological, biological, receptor binding, and signal transduction functions.

Assays for chemotaxis relating to neutrophils are described in Walz *et al.*, *Biochem. Biophys. Res. Commun.* (1987) *149*:755, Yoshimura *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1987) *84*:9233, and Schroder *et al.*, *J. Immunol.* (1987) *139*:3474; to lymphocytes, Larsen *et al.*, *Science* (1989) *243*:1464, Carr *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1994) *91*:3652; to tumor-infiltrating lymphocytes, Liao *et al.*, *J. Exp. Med* (1995). *182*:1301; to hematopoietic progenitors, Aiuti *et al.*, *J. Exp. Med.* (1997) *185*:111; to monocytes, Valente *et al.*, *Biochem.* (1988) *27*:4162; and to natural killer cells, Loetscher *et al.*, *J. Immunol.* (1996) *156*:322, and Allavena *et al.*, *Eur. J. Immunol.* (1994) *24*:3233.

Assays for determining the biological activity of attracting eosinophils are described in Dahinden *et al.*, *J. Exp. Med.* (1994) *179*:751, Weber *et al.*, *J. Immunol.* (1995) *154*:4166, and Noso *et al.*, *Biochem. Biophys. Res. Commun.* (1994) *200*:1470; for attracting dendritic cells, Sozzani *et al.*, *J. Immunol.* (1995) *155*:3292; for attracting basophils, in Dahinden *et al.*, *J. Exp. Med.* (1994) *179*:751, Alam *et al.*, *J. Immunol.* (1994) *152*:1298, Alam *et al.*, *J. Exp. Med.* (1992) *176*:781; and for activating neutrophils, Maghazaci *et al.*, *Eur. J. Immunol.* (1996) *26*:315, and Taub *et al.*, *J. Immunol.* (1995) *155*:3877. Native chemokines can act as mitogens for fibroblasts, assayed as described in Mullenbach *et al.*, *J. Biol. Chem.* (1986) *261*:719.

Native chemokines exhibit binding activity with a number of receptors. Description of such receptors and assays to detect binding are described in, for example, Murphy *et al.*, *Science* (1991) *253*:1280; Combadiere *et al.*, *J. Biol. Chem.* (1995) *270*:29671; Daugherty *et al.*, *J. Exp. Med.* (1996) *183*:2349; Samson *et al.*, *Biochem.* (1996) *35*:3362; Raport *et al.*, *J.*

Biol. Chem. (1996) *271*:17161; Combadiere *et al., J. Leukoc. Biol.* (1996) *60*:147; Baba *et al., J. Biol. Chem.* (1997) *23*:14893; Yosida *et al., J. Biol. Chem.* (1997) *272*:13803; Arvannitakis *et al., Nature* (1997) *385*:347, and other assays are known in the art.

Assays for kinase activation of chemokines are described by Yen *et al., J. Leukoc. Biol.* (1997) *61*:529; Dubois *et al., J. Immunol.* (1996) *156*:1356; Turner *et al., J. Immunol.* (1995) *155*:2437. Assays for inhibition of angiogenesis or cell proliferation are described in Maione *et al., Science* (1990) *247*:77. Glycosaminoglycan production can be induced by native chemokines, assayed as described in Castor *et al., Proc. Natl. Acad. Sci. (USA)* (1983) *80*:765. Chemokine-mediated histamine release from basophils is assayed as described in Dahinden *et al., J. Exp. Med.* (1989) *170*:1787; and White *et al., Immunol. Lett.* (1989) *22*:151. Heparin binding is described in Luster *et al., J. Exp. Med.* (1995) *182*:219.

Chemokines can possess dimerization activity, which can be assayed according to Burrows *et al., Biochem.* (1994) *33*:12741; and Zhang *et al., Mol. Cell. Biol.* (1995) *15*:4851. Native chemokines can play a role in the inflammatory response of viruses. This activity can be assayed as described in Bleul *et al., Nature* (1996) *382*:829; and Oberlin *et al., Nature* (1996) *382*:833. Exocytosis of monocytes can be promoted by native chemokines. The assay for such activity is described in Uguccioni *et al., Eur. J. Immunol.* (1995) *25*:64. Native chemokines also can inhibit hematopoietic stem cell proliferation. The method for testing for such activity is reported in Graham *et al., Nature* (1990) *344*:442.

Death Domain Proteins. Several protein families contain death domain motifs (Feinstein and Kimchi, *TIBS Letters* (1995) *20*:242). Some death domain containing proteins are implicated in cytotoxic intracellular signaling (Cleveland *et al., Cell* (1995) *81*:479, Pan *et al, Science* (1997) *276*:111; Duan *et al., Nature* (1997) *385*:86-89, and Chinnaiyan *et al, Science* (1996) *274*:990). U.S. Patent No. 5,563,039 describes a protein homologous to TRADD (Tumor Necrosis Factor Receptor-1 Associated Death Domain containing protein), and modifications of the active domain of TRADD that retain the functional characteristics of the protein, as well as apoptosis assays for testing the function of such death domain containing proteins. U.S. Patent No. 5,658,883 discloses biologically active TGF-B1 peptides. U.S. Patent No. 5,674,734 discloses RIP, which contains a C-terminal death domain and an N-terminal kinase domain.

Leukemia Inhibitory Factor (LIF). An LIF profile is constructed from sequences of leukemia inhibitor factor, CT-1 (cardiotrophin-1), CNTF (ciliary neurotrophic factor), OSM (oncostatin M), and IL-6 (interleukin-6). This profile encompasses a family of secreted cytokines that have pleiotropic effects on many cell types including hepatocytes, osteoclasts, neuronal cells and cardiac myocytes, and can be used to detect additional genes encoding such proteins. These molecules are all structurally related and share a common co-receptor gp130 which mediates intracellular signal transduction by cytoplasmic tyrosine kinases such as src.

Novel proteins related to this family are also likely to be secreted, to activate gp130 and to function in the development of a variety of cell types. Thus new members of this family would be candidates to be developed as growth or survival factors for the cell types that they stimulate. For more details on this family of cytokines, see Pennica *et al*, *Cytokine and Growth Factor Reviews* (1996) *7*:81-91. U.S. Patent No. 5,420,247 discloses LIF receptor and fusion proteins. U.S. Patent No. 5,443,825 discloses human LIF.

Angiopoietin. Angiopoietin-1 is a secreted ligand of the TIE-2 tyrosine kinase; it functions as an angiogenic factor critical for normal vascular development. Angiopoietin-2 is a natural antagonist of angiopoietin-1 and thus functions as an anti-angiogenic factor. These two proteins are structurally similar and activate the same receptor (Folkman *et al.*, *Cell* (1996) *87*:1153, and Davis *et al.*, *Cell* (1996) *87*:1161). The angiopoietin molecules are composed of two domains: a coiled-coil region and a region related to fibrinogen. The fibrinogen domain is found in many molecules including ficolin and tesascin, and is well defined structurally with many members.

Receptor Protein-Tyrosine Kinases. Receptor Protein-Tyrosine Kinases or RPTKs are described in Lindberg, *Annu. Rev. Cell Biol.* (1994) *10*:251-337.

Growth Factors: (Epidermal Growth Factor) EGF and (Fibroblast Growth Factor) FGF. For a discussion of growth factor superfamilies, see *Growth Factors: A Practical Approach*, (Appendix A1) (1993) McKay and Leigh, Oxford University Press, NY, 237-243. U.S. Patent No. 4,444,760 discloses acidic brain fibroblast growth factor, which is active in the promotion of cell division and wound healing. U.S. Patent No. 5,439,818 discloses DNA encoding human recombinant basic fibroblast growth factor, which is active in wound healing. U.S. Patent No. 5,604,293 discloses recombinant human basic fibroblast growth

factor, which is useful for wound healing. U.S. Patent No. 5,410,832 discloses brain-derived and recombinant acidic fibroblast growth factor, which act as mitogens for mesoderm and neuroectoderm-derived cells in culture, and promote wound healing in soft tissue, cartilaginous tissue and musculo-skeletal tissue. U.S. Patent No. 5,387,673 discloses biologically active fragments of FGF.

Proteins of the TNF Family. A profile derived from the TNF family is created by aligning sequences of the following TNF family members: nerve growth factor (NGF), lymphotoxin, Fas ligand, tumor necrosis factor (TNFα), CD40 ligand, TRAIL, ox40 ligand, 4-1BB ligand, CD27 ligand, and CD30 ligand. The profile is designed to identify sequences of proteins that constitute new members or homologues of this family of proteins. U.S. Patent No. 5,606,023 discloses mutant TNF proteins; U.S. Patent No. 5,597,899 and U.S. Patent No. 5,486,463 disclose TNF muteins; and U.S. Patent No. 5,652,353 discloses DNA encoding TNFα muteins.

Members of the TNF family of proteins have been show in vitro to multimerize, as described in Burrows *et al.*, *Biochem.* (1994) *33*:12741 and Zhang *et al.*, *Mol. Cell. Biol.* (1995) *15*:4851 and bind receptors as described in Browning *et al.*, *J. Immunol.* (1994) *147*:1230, Androlewicz *et al.*, *J. Biol. Chem.*(1992) *267*:2542, and Crowe *et al.*, *Science* (1994) *264*:707.

In vivo, TNFs proteolytically cleave a target protein as described in Kriegel *et al.*, *Cell* (1988) *53*:45 and Mohler *et al.*, *Nature* (1994) *370*:218 and demonstrate cell proliferation and differentiation activity. T-cell or thymocyte proliferation is assayed as described in Armitage *et al.*, *Eur. J. Immunol.* (1992) *22*:447; Current Protocols in Immunology, ed. J.E. Coligan *et al.*, 3.1-3.19; Takai *et al.*, *J. Immunol.* (1986) *137*:3494-3500, Bertagnoli *et al.*, *J. Immunol.* (1990) *145*:1706, Bertagnoli *et al.*, *J. Immunol.* (1991) *133*:327, Bertagnoli *et al.*, *J. Immunol.* (1992) *149*:3778, and Bowman *et al.*, *J. Immunol.* (1994) *152*:1756. B cell proliferation and Ig secretion are assayed as described in Maliszewski, *J. Immunol.* (1990) *144*:3028, and Assays for B Cell Function: In Vitro Antibody Production, Mond and Brunswick, Current Protocols in Immunol., Coligan Ed vol 1 pp 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994, Kehrl *et al.*, *Science* (1987) *238*:1144 and Boussiotis *et al.*, *PNAS USA* (1994) *91*:7007. Other in vivo activities include upregulation of cell surface antigens, upregulation of costimulatory molecules, and cellular

aggregation/adhesion as described in Barrett *et al.*, *J. Immunol.* (1991) *146*:1722; Bjorck *et al.*, *Eur. J. Immunol.* (1993) *23*:1771; Clark *et al.*, *Annu Rev. Immunol.* (1991) *9*:97; Ranheim *et al.*, *J. Exp. Med.* (1994) *177*:925; Yellin, *J. Immunol.* (1994) *153*:666; and Gruss *et al.*, *Blood* (1994) *84*:2305.

Proliferation and differentiation of hematopoietic and lymphopoietic cells has also been shown in vivo for TNFs, using assays for embryonic differentiation and hematopoiesis as described in Johansson *et al.*, *Cellular Biology* (1995) *15*:141, Keller *et al., Mol. Cell. Biol.* (1993) *13*:473, McClanahan *et al.*, *Blood* (1993) *81*:2903 and using assays to detect stem cell survival and differentiation as described in Culture of Hematopoietic Cells, Freshney *et al.* eds, pp 1-21, 23-29, 139-162, 163-179, and 265-268, Wiley-Liss, Inc., New York, NY, 1994, and Hirajama *et al.*, *PNAS USA* (1992) *89*:5907.

In vivo activities of TNFs also include lymphocyte survival and apoptosis, assayed as described in Darzynkewicz *et al.*, *Cytometry* (1992) *13*:795; Gorczca *et al.*, *Leukemia* (1993) *7*:659; Itoh *et al.*, *Cell* (1991) *66*:233; Zacharduk, *J. Immunol.* (1990) *145*:4037; Zamai *et al.*, *Cytometry* (1993) *14*:891; and Gorczyca *et al., Int'l J. Oncol.* (1992) *1*:639. Some members of the TNF family are cleaved from the cell surface; others remain membrane bound. The three-dimensional structure of TNF is discussed in Sprang and Eck, Tumor Necrosis Factors; *supra.*

TNF proteins include a transmembrane domain. The protein is cleaved into a shorter soluble version, as described in Kriegler *et al.*, *Cell* (1988) *53*:45, Perez *et al.*, *Cell* (1990) *63*:251, and Shaw *et al.*, *Cell* (1986) *46*:659. The transmembrane domain is between amino acid 46 and 77 and the cytoplasmic domain is between position 1 and 45 on the human form of TNFα. The 3-dimensional motifs of TNF include a sandwich of two pleated β sheets. Each sheet is composed of anti-parallel β strands. β strands facing each other on opposite sites of the sandwich are connected by short polypeptide loops, as described in Van Ostade *et al.*, *Protein Engineering* (1994) *7(1)*:5, and Sprang *et al.*, Tumor Necrosis Factors; *supra.* Residues of the TNF family proteins that are involved in the β sheet secondary structure have been identified as described in Van Ostade *et al., Protein Eng.* (1994) *7(1)*:5, and Sprang *et al., supra.*

TNF receptors are disclosed in U.S. Patent No. 5,395,760. A profile derived from the TNF receptor family is created by aligning sequences of the TNF receptor family, including

Apo1/Fas, TNFR I and II, death receptor 3 (DR3), CD40, ox40, CD27, and CD30. Thus, the profile is designed to identify from the polynucleotides of the invention sequences of proteins that constitute new members or homologues of this family of proteins.

Tumor necrosis factor receptors exist in two forms in humans: p55 TNFR and p75 TNFR, both of which provide intracellular signals upon binding with a ligand. The extracellular domains of these receptor proteins are cysteine rich. The receptors can remain membrane bound, although some forms of the receptors are cleaved forming soluble receptors. The regulation, diagnostic, prognostic, and therapeutic value of soluble TNF receptors is discussed in Aderka, *Cytokine and Growth Factor Reviews*, (1996) *7(3)*:231.

PDGF Family. U.S. Patent No. 5,326,695 discloses platelet derived growth factor agonists; bioactive portions of PDGF-B are used as agonists. U.S. Patent No. 4,845,075 discloses biologically active B-chain homodimers, and also includes variants and derivatives of the PDGF-B chain. U.S. Patent No. 5,128,321 discloses PDGF analogs and methods of use. Proteins having the same bioactivity as PDGF are disclosed, including A and B chain proteins.

Kinase (Including MKK) Family. U.S. Patent No. 5,650,501 discloses serine/threonine kinase, associated with mitotic and meiotic cell division; the protein has a kinase domain in its N-terminal and 3 PEST regions in the C-terminus. U.S. Patent No. 5,605,825 discloses human PAK65, a serine protein kinase.

The foregoing discussion provides a few examples of the protein profiles that can be compared with the polynucleotides of the invention. One skilled in the art can use these and other protein profiles to identify the genes that correlate with the provided polynucleotides.

C. Identification of Secreted & Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) *78*:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) *157*: 105-132; and RAOAR algorithm, Degli Esposti *et al., Eur. J. Biochem.* (1990) *190*: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

IV. Identification of the Function of an Expression Product of a Full-Length Gene Corresponding to a Polynucleotide

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al., Tet. Lett.* (1981) *22*:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA,

phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA. See Applied Biosystems User Bulletin 53 and Ogilvie *et al.*, *Pure & Applied Chem.* (1987) *59*:325.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiruam disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nucleotides can be synthesized, more typically, 100 nucleotides, more typically 50 nucleotides; even more typically 30 to 40 nucleotides. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al., supra.*

A. Ribozymes

Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect.

One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al., Current Opin. Struct. Biol.* (1996) *6*:527. Usman also discusses the therapeutic uses of ribozymes. Ribozymes can also be prepared and used as described in Long *et al., FASEB J.* (1993) *7*:25; Symons, *Ann. Rev. Biochem.* (1992) *61*:641; Perrotta *et al., Biochem.* (1992) *31*:16; Ojwang *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1992) *89*:10802; and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S.

Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No. 5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al.*, *Nucleic Acid Res.* (1989) *17*:7059. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al.*, *Nucleic Acids Res.* (1989) *17*:7059. Preparation and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) *20*:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) *15(3)*:273.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) *17*:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al., Eur. J. Biochem.* (1997) *245*:1.

Using the polynucleotide sequences of the invention and methods known in the art, ribozymes are designed to specifically bind and cut the corresponding mRNA species. Ribozymes thus provide a means to inhibit the expression of any of the proteins encoded by the disclosed polynucleotides or their full-length genes. The full-length gene need not be known in order to design and use specific inhibitory ribozymes. In the case of a polynucleotide or full-length cDNA of unknown function, ribozymes corresponding to that nucleotide sequence can be tested in vitro for efficacy in cleaving the target transcript. Those ribozymes that effect cleavage in vitro are further tested in vivo. The ribozyme can also be used to generate an animal model for a disease, as described in Birikh *et al., supra.* An effective ribozyme is used to determine the function of the gene of interest by blocking its transcription and detecting a change in the cell. Where the gene is found to be a mediator in a disease, an effective ribozyme is designed and delivered in a gene therapy for blocking transcription and expression of the gene.

Therapeutic and functional genomic applications of ribozymes proceed beginning with knowledge of a portion of the coding sequence of the gene to be inhibited. Thus, for many genes, a partial polynucleotide sequence provides adequate sequence for constructing

an effective ribozyme. A target cleavage site is selected in the target sequence, and a ribozyme is constructed based on the 5' and 3' nucleotide sequences that flank the cleavage site. Retroviral vectors are engineered to express monomeric and multimeric hammerhead ribozymes targeting the mRNA of the target coding sequence. These monomeric and multimeric ribozymes are tested in vitro for an ability to cleave the target mRNA. A cell line is stably transduced with the retroviral vectors expressing the ribozymes, and the transduction is confirmed by Northern blot analysis and reverse-transcription polymerase chain reaction (RT-PCR). The cells are screened for inactivation of the target mRNA by such indicators as reduction of expression of disease markers or reduction of the gene product of the target mRNA.

B. <u>Antisense</u>

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

One rationale for using antisense methods to determine the function of the gene corresponding to a disclosed polynucleotide is the biological activity of antisense therapeutics. Antisense therapy for a variety of cancers is in clinical phase and has been discussed extensively in the literature. Reed reviewed antisense therapy directed at the Bcl-2 gene in tumors; gene transfer-mediated overexpression of Bcl-2 in tumor cell lines conferred resistance to many types of cancer drugs. (Reed, J.C., *N.C.I.* (1997) *89*:988). The potential for clinical development of antisense inhibitors of *ras* is discussed by Cowsert, L.M., *Anti-Cancer Drug Design* (1997) *12*:359. Additional important antisense targets include

leukemia (Geurtz, A.M., *Anti-Cancer Drug Design* (1997) *12*:341); human C-ref kinase (Monia, B.P., *Anti-Cancer Drug Design* (1997) *12*:327); and protein kinase C (McGraw *et al., Anti-Cancer Drug Design* (1997) *12*:315.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells clearly is warranted.

Ogunbiyi *et al., Gastroenterology* (1997) *113(3)*:761 describe prognostic use of allelic loss in colon cancer; Barks *et al., Genes, Chromosomes, and Cancer* (1997) *19(4)*:278 describe increased chromosome copy number detected by FISH in malignant melanoma; Nishizake *et al., Genes, Chromosomes, and Cancer* (1997) *19(4)*:267 describe genetic alterations in primary breast cancer and their metastases and direct comparison using modified comparative genome hybridization; and Elo *et al., Cancer Research* (1997) *57(16)*:3356 disclose that loss of heterozygosity at 16z24.1-q24.2 is significantly associated with metastatic and aggressive behavior of prostate cancer.

C. Dominant Negative Mutations

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) *329*:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

V. Construction of Polypeptides of the Invention and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides. These polypeptides can also be encoded by nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS: 1-844 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By homolog is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described *supra*.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by

purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted. For example, substitutions between the following groups are conservative: Gly/Ala, Val/Ile/Leu, Asp/Glu, Lys/Arg, Asn/Gln, Ser/Cys, Thr, and Phe/Trp/Tyr.

Variants can be designed so as to retain biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). In a non-limiting example, Osawa *et al.*, *Biochem. Mol. Int.* (1994) *34*:1003, discusses the actin binding region of a protein from several different species. The actin binding regions of the these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, and S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go *et al*, *Int. J. Peptide Protein Res.* (1980) *15*:211, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid

residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Inter-group replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Additional guidance for production of polypeptide variants is provided in Querol *et al.*, *Prot. Eng.* (1996) *9*:265, which provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, *J. Gen. Microbiol.* (1991) *137*:579. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, *Science* (1984) *226*:555; Pantoliano *et al.*, *Biochemistry* (1987) *26*:2077; Matsumura *et al.*, *Nature* (1989) *342*:291; Nishikawa *et al.*, *Protein Eng.* (1990) *3*:443; Takagi *et al.*, *J. Biol. Chem.* (1990) *265*:6874; Clarke *et al.*, *Biochemistry* (1993) *32*:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) *7*:1379. Metal binding sites can be introduced, according to Toma *et al.*, *Biochemistry* (1991) *30*:97, and Haezerbrouck *et al.*, *Protein Eng.* (1993) *6*:643. Substitutions with prolines in loops can be made according to Masul *et al.*, *Appl. Env. Microbiol.* (1994) *60*:3579; and Hardy *et al.*, *FEBS Lett. 317*:89.

Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses substitution of cysteines with other amino acids, and methods for assaying biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such substitutions, for example to eliminate disulfide bond formation.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of

amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-844, or a homolog thereof.

The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

VI. Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form includes an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of

cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention include sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-844. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-844. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-844, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of

computer-readable files (*e.g.*, searchable files, executable files, *etc*, including, but not limited to, for example, search program software, *etc.*.).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul *et al.*, *supra.*) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif with the stored sequence information. Search means are used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but arc not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures,

promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks fragments of the genome possessing varying degrees of homology to a target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences and identifies the degree of sequence similarity contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOS:1-844, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-844 is represented on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art, including those described in 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742287; and EP 799897. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-844.

VII. Utilities

A. Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nucleotides of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Probes in Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. The references describe an example of a sandwich nucleotide hybridization assay. For example, in Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al.*, *Meth. Enzymol.* (1987) *155*:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer polynucleotides nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these

polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping. Polynucleotides of the present invention are used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387.

For example, fluorescence in situ hybridization (FISH) on normal metaphase spreads facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Curr. Opin. Biotechnol.* (1994) *8*:70; Kallioniemi *et al.*, *Sem. Cancer Biol.* (1993) *4*:41; Valdes *et al.*, *Methods in Molecular Biology* (1997) *68*:1, Boultwood, ed., Human Press, Totowa, NJ. Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence shown in the Sequence Listing are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label,

and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the probe.

Polynucleotides are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al., Advances in Genetics,* (1995) *33*:63-99; Walter *et al., Nature Genetics* (1994) *7*:22; Walter and Goodfellow, *Trends in Genetics* (1992) *9*:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at http:/F/shgc-www.stanford.edu; and http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at http://www.sph.umich.edu/group/statgen/software.

In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Polynucleotides based on the polynucleotides of the invention can be used to probe these regions. For example, if through profile searching a provided polynucleotide is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the polynucleotide constitutes a new material for isolating a specific protein that has potential for developing a cancer diagnostic or therapeutic.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods can be used to detect particular mRNA species, including but not limited to in situ hybridization and Northern blotting.

Use of Polymorphisms. A polynucleotide of the invention will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. Particular polymorphic forms of the provided polynucleotides can be used to either identify a sample as deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

B. Antibody Production

Expression products of a polynucleotide of the invention, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the polynucleotides of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly.

Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method known in the art, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, for example at least 15, 25, or 50 amino acids. A short sequence of a polynucleotide may then be unsuitable for use as an epitope to raise antibodies for identifying the corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies can be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a polynucleotide of the invention.

Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

To test for the presence of serum antibodies to the polypeptide of the invention in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies, according to methods well known in the art.

C. Use of Polynucleotides to Construct Arrays for Diagnostics

Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocelllose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/29212; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

As discussed in some detail above, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant polynucleotide sequences can be used to determine if any of the provided polynucleotides are differentially expressed between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) *8*:217; and Ramsay *Nature Biotechnol.* (1998) *16*:40.

D. Differential Expression

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families as described

above, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (*e.g.*, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

The polynucleotide-related genes in the two tissues are compared by any means known in the art. For example, the two genes can be sequenced, and the sequence of the gene in the tissue suspected of being diseased compared with the gene sequence in the normal tissue. The genes corresponding to a provided polynucleotide, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to detectably labeled nucleotide probes selected from a nucleotide sequence shown in the Sequence Listing. A difference in the nucleotide sequence of the isolated gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the gene product encoded by the subject polynucleotide in the disease, and provides guidance for preparing a therapeutic agent.

Alternatively, mRNA corresponding to a provided polynucleotide in the two tissues is compared. PolyA$^+$ RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of mRNA transcripts between the two tissues using Northern blots and detectably labeled

nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing. Increased or decreased expression of a given mRNA in a tissue sample suspected of being diseased, compared with the expression of the same mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a therapeutic agent.

The comparison can also be accomplished by analyzing polypeptides between the matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect polypeptides in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of expression of a given polypeptide in a tissue suspected of being diseased, compared with the same protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides guidance for preparing a therapeutic agent.

Similarly, comparison of polynucleotide sequences or of gene expression products, *e.g.*, mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons are made as described above. For example, increased or decreased expression of a gene corresponding to an inventive polynucleotide in the tissue suspected of being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of a given gene in the neoplastic tissue relative to expression of the same gene in normal tissue, or differences in the amount of increased expression of a given gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, malignant or non-malignant cells, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic

fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. Particular diagnostic and prognostic uses of the disclosed polynucleotides are described in more detail below.

E. Diagnostic, Prognostic, and Other Uses Based On Differential Expression

In general, diagnostic methods of the invention for involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.*, breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.*, cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease.

The term "differentially expressed gene" is intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at

least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

"Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) having a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art, where particular methods of interest include those described in: Pietu *et al. Genome Res.*

(1996) 6:492; Zhao *et al.*, *Gene* (1995) *156*:207; Soares , *Curr. Opin. Biotechnol.* (1977) *8*: 542; Raval, *J. Pharmacol Toxicol Methods* (1994) *32*:125; Chalifour *et al., Anal. Biochem* (1994) *216*:299; Stolz *et al., Mol. Biotechnol.* (1996) *6*:225; Hong *et al., Biosci. Reports* (1982) *2*:907; and McGraw, *Anal. Biochem.* (1984) *143*:298. Also of interest are the methods disclosed in WO 97/27317, the disclosure of which is herein incorporated by reference.

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-844. The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

In the assays of the invention, the diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-844, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-844 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. For example, a higher level of expression of a polynucleotide corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of a polynucleotide corresponding to SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient. Further examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes,(*e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.* ^{32}P, ^{35}S, ^{3}H, *etc.*), and the like. The detectable label can involve a two stage systems (*e.g.*, biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

<u>Polypeptide detection in diagnosis.</u> In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (*e.g.*, using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (*e.g.*, biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, *e.g.* fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can of qualitative or quantitative

detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

In general, the detected level of differentially expressed polypeptide in the test sample is compared to a level of the differentially expressed gene product in a reference or control sample, *e.g.*, in a normal cell (negative control) or in a cell having a known disease state (positive control). For example, a higher level of expression of a polypeptide encoded by SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of the polypeptide encoded by SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

<u>mRNA detection.</u> The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. For example, the level of mRNA of the invention in a tissue sample suspected of being cancerous or dysplastic is compared with the expression of the mRNA in a reference sample, *e.g.*, a positive or negative control sample (*e.g.*, normal tissue, cancerous tissue, *etc.*). In a specific non-limiting example, a higher level of mRNA corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of mRNA corresponding to SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

Any suitable method for detecting and comparing mRNA expression levels in a sample can be used in connection with the diagnostic methods of the invention (see, *e.g.*, U.S. 5,804,382). For example, mRNA expression levels in a sample can be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used

to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein.

Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (Velculescu et al., *Science* (1995) *270*:484). In short, SAGE involves the isolation of short unique sequence tags from a specific location within each transcript (*e.g.*, a sequence of any one of SEQ ID NOS:1-6). The sequence tags are concatenated, cloned, and sequenced. The frequency of particular transcripts within the starting sample is reflected by the number of times the associated sequence tag is encountered with the sequence population.

Gene expression in a test sample can also be analyzed using differential display (DD) methodology. In DD, fragments defined by specific sequence delimiters (*e.g.*, restriction enzyme sites) are used as unique identifiers of genes, coupled with information about fragment length or fragment location within the expressed gene. The relative representation of an expressed gene with a sample can then be estimated based on the relative representation of the fragment associated with that gene within the pool of all possible fragments. Methods and compositions for carrying out DD are well known in the art, see, *e.g.*, U.S. 5,776,683; and U.S. 5,807,680.

Alternatively, gene expression in a sample using hybridization analysis, which is based on the specificity of nucleotide interactions. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (*e.g.*, mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

Changes in the promoter or enhancer sequence that affect expression levels of an differentially gene can be compared to expression levels of the normal allele by various methods known in the art. Methods for determining promoter or enhancer strength include quantitation of the expressed natural protein; insertion of the variant control element into a vector with a reporter gene such as β-galactosidase, luciferase, chloramphenicol acetyltransferase, *etc.* that provides for convenient quantitation; and the like.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. The use of the polymerase chain reaction is described in Saiki, *et al.*, *Science* (1985) *239*:487, and a review of techniques can be found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, (1989) pp. 14.2. Alternatively, various methods are known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, for examples see Riley *et al.*, *Nucl. Acids Res.* (1990) *18*:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) *58*:1239.

The sample nucleic acid, *e.g.* amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type

sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.)*. The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in an differentially expressed gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOS:1-844. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of

polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative

breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

"Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (*e.g.*, a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can be compared to previously generated and stored REPs.

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

Methods for collection of data from hybridization of samples with a reference arrays are also well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label. Methods and devices for detecting fluorescently marked targets on devices are known in the art. Generally, such detection devices include a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent no. 5,631,734. A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) *6*:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (*e.g.*, a test

sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.* data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays), design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

F. <u>Use of the Polynucleotides of the Invention in Cancer</u>

Oncogenesis involves the unbridled growth, dedifferentiation and abnormal migration of cells. Cancerous cells can have the ability to compress, invade, and destroy normal tissue. Cancerous cells may also metastasize to other parts of the body via the

bloodstream or the lymph system and colonize in these other areas. Different cancers are classified by the cell from which the cancerous cell is derived and from its cellular morphology and/or state of differentiation.

Somatic genetic abnormalities cause cancer initiation and progression. Cancer generally is clonally formed, *i.e.* gain of function of oncogenes and loss of function of tumor suppressor genes within a single cell transform the cell to be cancerous, and that single cell grows and divides to form a cancerous lesion. The genes known to be involved in cancer initiation and progression are involved in numerous cellular functions, including developmental differentiation, cell cycle regulation, cell signaling, immunological response, DNA replication, and DNA repair.

The identification and characterization of genetic or biochemical markers in blood or tissues that will detect the earliest changes along the carcinogenesis pathway and monitor the efficacy of various therapies and preventive interventions is a major goal of cancer research. Scientists have identified genetic changes in stool specimens that indicate the stages of colon cancer, and other biomarkers such as gene mutations, hormone receptors, proteins that inhibit metastasis, and enzymes that metabolize drugs are all being used to determine the severity and predict the course of breast, prostate, lung, and other cancers.

Recent advances in the pathogenesis of certain cancers has been helpful in determining patient treatment. The level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients has defined certain prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Moreover, a promising level of one or more marker polynucleotides can provide impetus for not aggressively treating a particular patient, thus sparing the patient the deleterious side effects of aggressive therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient.

Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Different staging systems are used for different types of cancer, but each generally involves the following determinations: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. This system of staging is called the TNM system. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or another site, are called Stage IV, the most advanced stage.

Currently, the determination of staging is done using pathological techniques and is based more on the presence or absence of malignant tissue rather than the characteristics of the tumor type. Presence or absence of malignant tissue is based primarily on the gross morphology of the cells in the areas biopsied. The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggresivity of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. Based on the microscopic appearance of a tumor, pathologists will identify the grade of a tumor based on parameters such as cell morphology,

cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness. That is, undifferentiated or high-grade tumors grow more quickly than well differentiated or low-grade tumors. Information about tumor grade is useful in planning treatment and predicting prognosis.

The American Joint Commission on Cancer has recommended the following guidelines for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. Although grading is used by pathologists to describe most cancers, it plays a more important role in treatment planning for certain types than for others. An example is the Gleason system that is specific for prostate cancer, which uses grade numbers to describe the degree of differentiation. Lower Gleason scores indicate well-differentiated cells. Intermediate scores denote tumors with moderately differentiated cells. Higher scores describe poorly differentiated cells. Grade is also important in some types of brain tumors and soft tissue sarcomas.

The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Familial Cancer Genes. A number of cancer syndromes are linked to Mendelian inheritance of a predisposition to develop particular cancers. The following table contains a list of cancer types that can be inherited, and for which the gene or genes responsible have been identified. Most of the cancer types listed can occur as part of several different genetic conditions, each caused by alterations in a different gene.

Cancer Type	Genetic Condition	Gene
Brain	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
	Neurofibromatosis 2	NF2
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Breast	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Colon	Familial adenomatous polyposis (FAP)	APC
	Hereditary non-polyposis colon cancer (HNPCC) 1	HMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1

Cancer Type	Genetic Condition	Gene
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
Endocrine (parathyroid, pituitary, GI endocrine)	Multiple endocrine neoplasia 1 (MEN1)	MEN1
Endocrine (pheochromacytoma, medullary thyroid)	Multiple endocrine neoplasia 2 (MEN2)	RET
Endometrial	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
Eye	Hereditary retinoblastoma	RB1
Hematologic (lymphomas and leukemia)	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Kidney	Hereditary Wilms' tumor	WT1
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Ovary	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
Sarcoma	Hereditary retinoblastoma	RB1
	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
Skin	Hereditary melanoma 1	CDKN2
	Hereditary melanoma 2	CDK4
	Basal cell naevus (Gorlin) syndrome	PTCH
Stomach	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2

The polynucleotides of the invention can be especially useful to monitor patients having any of the above syndromes to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. As can be seen from the table, a number of genes are involved in multiple forms of cancer. Thus, a polynucleotide of the invention identified as important for metastatic colon cancer can also have clinical implications for a patient diagnosed with stomach cancer or endometrial cancer.

Lung Cancer. Lung cancer is one of the most common cancers in the United States, accounting for about 15 percent of all cancer cases, or 170,000 new cases each year. At this time, over half of the lung cancer cases in the United States are in men, but the number found in women is increasing and will soon equal that in men. Today more women die of lung cancer than of breast cancer. Lung cancer is especially difficult to diagnose and treat because of the large size of the lungs, which allows cancer to develop for years undetected.

In fact, lung cancer can spread outside the lungs without causing any symptoms. Adding to the confusion, the most common symptom of lung cancer, a persistent cough, can often be mistaken for a cold or bronchitis.

Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma), which usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

Currently, CT scans, MRIs, X-rays, sputum cytology, and biopsies are used to diagnose nonsmall cell lung cancer. The form and cellular origin of the lung cancer is diagnosed primarily through biopsy from either a surgical biopsy or a needle aspiration of lung tissue, and usually the biopsy is prompted from an abnormality identified on an X-ray. In some cases, sputum cytology can reveal lung cancers in patients with normal X-rays or can determine the type of lung cancer, but because it cannot pinpoint the tumor's location, a positive sputum cytology test is usually followed by further tests. Since these tests are based in large part on gross morphology of the tissue, the diagnosis of a particular kind of tumor is largely subjective, and the diagnosis can vary significantly between clinicians.

The polynucleotides of the invention can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the

surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a polynucleotide in hyperplasia can be used as a diagnostic marker for metastatic lung cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between high metastatic versus low metastatic lung cancer , *i.e.* SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 381, 395, and 400. Detection of malignant lung cancer with a higher metastatic potential can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of other known genes.

<u>Breast Cancer.</u> The National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States will develop breast cancer during her lifetime. Clinical breast examination and mammography are recommended as combined modalities for breast cancer screening, and the nature of the cancer will often depend upon the location of the tumor and the cell type from which the tumor is derived. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows:

Ductal carcinoma in situ (DCIS): Ductal carcinoma in situ is the most common type of noninvasive breast cancer. In DCIS, the malignant cells have not metastasized through the walls of the ducts into the fatty tissue of the breast. Comedocarcinoma is a type of DCIS that is more likely than other types of DCIS to come back in the same area after lumpectomy. It is more closely linked to eventual development of invasive ductal carcinoma than other forms of DCIS.

Infiltrating (or invasive) ductal carcinoma (IDC): this type of cancer has metastasized through the wall of the duct and invaded the fatty tissue of the breast. At this point, it has the potential to use the lymphatic system and bloodstream for metastasis to more distant parts of the body. Infiltrating ductal carcinoma accounts for about 80% of breast cancers.

Lobular carcinoma in situ (LCIS): While not a true cancer, LCIS (also called lobular neoplasia) is sometimes classified as a type of noninvasive breast cancer. It does not penetrate through the wall of the lobules. Although it does not itself usually become an

invasive cancer, women with this condition have a higher risk of developing an invasive breast cancer in the same breast, or in the opposite breast.

Infiltrating (or invasive) lobular carcinoma (ILC): ILC is similar to IDC, in that it has the potential metastasize elsewhere in the body. About 10% to 15% of invasive breast cancers are invasive lobular carcinomas. ILC can be more difficult to detect by mammogram than IDC.

Inflammatory breast cancer: This rare type of invasive breast cancer accounts for about 1% of all breast cancers and is extremely aggressive. Multiple skin symptoms associated with this cancer are caused by cancer cells blocking lymph vessels or channels in the skin over the breast.

Medullary carcinoma: This special type of infiltrating breast cancer has a relatively well defined, distinct boundary between tumor tissue and normal tissue. It accounts for about 5% of breast cancers. The prognosis for this kind of breast cancer is better than for other types of invasive breast cancer.

Mucinous carcinoma: This rare type of invasive breast cancer originates from mucus-producing cells. The prognosis for mucinous carcinoma is better than for the more common types of invasive breast cancer.

Paget's disease of the nipple: This type of breast cancer starts in the ducts and spreads to the skin of the nipple and the areola. It is a rare type of breast cancer, occurring in only 1% of all cases. Paget's disease can be associated with in situ carcinoma, or with infiltrating breast carcinoma. If no lump can be felt in the breast tissue, and the biopsy shows DCIS but no invasive cancer, the prognosis is excellent.

Phyllodes tumor: This very rare type of breast tumor forms from the stroma of the breast, in contrast to carcinomas which develop in the ducts or lobules. Phyllodes (also spelled phylloides) tumors are usually benign, but are malignant on rare occasions. Nevertheless, malignant phyllodes tumors are very rare and less than 10 women per year in the US die of this disease. Benign phyllodes tumors are successfully treated by removing the mass and a narrow margin of normal breast tissue.

Tubular carcinoma: Accounting for about 2% of all breast cancers, tubular carcinomas are a special type of infiltrating breast carcinoma. They have a better prognosis than usual infiltrating ductal or lobularcarcinomas.

High-quality mammography combined with clinical breast exam remains the only screening method clearly tied to reduction in breast cancer mortality. Lower dose x-rays, digitized computer rather than film images, and the use of computer programs to assist diagnosis, are almost ready for widespread dissemination. Other technologies also are being developed, including magnetic resonance imaging and ultrasound. In addition, a very low radiation exposure technique, positron emission tomography has the potential for detecting early breast cancer.

It is also possible to differentiate between non-cancerous breast tissue and malignant breast tissue by analyzing differential gene expression between tissues. In addition, there may be several possible alterations that lead to the various possible types of breast cancer. The different types of breast tumors (*e.g.*, invasive vs. non-invasive, ductal vs. axillary lymph node) can be differentiable from one another by the identification of the differences in genes expressed by different types of breast tumor tissues (Porter-Jordan *et al.*, *Hematol Oncol Clin North Am* (1994) *8*:73). Breast cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with breast tumors. Where enough information is available about the differential gene expression between various types of breast tumor tissues, the specific type of breast tumor can also be diagnosed.

For example, increased estrogen receptor (ER) expression in normal breast epithileum, while not itself indicative of malignant tissue, is a known risk marker for development of breast cancer. Khan SA *et al.*, *Cancer Res* (1994) *54*:993. Malignant breast cancer is often divided into two groups, ER-positive and ER-negative, based on the estrogen receptor status of the tissue. The ER status represents different survival length and response to hormone therapy, and is thought to represent either: 1) an indicator of different stages of the disease, or 2) an indicator that allows differentiation between two similar but distinct diseases. K. Zhu *et al.*, *Med. Hypoth.* (1997) *49*:69. A number of other genes are known to vary expression between either different stages of cancer or different types of similar breast cancer.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer. The differential expression of a polynucleotide in human breast tumor tissue can be used as a diagnostic marker for human breast cancer. The polynucleotides of the invention that would be especially useful for this purpose are

those that exhibit differential expression between breast cancer tissue with a high metastatic potential and a low metastatic potential, *i.e.* SEQ ID NOS: 9, 42, 52, 62, 65, 66, 68, 114, 123, 144, 172, 178, 214, 219, 223, 258, 317, and 379. Detection of breast cancer can be determined using expression levels of any of these sequences alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.* ER expression. In addition, development of breast cancer can be detected by examining the ratio of SEQ ID NO: to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Diagnosis of breast cancer can also involve comparing the expression of a polynucleotide of the invention with the expression of other sequences in non-malignant breast tissue samples in comparison to one or more forms of the diseased tissue. A comparison of expression of one or more polynucleotides of the invention between the samples provides information on relative levels of these polynucleotides as well as the ratio of these polynucleotides to the expression of other sequences in the tissue of interest compared to normal.

This risk of breast cancer is elevated significantly by the presence of an inherited risk for breast cancer, such as a mutation in BRCA-1 or BRCA-2. New diagnostic tools are being developed to address the needs of higher risk patients to complement mammography and physical examinations for early detection of breast cancer, particularly among younger women. The presence of antigen or expression markers in nipple aspirate fluid (NAF) samples collected from one or both breasts can be useful for useful for risk assessment or early cancer detection. Breast cytology and biomarkers obtained by random fine needle aspiration have been used to identify hyperplasia with atypia and overexpression of p53 and EGFR. The polynucleotides of the invention can be used in multivariate analysis with expression studies with genes such as p53 and EGFR as risk predictors and as surrogate endpoint biomarkers for breast cancer.

As well as being used for diagnosis and risk assessment, the expression of certain genes can also correlated to prognosis of a disease state. The expression of particular gene have been used as prognostic indicators for breast cancer including increased expression of *c-erbB-2*, pS2, ER, progesterone receptor, epidermal growth factor receptor (EGFR), *neu*, *myc*, *bcl-2*, *int2*, cytosolic tyrosine kinase, cyclin E, *prad-1*, *hst*, uPA, PAI-1, PAI-2, cathepsin D, as well as the presence of a number of cancer-specific antigens, *e.g.* CEA, CA M26, CA M29 and CA 15.3. Davis, *Br. J. Biomed Sci.* (1996) *53*:157. Poor prognosis has also been linked to a decrease in expression of certain genes, such as *p53, Rb, nm23.* The expression of the polynucleotides of the invention can be of prognostic value for determining the metastatic potential of a malignant breast cancer, as this molecules are differentially expressed between high and low metastatic potential tissues tumors. The levels of these polynucleotides in patients with malignant breast cancer can compared to normal tissue, malignant tissue with a known high potential metastatic level, and malignant tissue with a known lower level of metastatic potential to provide a prognosis for a particular patient. Such a prognosis is predictive of the extent and nature of the cancer. The determined prognosis is useful in determining the prognosis of a patient with breast cancer, both for initial treatment of the disease and for longer-term monitoring of the same patient. If samples are taken from the same individual over a period of time, differences in polynucleotide expression that are specific to that patient can be identified and closely watched.

<u>Colon Cancer.</u> Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Indeed, colorectal cancer is the second most preventable cancer, after lung cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. About 20 percent of all cases of colon cancer are thought to be related to heredity. Currently, multiple familial colorectal cancer disorders have been identified, which are summarized as follows:

Familial adenomatous polyposis (FAP): This condition results in a person having hundreds or even thousands of polyps in the colon and rectum that usually first appear during

the teenage years. Cancer nearly always develops in one or more of these polyps between the ages of 30 and 50.

Gardner's syndrome: Like FAP, Gardner's syndrome results in polyps and colorectal cancers that develop at a young age. It can also cause benign tumors of the skin, soft connective tissue and bones.

Hereditary nonpolyposis colon cancer (HNPCC): People with this condition tend to develop colorectal cancer at a young age, without first having many polyps. HNPCC has an autosomal dominant pattern of inheritance with variable but high penetrance estimated to be about 90%. HNPCC underlies 0.5%-10% of all cases of colorectal cancer. An understanding of the mechanisms behind the development of HNPCC is emerging, and genetic presymptomatic testing, now being conducted in research settings, soon will be available on a widespread basis for individuals identified at risk for this disease.

Familial colorectal cancer in Ashkenazi Jews: Recent research has found an inherited tendency to developing colorectal cancer among some Jews of Eastern European descent. Like people with FAP, Gardner's syndrome, and HNPCC, their increased risk is due to an inherited mutation present in about 6% of American Jews.

Several tests are currently used to screen for colorectal cancer, including digital rectal examination, fecal occult blood test, sigmoidoscopy, colonoscopy, virtual colonoscopy and MRI. Each of these tests identifies potential colorectal cancer lesions, or a risk of development of these lesions, at a fairly gross morphological level.

The sequential alteration of a number of genes is associated with malignant adenocarcinoma, including the genes DCC, p53, ras, and FAP. For a review, see *e.g.* Fearon ER, *et al.*, *Cell* (1990) *61(5)*:759; Hamilton SR *et al.*, *Cancer* (1993) *72*:957; Bodmer W, *et al.*, *Nat Genet.* (1994) *4(3)*:217; Fearon ER, *Ann N Y Acad Sci.* (1995) *768*:101. Molecular genetic alterations are thus promising as potential diagnostic and prognostic indicators in colorectal carcinoma and molecular genetics of colorectal carcinoma since it is possible to differentiate between different types of colorectal neoplasias using molecular markers. Colorectal cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with colorectal tumors.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a

polynucleotide in hyperplasia can be used as a diagnostic marker for colon cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between malignant metastatic colon cancer and normal patient tissue , *i.e.* SEQ ID NOS: 52, 119, 172, 288. Detection of malignant colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression.

Determination of the aggressive nature and/or the metastatic potential of a colon cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.* p53 expression. In addition, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

G. Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides.

A library of peptides can be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175 ('175), and in WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (*e.g.*, a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (*e.g.*, hexamers) is formed. Note that one need not include all amino acids in each step: one can include only one or two amino acids in some steps (*e.g.*, where it is

known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin. The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction can be easily driven to completion. Additionally, one can maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, *e.g.*, 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, *e.g.*, 20-100 candidates, and reassayed. Positive sub-subpools can be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO 91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis can be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at

concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

H. Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions can comprise polypeptides, antibodies, or polynucleotides of the claimed invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a

therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

<u>Delivery Methods.</u> Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); (2) delivered ex vivo, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy); or (3) delivered *in vitro* for expression of recombinant proteins (*e.g.*, polynucleotides). Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO

93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide or corresponding polypeptide.

Preparation of antisense polynucleotides is discussed above. Neoplasias that are treated with the antisense composition include, but are not limited to, cervical cancers, melanomas, colorectal adenocarcinomas, Wilms' tumor, retinoblastoma, sarcomas, myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and myeloid leukemia, and lymphomas, such as histiocytic lymphoma. Proliferative disorders that are treated with the therapeutic composition include disorders such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin, are treated with antisense therapeutic compositions based upon a polynucleotide of the invention. Even in disorders in which mutations in the corresponding gene are not implicated, downregulation or inhibition of expression of a gene corresponding to a polynucleotide of the invention can have therapeutic application. For example, decreasing gene expression can help to suppress tumors in which enhanced expression of the gene is implicated.

Both the dose of the antisense composition and the means of administration are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. Administration of the therapeutic antisense agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized

administration, and topical administration. Preferably, the therapeutic antisense composition contains an expression construct comprising a promoter and a polynucleotide segment of at least 12, 22, 25, 30, or 35 contiguous nucleotides of the antisense strand of a polynucleotide disclosed herein. Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter.

Various methods are used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues is also used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) *11*:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) *263*:621; Wu *et al.*, *J. Biol. Chem.* (1994) *269*:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) *87*:3655; Wu *et al.*, *J. Biol. Chem.* (1991) *266*:338. Preferably, receptor-mediated targeted delivery of therapeutic compositions containing antibodies of the invention is used to deliver the antibodies to specific tissue.

Therapeutic compositions containing antisense subgenomic polynucleotides are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μg to about 2 mg, about 5 μg to about 500 μg, and about 20 μg to about 100 μg of DNA can also be used during a gene therapy protocol. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is

desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. A more complete description of gene therapy vectors, especially retroviral vectors, is contained in U.S. Serial No. 08/869,309, which is expressly incorporated herein, and in section G below.

For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173. Therapeutic agents also include antibodies to proteins and polypeptides encoded by the polynucleotides of the invention and related genes, as described in U.S. Patent No. 5,654,173.

I. Gene Therapy

The therapeutic polynucleotides and polypeptides of the present invention can be utilized in gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) *1*:51; Kimura, *Human Gene Therapy* (1994) *5*:845; Connelly, *Human Gene Therapy* (1995) *1*:185; and Kaplitt, *Nature Genetics* (1994) *6*:148). Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches. Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

The present invention can employ recombinant retroviruses which are constructed to carry or express a selected nucleic acid molecule of interest. Retrovirus vectors that can be employed include those described in EP 0 415 731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; Vile and Hart, *Cancer Res.* (1993) *53*:3860; Vile *et al.*, *Cancer Res.* (1993) *53*:962; Ram et al., *Cancer Res.* (1993) *53*:83; Takamiya *et al.*, J. *Neurosci. Res.* (1992) *33*:493; Baba et al., *J. Neurosurg.* (1993) *79*:729; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; and EP 0 345 242. Preferred recombinant retroviruses include those described in WO 91/02805.

Packaging cell lines suitable for use with the above-described retroviral vector constructs can be readily prepared (see, *e.g.*, WO 95/30763 and WO 92/05266), and used to create producer cell lines (also termed vector cell lines) for the production of recombinant vector particles. Within particularly preferred embodiments of the invention, packaging cell lines are made from human (such as HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviruses that can survive inactivation in human serum.

The present invention also employs alphavirus-based vectors that can function as gene delivery vehicles. Such vectors can be constructed from a wide variety of alphaviruses, including, for example, Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532). Representative examples of such vector systems include those described in U.S. Patent Nos. 5,091,309; 5,217,879; and 5,185,440; WO 92/10578; WO 94/21792; WO 95/27069; WO 95/27044; and WO 95/07994. Gene delivery vehicles of the present invention can also employ parvovirus such as adeno-associated virus (AAV) vectors. Representative examples include the AAV vectors disclosed by Srivastava in WO 93/09239, Samulski et al., *J. Virol.* (1989) *63*:3822; Mendelson et al., *Virol.* (1988) *166*:154; and Flotte *et al.*, *PNAS* (1993) *90*:10613.

Representative examples of adenoviral vectors include those described by Berkner, *Biotechniques* (1988) *6*:616; Rosenfeld *et al.*, *Science* (1991) *252*:431; WO 93/19191; Kolls *et al.*, *PNAS* (1994) *91*:215; Kass-Eisler *et al.*, *PNAS* (1993) *90*:11498; Guzman *et al.*, *Circulation* (1993) *88*:2838; Guzman *et al.., Cir. Res.* (1993) *73*:1202; Zabner *et al.*, *Cell* (1993) *75*:207; Li *et al.*, *Hum. Gene Ther.* (1993) *4*:403; Cailaud *et al.*, *Eur. J. Neurosci.* (1993) *5*:1287; Vincent *et al.*, *Nat. Genet.* (1993) *5*:130; Jaffe *et al.*, *Nat. Genet.* (1992) *1*:372; and Levrero *et al.*, *Gene* (1991) *101*:195. Exemplary adenoviral gene therapy vectors employable in this invention also include those described in WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655. Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) *3*:147 can be employed.

Other gene delivery vehicles and methods can be employed, including polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example Curiel, *Hum. Gene Ther.* (1992) *3*:147; ligand linked DNA, for example see Wu, *J. Biol. Chem.* (1989) *264*:16985; eukaryotic cell delivery vehicles cells, for example see U.S. Pat. No. 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338; deposition of photopolymerized hydrogel materials; hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; ionizing radiation as described in U.S. Patent No. 5,206,152 and in WO92/11033; nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) *14*:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) *91*:1581.

Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Uptake efficiency can be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method can be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) *91*(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Patent No. 5,206,152 and WO 92/11033.

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

The present invention is now illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, these embodiments are illustrative and are not meant to be construed as restricting the invention in any way.

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

Human colon cancer cell line Km12L4-A (Morika, W. A. K. et al., *Cancer Research* (1988) *48*:6863) was used to construct a cDNA library from mRNA isolated from the cells. As described in the above overview, a total of 4,693 sequences expressed by the Km12L4-A cell line were isolated and analyzed; most sequences were about 275-300 nucleotides in length. The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B_2 surgical specimen (Morikawa *et al. Cancer Res.* (1988) *48*:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman *et al. Nucl. Acids. Res.* (1995) *23*:4007; Bao-Ling *et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) *21*:3269). The KM12C and KM12C-derived cell lines (*e.g.*, KM12L4, KM12L4-A, *etc.*) are well-recognized in the art as a model cell line for the study of colon cancer (see, *e.g.*, Moriakawa *et al.*, *supra*; Radinsky *et al. Clin. Cancer Res.* (1995) *1*:19; Yeatman *et al.*, (1995) *supra*; Yeatman *et al. Clin. Exp. Metastasis* (1996) *14*:246).

The sequences were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate of relative little interest due to their lox complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. Masking resulted in the elimination of 43 sequences. The remaining sequences were then used in a BLASTN vs. Genbank search with search parameters of greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40}, which search resulted in the discarding of 1,432 sequences. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). This search resulted in discard of 98 sequences as having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40}.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search resulted in discard of 1771 sequences (sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40}; sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded). Second, a BLASTN vs. Patent GeneSeq database resulted in discard of 15 sequences (greater than 99% identity; p value less than 1×10^{-40}; greater than 99% overlap).

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 404 sequences listed in the accompanying Sequence Listing. The Sequence Listing is arranged beginning with sequences with no similarity to any sequence in a database searched, and ending with sequences with the greatest similarity. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides and were assigned sequence identification numbers SEQ ID NOS: 1-404. The DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing. The majority of the sequences are presented in the Sequence Listing in the 5' to 3' direction. A small number, 25, are listed in the Sequence Listing in the 5' to 3' direction but the sequence as written is actually 3' to 5'. These sequences are readily identified with the designation "AR" in the Sequence Name in Table 1 (inserted before the claims). The sequences correctly listed in the 5' to 3' direction in the Sequence Listing are designated "AF." The Sequence Listing filed herewith therefore contains 25 sequences listed in the reverse order, namely SEQ ID NOS:47, 97, 137, 171, 173, 179, 182, 194, 200, 202, 213, 227, 258, 264, 275, 302, 313, 324, 329, 330, 331, 338, 358, 379, and 404.

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

In order to confirm the sequences of SEQ ID NOS:1-404, inserts of the clones corresponding to these polynucleotides were re-sequenced. These "validation" sequences are provided in SEQ ID NOS:405-800. These validation sequences were often longer than the original polynucleotide sequences. They validate, and thus often provide additional sequence information. Validation sequences can be correlated with the original sequences they validate by identifying those sequences of SEQ ID NOS:1-404 and the validation sequences of SEQ ID NOS:405-800 that share the same clone name in Table 1.

Example 2: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-404, as well as the validation sequences SEQ ID NOS:405-800, were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at http://ww.ncbi.nlm.nih.gov/BLAST/. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Table 2 (inserted before the claims) shows the results of the alignments. Table 2 refers to each sequence by its SEQ ID NO:, the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values of the search results. Table 1 identifies each SEQ ID NO: by SEQ name, clone ID, and cluster. As discussed above, a single cluster includes polynucleotides representing the same gene or gene family, and generally represents sequences encoding the same gene product.

For each of SEQ ID NOS:1-800, the best alignment to a protein or DNA sequence is included in Table 2. The activity of the polypeptide encoded by SEQ ID NOS:1-800 is the same or similar to the nearest neighbor reported in Table 2. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOS:1-800. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID NOS:1-800.

SEQ ID NOS:1-800 and the translations thereof may be human homologs of known genes of other species or novel allelic variants of known human genes. In such cases, these new human sequences are suitable as diagnostics or therapeutics. As diagnostics, the human sequences SEQ ID NOS:1-800 exhibit greater specificity in detecting and differentiating human cell lines and types than homologs of other species. The human polypeptides encoded by SEQ ID NOS:1-800 are likely to be less immunogenic when administered to humans than homologs from other species. Further, on administration to humans, the polypeptides encoded by SEQ ID NOS:1-800 can show greater specificity or can be better regulated by other human proteins than are homologs from other species.

Example 3: Members of Protein Families

After conducting a profile search as described in the specification above, several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 3). Thus the invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
24	4 transmembrane segments integral membrane proteins	1218	578	rev
41	4 transmembrane segments integral membrane proteins	1086	413	rev
101	4 transmembrane segments integral membrane proteins	1206	544	rev
157	4 transmembrane segments integral membrane proteins	721	33	rev
341	4 transmembrane segments integral membrane proteins	1253	613	rev
395	4 transmembrane segments integral membrane proteins	530	10	for
395	4 transmembrane segments integral membrane proteins	696	17	for
395	4 transmembrane segments integral membrane proteins	471	39	rev
24	7 transmembrane receptor (Secretin family)	1301	491	rev
41	7 transmembrane receptor (Secretin family)	1309	10	rev
101	7 transmembrane receptor (Secretin family)	1330	296	rev
157	7 transmembrane receptor (Secretin family)	1173	249	rev
291	7 transmembrane receptor (Secretin family)	1400	269	rev

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
291	7 transmembrane receptor (Secretin family)	712	130	for
305	7 transmembrane receptor (Secretin family)	926	4	for
305	7 transmembrane receptor (Secretin family)	753	55	rev
315	7 transmembrane receptor (Secretin family)	1058	270	rev
341	7 transmembrane receptor (Secretin family)	1265	534	rev
116	Ank repeat	141	218	for
251	Ank repeat	290	207	for
251	Ank repeat	467	387	for
63	ATPases Associated with Various Cellular Activities	543	60	for
116	ATPases Associated with Various Cellular Activities	802	313	for
134	ATPases Associated with Various Cellular Activities	525	57	rev
136	ATPases Associated with Various Cellular Activities	712	163	for
151	ATPases Associated with Various Cellular Activities	719	73	for
151	ATPases Associated with Various Cellular Activities	386	13	for
384	ATPases Associated with Various Cellular Activities	664	140	for
404	ATPases Associated with Various Cellular Activities	704	52	for
374	Basic region plus leucine zipper transcription factors	298	146	for
97	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)	230	63	for
136	EF-hand	121	207	for
242	EF-hand	238	155	for
379	EF-hand	212	126	for
308	Eukaryotic aspartyl proteases	1300	461	rev
213	GATA family of transcription factors	720	377	for
367	G-protein alpha subunit	971	467	rev
188	Phorbol esters/diacylglycerol binding	91	177	for
251	Phorbol esters/diacylglycerol binding	133	219	for
202	protein kinase	482	1	rev
202	protein kinase	970	1	rev
315	protein kinase	739	158	for
315	protein kinase	1023	197	for
367	protein kinase	1046	285	rev
397	protein kinase	511	6	for
256	Protein phosphatase 2C	13	90	for
256	Protein phosphatase 2C	163	86	for
382	Protein Tyrosine Phosphatase	261	2	for
306	SH3 Domain	141	296	for
386	SH3 Domain	359	209	for
169	Trypsin	764	164	rev
188	WD domain, G-beta repeats	480	382	for
188	WD domain, G-beta repeats	206	117	for
335	WD domain, G-beta repeats	3	92	for
23	wnt family of developmental signaling proteins	1151	335	rev
291	wnt family of developmental signaling proteins	779	89	rev
291	wnt family of developmental signaling proteins	1347	382	rev
324	wnt family of developmental signaling proteins	1180	499	rev
330	wnt family of developmental signaling proteins	1180	499	rev
341	wnt family of developmental signaling proteins	1399	560	rev

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
353	wnt family of developmental signaling proteins	880	49	rev
188	WW/rsp5/WWP domain containing proteins	431	354	for
379	WW/rsp5/WWP domain containing proteins	12	89	for
395	WW/rsp5/WWP domain containing proteins	153	76	for
395	WW/rsp5/WWP domain containing proteins	156	64	for
61	Zinc finger, C2H2 type	254	192	for
306	Zinc finger, C2H2 type	428	367	for
386	Zinc finger, C2H2 type	191	253	for
322	Zinc finger, CCHC class	553	503	for
306	Zinc-binding metalloprotease domain	101	60	rev
395	Zinc-binding metalloprotease domain	28	69	rev

Start and stop indicate the position within the individual sequenes that align with the query sequence having the indicated SEQ ID NO. The direction (Dir) indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

<u>a) Four Transmembrane Integral Membrane Proteins.</u> SEQ ID NOS: 24, 41, 101, 157, 341, and 395 correspond to a sequence encoding a polypeptide that is a member of the 4 transmembrane segments integral membrane protein family (transmembrane 4 family). The transmembrane 4 family of proteins includes a number of evolutionarily-related eukaryotic cell surface antigens (Levy *et al.*, *J. Biol. Chem.*, (1991) *266*:14597; Tomlinson *et al.*, *Eur. J. Immunol.* (1993) *23*:136; Barclay *et al.* The leucocyte antigen factbooks. (1993) Academic Press, London/San Diego). The proteins belonging to this family include: 1) Mammalian antigen CD9 (MIC3), which is involved in platelet activation and aggregation; 2) Mammalian leukocyte antigen CD37, expressed on B lymphocytes; 3) Mammalian leukocyte antigen CD53 (OX-44), which is implicated in growth regulation in hematopoietic cells; 4) Mammalian lysosomal membrane protein CD63 (melanoma-associated antigen ME491; antigen AD1); 5) Mammalian antigen CD81 (cell surface protein TAPA-1), which is implicated in regulation of lymphoma cell growth; 6) Mammalian antigen CD82 (protein

R2; antigen C33; Kangai 1 (KAI1)), which associates with CD4 or CD8 and delivers costimulatory signals for the TCR/CD3 pathway; 7) Mammalian antigen CD151 (SFA-1; platelet-endothelial tetraspan antigen 3 (PETA-3)); 8) Mammalian cell surface glycoprotein A15 (TALLA-1; MXS1); 9) Mammalian novel antigen 2 (NAG-2); 10) Human tumor-associated antigen CO-029; 11) Schistosoma mansoni and japonicum 23 Kd surface antigen (SM23 / SJ23).

The members of the 4 transmembrane family share several characteristics. First, they all are apparently type III membrane proteins, which are integral membrane proteins containing an N-terminal membrane-anchoring domain which is not cleaved during biosynthesis and which functions both as a translocation signal and as a membrane anchor. The family members also contain three additional transmembrane regions, at least seven conserved cysteines residues, and are of approximately the same size (218 to 284 residues). These proteins are collectively know as the "transmembrane 4 superfamily" (TM4) because they span plasma membrane four times. A schematic diagram of the domain structure of these proteins is as follows:

```
+-+-----+-------+----+-----+-----+----------------------+-----+----+
| | TMa | Extra | TM2| Cyt | TM3 | Extracellular        | TM4 | Cyt|
+-+-----+-------+----C-----C-----+--------CC---C-----C---+-----C----+
                                          *********
```

where Cyt is the cytoplasmic domain, TMa is the transmembrane anchor; TM2 to TM4 represents transmembrane regions 2 to 4, 'C' are conserved cysteines, and '* 'indicates the position of the consensus pattern. The consensus pattern spans a conserved region including two cysteines located in a short cytoplasmic loop between two transmembrane domains: Consensus pattern: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-[STA]- x(2)-[EG]-x(2)-[CWN]-[LIVM](2).

b) Seven Transmembrane Integral Membrane Proteins. SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, and 341 correspond to a sequence encoding a polypeptide that is a member of the seven transmembrane receptor family. G-protein coupled receptors (Strosberg, *Eur. J. Biochem.* (1991) *196*:1; Kerlavage, *Curr. Opin. Struct. Biol.* (1991) *1*:394; and Probst *et al.*, *DNA Cell Biol.* (1992) *11*:1; and Savarese *et al.*, *Biochem. J.* (1992) *293*:1) (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. The tertiary structure of these receptors is thought to be highly similar. They have seven hydrophobic regions, each of which most probably spans

the membrane. The N-terminus is located on the extracellular side of the membrane and is often glycosylated, while the C-terminus is cytoplasmic and generally phosphorylated. Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. Most, but not all of these receptors, lack a signal peptide. The most conserved parts of these proteins are the transmembrane regions and the first two cytoplasmic loops. A conserved acidic-Arg-aromatic triplet is present in the N-terminal extremity of the second cytoplasmic loop (Attwood *et al.*, *Gene* (1991) *98*:153) and could be implicated in the interaction with G proteins.

To detect this widespread family of proteins a pattern is used that contains the conserved triplet and that also spans the major part of the third transmembrane helix. Additional information about the seven transmembrane receptor family, and methods for their identification and use, is found in U.S. Patent No. 5,759,804. Due in part to their expression on the cell surface and other attractive characteristics, seven transmembrane protein family members are of particular interest as drug targets, as surface antigen markers, and as drug delivery targets (*e.g.*, using antibody-drug complexes and/or use of anti-seven transmembrane protein antibodies as therapeutics in their own right).

c) <u>Ank Repeats.</u> SEQ ID NOS: 116 and 251 represent polynucleotides encoding Ank repeat-containing proteins. The ankyrin motif is a 33 amino acid sequence named after the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breeden *et al., Nature* (1987) *329*:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno *et al., Development* (1997) *124(21)*:4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-protein interactions (Bork, *Proteins* (1993) *17(4)*:363; Lambert and Bennet, *Eur. J. Biochem.* (1993) *211*:1; Kerr *et al., Current Op. Cell Biol.* (1992) *4*:496; Bennet *et al., J. Biol. Chem.* (1980) *255*:6424).

The 90 kD N-terminal domain of ankyrin contains a series of 24 33-amino-acid ank repeats. (Lux *et al., Nature* (1990) *344*:36-42, Lambert *et al., PNAS USA* (1990) *87*:1730.) The 24 ank repeats form four folded subdomains of 6 repeats each. These four repeat subdomains mediate interactions with at least 7 different families of membrane proteins. Ankyrin contains two separate binding sites for anion exchanger dimers. One site utilizes repeat subdomain two (repeats 7-12) and the other requires both repeat subdomains 3 and 4 (repeats 13-24). Since the anion exchangers exist in dimers, ankyrin binds 4 anion

exchangers at the same time. (Michaely and Bennett, *J. Biol. Chem.* (1995) *270(37)*:22050) The repeat motifs are involved in ankyrin interaction with tubulin, spectrin, and other membrane proteins. (Lux *et al.*, *Nature* (1990) *344*:36.)

The Rel/NF-kappaB/Dorsal family of transcription factors have activity that is controlled by sequestration in the cytoplasm in association with inhibitory proteins referred to as I-kappaB. (Gilmore, *Cell* (1990) *62*:841; Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) *2*:211; Baeuerle, *Biochim Biophys Acta* (1991) *1072*:63; Schmitz *et al.*, *Trends Cell Biol.* (1991) *1*:130.) I-kappaB proteins contain 5 to 8 copies of 33 amino acid ankyrin repeats and certain NF-kappaB/rel proteins are also regulated by cis-acting ankyrin repeat containing domains including p105NF-kappaB which contains a series of ankyrin repeats (Diehl and Hannink, *J. Virol.* (1993) *67(12)*:7161). The I-kappaBs and Cactus (also containing ankyrin repeats) inhibit activators through differential interactions with the Rel-homology domain. The gene family includes proto-oncogenes, thus broadly implicating I-kappaB in the control of both normal gene expression and the aberrant gene expression that makes cells cancerous. (Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) *2(2)*:211-220). In the case of rel/NF-kappaB and pp40/I-kappaBβ, both the ankyrin repeats and the carboxy-terminal domain are required for inhibiting DNA-binding activity and direct association of pp40/I-kappaBβ with rel/NF-kappaB protein. The ankyrin repeats and the carboxy-terminal of pp40/I-kappaBβ (form a structure that associates with the rel homology domain to inhibit DNA binding activity (Inoue *et al.*, *PNAS USA* (1992) *89*:4333).

The 4 ankyrin repeats in the amino terminus of the transcription factor subunit GABPβ are required for its interaction with the GABPα subunit to form a functional high affinity DNA-binding protein. These repeats can be crosslinked to DNA when GABP is bound to its target sequence. (Thompson *et al.*, *Science* (1991) *253*:762; LaMarco *et al.*, *Science* (1991) *253*:789).

Myotrophin, a 12.5 kDa protein having a key role in the initiation of cardiac hypertrophy, comprises ankyrin repeats. The ankyrin repeats are characteristic of a hairpin-like protruding tip followed by a helix-turn-helix motif. The V-shaped helix-turn-helix of the repeats stack sequentially in bundles and are stabilized by compact hydrophobic cores, whereas the protruding tips are less ordered.

d) <u>ATPases Associated with Various Cellular Activities (AAA).</u> SEQ ID NOS: 63, 116, 134, 136, 151, 384, and 404 polynucleotides encoding novel members of the "ATPases Associated with diverse cellular Activities" (AAA) protein family The AAA protein family

is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich *et al., J. Cell Biol.* (1991) *114*:443; Erdmann *et al. Cell* (1991) *64*:499; Peters *et al., EMBO J.* (1990) *9*:1757; Kunau *et al., Biochimie* (1993) *75*:209-224; Confalonieri *et al., BioEssays* (1995) *17*:639; http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html). The proteins that belong to this family either contain one or two AAA domains.

Proteins containing two AAA domains include: 1) Mammalian and drosophila NSF (N-ethylmaleimide-sensitive fusion protein) and the fungal homolog, SEC18, which are involved in intracellular transport between the endoplasmic reticulum and Golgi, as well as between different Golgi cisternae; 2) Mammalian transitional endoplasmic reticulum ATPase (previously known as p97 or VCP), which is involved in the transfer of membranes from the endoplasmic reticulum to the golgi apparatus. This ATPase forms a ring-shaped homooligomer composed of six subunits. The yeast homolog, CDC48, plays a role in spindle pole proliferation; 3) Yeast protein PAS1 essential for peroxisome assembly and the related protein PAS1 from Pichia pastoris; 4) Yeast protein AFG2; 5) Sulfolobus acidocaldarius protein SAV and Halobacterium salinarium cdcH, which may be part of a transduction pathway connecting light to cell division.

Proteins containing a single AAA domain include: 1) Escherichia coli and other bacteria ftsH (or hflB) protein. FtsH is an ATP-dependent zinc metallopeptidase that degrades the heat-shock sigma-32 factor, and is an integral membrane protein with a large cytoplasmic C-terminal domain that contain both the AAA and the protease domains; 2) Yeast protein YME1, a protein important for maintaining the integrity of the mitochondrial compartment. YME1 is also a zinc-dependent protease; 3) Yeast protein AFG3 (or YTA10). This protein also contains an AAA domain followed by a zinc-dependent protease domain; 4) Subunits from regulatory complex of the 26S proteasome (Hilt *et al., Trends Biochem. Sci.* (1996) *21*:96), which is involved in the ATP-dependent degradation of ubiquitinated proteins, which subunits include: a) Mammalian 4 and homologs in other higher eukaryotes, in yeast (gene YTA5) and fission yeast (gene mts2); b) Mammalian 6 (TBP7) and homologs in other higher eukaryotes and in yeast (gene YTA2); c) Mammalian subunit 7 (MSS1) and homologs in other higher eukaryotes and in yeast (gene CIM5 or YTA3); d) Mammalian subunit 8 (P45) and homologs in other higher eukaryotes and in yeast (SUG1 or CIM3 or TBY1) and fission yeast (gene let1); e) Other probable subunits include human TBP1, which influences HIV gene expression by interacting with the virus tat transactivator protein, and yeast YTA1 and YTA6; 5) Yeast protein BCS1, a mitochondrial protein essential for the

expression of the Rieske iron-sulfur protein; 6) Yeast protein MSP1, a protein involved in intramitochondrial sorting of proteins; 7) Yeast protein PAS8, and the corresponding proteins PAS5 from Pichia pastoris and PAY4 from Yarrowia lipolytica; 8) Mouse protein SKD1 and its fission yeast homolog (SpAC2G11.06); 9) Caenorhabditis elegans meiotic spindle formation protein mei-1; 10) Yeast protein SAP1' 11) Yeast protein YTA7; and 12) Mycobacterium leprae hypothetical protein A2126A.

In general, the AAA domains in these proteins act as ATP-dependent protein clamps(Confalonieri *et al.* (1995) *BioEssays 17*:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]- D-x-A-[LIFA]-x-R.

e) <u>Basic Region Plus Leucine Zipper Transcription Factors.</u> SEQ ID NO:374 correspond to a polynucleotide encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) *2*:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) *4*:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. Members of the family include transcription factor AP-1, which binds selectively to enhancer elements in the cis control regions of SV40 and metallothionein IIA. AP-1, also known as c-jun, is the cellular homolog of the avian sarcoma virus 17 (ASV17) oncogene v-jun.

Other members of this protein family include jun-B and jun-D, probable transcription factors that are highly similar to jun/AP-1; the fos protein, a proto-oncogene that forms a non-covalent dimer with c-jun; the fos-related proteins fra-1, and fos B; and mammalian cAMP response element (CRE) binding proteins CREB, CREM, ATF-1, ATF-3, ATF-4, ATF-5, ATF-6 and LRF-1. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

f) <u>Bromodomain.</u> SEQ ID NO:97 corresponds to a polynucleotide encoding a polypeptide having a bromodomain region (Haynes et al., 1992, Nucleic Acids Res. 20:2693-2603, Tamkun et al., 1992, Cell 68:561-572, and Tamkun, 1995, Curr. Opin. Genet. Dev. 5:473-477), which is a conserved region of about 70 amino acids found in the following proteins: 1) Higher eukaryotes transcription initiation factor TFIID 250 Kd subunit (TBP-associated factor p250) (gene CCG1); P250 is associated with the TFIID TATA-box binding protein and seems essential for progression of the G1 phase of the cell

cycle. 2) Human RING3, a protein of unknown function encoded in the MHC class II locus; 3) Mammalian CREB-binding protein (CBP), which mediates cAMP-gene regulation by binding specifically to phosphorylated CREB protein; 4) Mammalian homologs of brahma, including three brahma-like human: SNF2a(hBRM), SNF2b, and BRG1; 5) Human BS69, a protein that binds to adenovirus E1A and inhibits E1A transactivation; 6) Human peregrin (or Br140).

The bromodomain is thought to be involved in protein-protein interactions and may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. The consensus pattern, which spans a major part of the bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

g) <u>EF-Hand.</u> SEQ ID NOS:136, 242, and 379 correspond to polynucleotides encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins belong to the same evolutionary family and share a type of calcium-binding domain known as the EF-hand (Kawasaki *et al.*, *Protein. Prof.* (1995) *2*:305-490). This type of domain consists of a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand).

Proteins known to contain EF-hand regions include: Calmodulin (Ca=4, except in yeast where Ca=3) ("Ca=" indicates approximate number of EF-hand regions); diacylglycerol kinase (EC 2.7.1.107) (DGK) (Ca=2); 2) FAD-dependent glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) from mammals (Ca=1); guanylate cyclase activating protein (GCAP) (Ca=3); MIF related proteins 8 (MRP-8 or CFAG) and 14 (MRP-14) (Ca=2); myosin regulatory light chains (Ca=1); oncomodulin (Ca=2); osteonectin (basement membrane protein BM-40) (SPARC); and proteins that contain an "osteonectin" domain (QR1, matrix glycoprotein SC1).

The consensus pattern includes the complete EF-hand loop as well as the first residue which follows the loop and which seem to always be hydrophobic.

Consensus pattern: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW]

h) Eukaryotic Aspartyl Proteases. SEQ ID NO:308 corresponds to a gene encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) *17*:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) *19*:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) *30*:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The two domains most probably evolved from the duplication of an ancestral gene encoding a primordial domain. Currently known eukaryotic aspartyl proteases include: 1) Vertebrate gastric pepsins A and C (also known as gastricsin); 2) Vertebrate chymosin (rennin), involved in digestion and used for making cheese; 3) Vertebrate lysosomal cathepsins D (EC 3.4.23.5) and E (EC 3.4.23.34); 4) Mammalian renin (EC 3.4.23.15) whose function is to generate angiotensin I from angiotensinogen in the plasma; 5) Fungal proteases such as aspergillopepsin A (EC 3.4.23.18), candidapepsin (EC 3.4.23.24), mucoropepsin (EC 3.4.23.23) (mucor rennin), endothiapepsin (EC 3.4.23.22), polyporopepsin (EC 3.4.23.29), and rhizopuspepsin (EC 3.4.23.21); and 6) Yeast saccharopepsin (EC 3.4.23.25) (proteinase A) (gene PEP4). PEP4 is implicated in posttranslational regulation of vacuolar hydrolases; 7) Yeast barrierpepsin (EC 3.4.23.35) (gene BAR1); a protease that cleaves alpha-factor and thus acts as an antagonist of the mating pheromone; and 8) Fission yeast sxa1 which is involved in degrading or processing the mating pheromones.

Most retroviruses and some plant viruses, such as badnaviruses, encode for an aspartyl protease which is an homodimer of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. It is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. Because the sequence around the two aspartates of eukaryotic aspartyl proteases and around the single active site of the viral proteases is conserved, a single signature pattern can be used to identify members of both groups of proteases. The consensus pattern is: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]- x-[LIVMFSTNC]-x-[LIVMFGTA], where D is the active site residue.

i) GATA Family of Transcription Factors. SEQ ID NO:213 corresponds to a novel member of the GATA family of transcription factors. The GATA family of transcription factors are proteins that bind to DNA sites with the consensus sequence (A/T)GATA(A/G), found within the regulatory region of a number of genes. Proteins currently known to belong

to this family are: 1) GATA-1 (Trainor, C.D., *et al.*, *Nature* (1990) *343*:92) (also known as Eryfl, GF-1 or NF-E1), which binds to the GATA region of globin genes and other genes expressed in erythroid cells. It is a transcriptional activator which probably serves as a general 'switch' factor for erythroid development; 2) GATA-2 (Lee, M.E., *et al.*, *J. Biol. Chem.* (1991) *266*:16188), a transcriptional activator which regulates endothelin-1 gene expression in endothelial cells; 3) GATA-3 (Ho, I.-C., *et al.*, *EMBO J.* (1991) *10*:1187), a transcriptional activator which binds to the enhancer of the T-cell receptor alpha and delta genes; 4) GATA-4 (Spieth, J., *et al.*, *Mol. Cell. Biol.* (1991) *11*:4651), a transcriptional activator expressed in endodermally derived tissues and heart; 5) Drosophila protein pannier (or DGATAa) (gene pnr) which acts as a repressor of the achaete-scute complex (as-c); 6) Bombyx mori BCFI (Drevet, J.R., *et al.*, *J. Biol. Chem.* (1994) *269*:10660), which regulates the expression of chorion genes; 7) Caenorhabditis elegans elt-1 and elt-2, transcriptional activators of genes containing the GATA region, including vitellogenin genes (Hawkins, M.G., *et al.*, *J. Biol. Chem.* (1995) *270*:14666); 8) Ustilago maydis urbs1 (Voisard, C.P.O., *et al.*, *Mol. Cell. Biol.* (1993) *13*:7091), a protein involved in the repression of the biosynthesis of siderophores; 9) Fission yeast protein GAF2.

All these transcription factors contain a pair of highly similar 'zinc finger' type domains with the consensus sequence C-x2-C-x17-C-x2-C. Some other proteins contain a single zinc finger motif highly related to those of the GATA transcription factors. These proteins are: 1) Drosophila box A-binding factor (ABF) (also known as protein serpent (gene srp)) which may function as a transcriptional activator protein and may play a key role in the organogenesis of the fat body; 2) Emericella nidulans are (Arst, H.N., Jr., *et al.*, *Trends Genet.* (1989) *5*:291) a transcriptional activator which mediates nitrogen metabolite repression; 3) Neurospora crassa nit-2 (Fu, Y.-H., *et al.*, *Mol. Cell. Biol.* (1990) *10*:1056), a transcriptional activator which turns on the expression of genes coding for enzymes required for the use of a variety of secondary nitrogen sources, during conditions of nitrogen limitation; 4) Neurospora crassa white collar proteins 1 and 2 (WC-1 and WC-2), which control expression of light-regulated genes; 5) Saccharomyces cerevisiae DAL81 (or UGA43), a negative nitrogen regulatory protein; 6) Saccharomyces cerevisiae GLN3, a positive nitrogen regulatory protein; 7) Saccharomyces cerevisiae GAT1; 8) Saccharomyces cerevisiae GZF3.

The consensus pattern for the GATA family is: C-x-[DN]-C-x(4,5)-[ST]-x(2)-W-[HR]-[RK]-x(3)-[GN]-x(3,4)-C-N-[AS]-C, where the four C's are zinc ligands.

j) G-Protein Alpha Subunit. SEQ ID NO:367 corresponds to a gene encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to intracellular effectors, such as ion channels and enzymes that vary the concentration of second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit has a molecule of guanosine diphosphate (GDP) bound to it. Stimulation of the G-protein by an activated receptor leads to its exchange for GTP (guanosine triphosphate). This results in the separation of the alpha from the beta and gamma subunits, which always remain tightly associated as a dimer. Both the alpha and beta-gamma subunits are then able to interact with effectors, either individually or in a cooperative manner. The intrinsic GTPase activity of the alpha subunit hydrolyses the bound GTP to GDP. This returns the alpha subunit to its inactive conformation and allows it to reassociate with the beta-gamma subunit, thus restoring the system to its resting state.

G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals. These fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon *et al.*, *Science* (1993) *252*:802). Many alpha subunits are substrates for ADP-ribosylation by cholera or pertussis toxins. They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications are probably important for membrane association and high- affinity interactions with other proteins. The atomic structure of the alpha subunit of the G-protein involved in mammalian vision, transducin, has been elucidated in both GTP- and GDB-bound forms, and shows considerable similarity in both primary and tertiary structure in the nucleotide-binding regions to other guanine nucleotide binding proteins, such as p21-ras and EF-Tu.

k) Phorbol Esters/Diacylglycerol Binding. SEQ ID NO:188 and 251 represent polynucleotides encoding a protein belonging to the family including phorbol esters/diacylglycerol binding proteins. Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC) (Azzi *et al.*, *Eur. J. Biochem.* (1992) *208*:547). Phorbol esters can directly stimulate PKC. The N-terminal region of PKC, known as C1, has been shown (Ono *et al.*, *Proc. Natl.*

Acad. Sci. USA (1989) *86*:4868) to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Such a domain has also been found in, for example, the following proteins.

(1) Diacylglycerol kinase (EC 2.7.1.107) (DGK) (Sakane *et al.*, *Nature* (1990) *344*:345), the enzyme that converts DAG into phosphatidate. It contains two copies of the DAG/PE-binding domain in its N-terminal section. At least five different forms of DGK are known in mammals; and

(2) N-chimaerin, a brain specific protein which shows sequence similarities with the BCR protein at its C-terminal part and contains a single copy of the DAG/PE-binding domain at its N-terminal part. It has been shown (Ahmed *et al.*, *Biochem. J.* (1990) *272*:767, and Ahmed *et al.*, *Biochem. J.* (1991) *280*:233) to be able to bind phorbol esters.

The DAG/PE-binding domain binds two zinc ions; the ligands of these metal ions are probably the six cysteines and two histidines that are conserved in this domain. The signature pattern completely spans the DAG/PE domain. The consensus pattern is: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C. All the C and H are probably involved in binding zinc.

l) <u>Protein Kinase.</u> SEQ ID NOS:202, 315, 367, and 397 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., *et al.*, *FASEB J.* (1995) *9*:576; Hunter T., *Meth. Enzymol.* (1991) *200*:3; Hanks S.K., *et al.*, *Meth. Enzymol.* (1991) *200*:38; Hanks S.K., *Curr. Opin. Struct. Biol.* (1991) *1*:369; Hanks S.K., *et al.*, *Science* (1988) *241*:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. Two of the conserved regions are the basis for the signature pattern in the protein kinase profile. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R., *et al.*, *Science* (1991) *253*:407). The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is

based on the alignment in (Hanks S.K., *et al.*, *FASEB J.* (1995) *9*:576) and covers the entire catalytic domain. The consensus patterns are as follows:

1) Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP. The majority of known protein kinases are detected by this pattern. Proteins kinases that are not detected by this consensus include viral kinases, which are quite divergent in this region and are completely missed by this pattern.

2) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue. This consensus sequence identifies most serine/threonine-specific protein kinases with only 10 exceptions. Half of the exceptions are viral kinases, while the other exceptions include Epstein-Barr virus BGLF4 and Drosophila ninaC, which have Ser and Arg, respectively, instead of the conserved Lys. These latter two protein kinases are detected by the tyrosine kinase specific pattern described below.

3) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue. All tyrosine-specific protein kinases are detected by this consensus pattern, with the exception of human ERBB3 and mouse blk. This pattern also detects most bacterial aminoglycoside phosphotransferases (Benner S., *Nature* (1987) *329*:21; Kirby R., *J. Mol. Evol.* (1992) *30*:489) and herpesviruses ganciclovir kinases (Littler E., *et al.*, *Nature* (1992) *358*:160), which are structurally and evolutionary related to protein kinases.

The protein kinase profile also detects receptor guanylate cyclases and 2-5A-dependent ribonucleases. Sequence similarities between these two families and the eukaryotic protein kinase family have been noticed previously. The profile also detects Arabidopsis thaliana kinase-like protein TMKL1 which seems to have lost its catalytic activity.

If a protein analyzed includes the two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type protein kinases have also been found in prokaryotes such as Myxococcus xanthus (Munoz-Dorado J., *et al.*, *Cell* (1991) *67*:995) and Yersinia pseudotuberculosis. The patterns shown above has been updated since their publication in (Bairoch A., *et al.*, *Nature* (1988) *331*:22).

m) Protein Phosphatase 2C. SEQ ID NO:256 corresponds to a polynucleotide encoding a novel protein phosphatase 2C (PP2C), which is one of the four major classes of mammalian serine/threonine specific protein phosphatases. PP2C (Wenk *et al.*, *FEBS Lett.*

(1992) *297*:135) is a monomeric enzyme of about 42 Kd which shows broad substrate specificity and is dependent on divalent cations (mainly manganese and magnesium) for its activity. Three isozymes are currently known in mammals: PP2C-alpha, -beta and -gamma.

n) Protein Tyrosine Phosphatase. SEQ ID NO:382 represents a polynucleotide encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer *et al., Science* (1991) *253*:401; Charbonneau *et al., Annu. Rev. Cell Biol.* (1992) *8*:463; Trowbridge, *J. Biol. Chem.* (1991) *266*:23517; Tonks *et al., Trends Biochem. Sci.* (1989) *14*:497; and Hunter, *Cell* (1989) *58*:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s).

Soluble PTPases include PTPN3 (H1) and PTPN4 (MEG), enzymes that contain an N-terminal band 4.1-like domain and could act at junctions between the membrane and cytoskeleton; PTPN6 (PTP-1C; HCP; SHP) and PTPN11 (PTP-2C; SH-PTP3; Syp), enzymes that contain two copies of the SH2 domain at its N-terminal extremity.

Dual specificity PTPases include DUSP1 (PTPN10; MAP kinase phosphatase-1; MKP-1) which dephosphorylates MAP kinase on both Thr-183 and Tyr-185; and DUSP2 (PAC-1), a nuclear enzyme that dephosphorylates MAP kinases ERK1 and ERK2 on both Thr and Tyr residues.

Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. Some of the receptor PTPases contain fibronectin type III (FN-III) repeats, immunoglobulin-like domains, MAM domains or carbonic anhydrase-like domains in their extracellular region. The cytoplasmic region generally contains two copies of the PTPAse domain. The first seems to have enzymatic activity, while the second is inactive but seems to affect substrate specificity of the first. In these domains, the catalytic cysteine is generally conserved but some other, presumably important, residues are not.

PTPase domains consist of about 300 amino acids. There are two conserved cysteines and the second one has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.

o) SH3 Domain. SEQ ID NO:306 and 386 represent polynucleotides encoding SH3 domain proteins. The Src homology 3 (SH3) domain is a small protein domain of about 60 amino acid residues first identified as a conserved sequence in the non-catalytic part of several cytoplasmic protein tyrosine kinases (e.g. Src, Abl, Lck) (Mayer *et al.*, *Nature* (1988) *332*:272). The domain has also been found in a variety of intracellular or membrane-associated proteins (Musacchio *et al.*, *FEBS Lett.* (1992) *307*:55; Pawson *et al.*, *Curr. Biol.* (1993) *3*:434; Mayer *et al.*, *Trends Cell Biol.* (1993) *3*:8; and Pawson *et al.*, *Nature* (1995) *373*:573).

The SH3 domain has a characteristic fold that consists of five or six beta-strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices (Kuriyan *et al.*, *Curr. Opin. Struct. Biol.* (1993) *3*:828). It is believed that SH3 domain-containing proteins mediate assembly of specific protein complexes via binding to proline-rich peptides (Morton *et al.*, *Curr. Biol.* (1994) *4*:615). In general, SH3 domains are found as single copies in a given protein, but there is a significant number of proteins with two SH3 domains and a few with 3 or 4 copies.

SH3 domains have been identified in, for example, protein tyrosine kinases, such as the Src, Abl, Bkt, Csk and ZAP70 families of kinases; mammalian phosphatidylinositol-specific phospholipase C-gamma-1 and -2; mammalian phosphatidyl inositol 3-kinase regulatory p85 subunit; mammalian Ras GTPase-activating protein (GAP); mammalian Vav oncoprotein, a guanine nucleotide exchange factor of the CDC24 family; Drosophila lethal(1)discs large-1 tumor suppressor protein (gene Dlg1); mammalian tight junction protein ZO-1; vertebrate erythrocyte membrane protein p55; Caenorhabditis elegans protein lin-2; rat protein CASK; and mammalian synaptic proteins SAP90/PSD-95, CHAPSYN-110/PSD-93, SAP97/DLG1 and SAP102. Novel SH3-domain containing polypeptides will facilitate elucidation of the role of such proteins in important biological pathways, such as ras activation.

p) Trypsin. SEQ ID NO:169 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* (1988) *334*:528). Proteases known to belong to the trypsin family include: 1) Acrosin; 2) Blood coagulation factors VII, IX, X, XI and XII, thrombin, plasminogen, and protein C; 3) Cathepsin G; 4) Chymotrypsins; 5) Complement components C1r, C1s, C2, and complement

factors B, D and I; 6) Complement-activating component of RA-reactive factor; 7) Cytotoxic cell proteases (granzymes A to H); 8) Duodenase I; 9) Elastases 1, 2, 3A, 3B (protease E), leukocyte (medullasin).; 10) Enterokinase (EC 3.4.21.9) (enteropeptidase); 11) Hepatocyte growth factor activator; 12) Hepsin; 13) Glandular (tissue) kallikreins (including EGF-binding protein types A, B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin); 14) Plasma kallikrein; 15) Mast cell proteases (MCP) 1 (chymase) to 8; 16) Myeloblastin (proteinase 3) (Wegener's autoantigen); 17) Plasminogen activators (urokinase-type, and tissue-type); 18) Trypsins I, II, III, and IV; 19) Tryptases; 20) Snake venom proteases such as ancrod, batroxobin, cerastobin, flavoxobin, and protein C activator; 21) Collagenase from common cattle grub and collagenolytic protease from Atlantic sand fiddler crab; 22) Apolipoprotein(a); 23) Blood fluke cercarial protease; 24) Drosophila trypsin like proteases: alpha, easter, snake-locus; 25) Drosophila protease stubble (gene sb); and 26) Major mite fecal allergen Der p III. All the above proteins belong to family S1 in the classification of peptidases (Rawlings N.D., *et al.*, *Meth. Enzymol.* (1994) *244*:19; http://www.expasy.ch/cgi-bin/lists?peptidas.txt) and originate from eukaryotic species. It should be noted that bacterial proteases that belong to family S2A are similar enough in the regions of the active site residues that they can be picked up by the same patterns.

The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue. All sequences known to belong to this class detected by the pattern, except for complement components C1r and C1s, pig plasminogen, bovine protein C, rodent urokinase, ancrod, gyroxin and two insect trypsins; 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

q) WD Domain, G-Beta Repeats. SEQ ID NOS:188 and 335 represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) *56*:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but

they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). Such a repetitive segment has been shown to exist in a number of other proteins including: human LIS1, a neuronal protein involved in type-1 lissencephaly; and mammalian coatomer beta' subunit (beta'-COP), a component of a cytosolic protein complex that reversibly associates with Golgi membranes to form vesicles that mediate biosynthetic protein transport.

The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

r) <u>wnt Family of Developmental Signaling Proteins.</u> SEQ ID NO: 23, 291, 324, 330, 341, and 353 correspond to novel members of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., *Trends Genet.* (1988) *4*:291) is a proto-oncogene induced by the integration of the mouse mammary tumor virus. It is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). The sequence of wnt-1 is highly conserved in mammals, fish, and amphibians. Wnt-1 was found to be a member of a large family of related proteins (Nusse R., *et al.*, *Cell* (1992) *69*:1073; McMahon A.P., *Trends Genet.* (1992) *8*:1; Moon R.T., *BioEssays* (1993) *15*:91) that are all thought to be developmental regulators. These proteins are known as wnt-2 (also known as irp), wnt-3, -3A, -4, -5A, -5B, -6, -7A, -7B, -8, -8B, -9 and -10. At least four members of this family are present in Drosophila; one of them, wingless (wg), is implicated in segmentation polarity. All these proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C. All sequences known to belong to this family are detected by the provided consensus pattern.

s) <u>Ww/rsp5/WWP Domain-Containing Proteins.</u> SEQ ID NOS:188, 379 , and 395 represent polynucleotides encoding a polypeptide in the family of WW/rsp5/WWP domain-

containing proteins. The WW domain (Bork *et al.*, *Trends Biochem. Sci.* (1994) *19*:531; Andre *et al.*, *Biochem. Biophys. Res. Commun.* (1994) *205*:1201; Hofmann *et al.*, *FEBS Lett.* (1995) *358*:153; and Sudol *et al.*, *FEBS Lett.* (1995) *369*:67), also known as rsp5 or WWP), was originally discovered as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown (Chen *et al.*, *Proc. Natl. Acad. Sci. USA* (1995) *92*:7819) to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions, generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

Proteins containing the WW domain include:

1. Dystrophin, a multidomain cytoskeletal protein. Its longest alternatively spliced form consists of an N-terminal actin-binding domain, followed by 24 spectrin-like repeats, a cysteine-rich calcium-binding domain and a C-terminal globular domain. Dystrophins form tetramers and is thought to have multiple functions including involvement in membrane stability, transduction of contractile forces to the extracellular environment and organization of membrane specialization. Mutations in the dystrophin gene lead to muscular dystrophy of Duchenne or Becker type. Dystrophin contains one WW domain C-terminal of the spectrin-repeats.

2. Vertebrate YAP protein, which is a substrate of an unknown serine kinase. It binds to the SH3 domain of the Yes oncoprotein via a proline-rich region. This protein appears in alternatively spliced isoforms, containing either one or two WW domains.

3. IQGAP, which is a human GTPase activating protein acting on ras. It contains an N-terminal domain similar to fly muscle mp20 protein and a C-terminal ras GTPase activator domain.

For the sensitive detection of WW domains, the profile spans the whole homology region as well as a pattern. The consensus for this family is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

t) <u>Zinc Finger, C2H2 Type.</u> SEQ ID NO:61, 306, and 386 correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug *et al.*, *Trends Biochem. Sci.* (1987) *12*:464; Evans *et al.*, *Cell* (1988) *52*:1; Payre *et al.*, *FEBS Lett.* (1988) *234*:245; Miller *et al.*, *EMBO J.* (1985) *4*:1609;

and Berg, *Proc. Natl. Acad. Sci. USA* (1988) *85*:99) are nucleic acid-binding protein structures first identified in the Xenopus transcription factor TFIIIA. These domains have since been found in numerous nucleic acid-binding proteins. A zinc finger domain is composed of 25 to 30 amino acid residues. Two cysteine or histidine residues are positioned at both extremities of the domain, which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with about five nucleotides.

Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine residues involved in the zinc atom coordination. In the first class to be characterized, called C2H2, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc-dependent DNA or RNA binding property of some members of this class.

Mammalian proteins having a C2H2 zipper include (number in parenthesis indicates number of zinc finger regions in the protein): basonuclin (6), BCL-6/LAZ-3 (6), erythroid krueppel-like transcription factor (3), transcription factors Sp1 (3), Sp2 (3), Sp3 (3) and Sp(4) 3, transcriptional repressor YY1 (4), Wilms' tumor protein (4), EGR1/Krox24 (3), EGR2/Krox20 (3), EGR3/Pilot (3), EGR4/AT133 (4), Evi-1 (10), GLI1 (5), GLI2 (4+), GLI3 (3+), HIV-EP1/ZNF40 (4), HIV-EP2 (2), KR1 (9+), KR2 (9), KR3 (15+), KR4 (14+), KR5 (11+), HF.12 (6+), REX-1 (4), ZfX (13), ZfY (13), Zfp-35 (18), ZNF7 (15), ZNF8 (7), ZNF35 (10), ZNF42/MZF-1 (13), ZNF43 (22), ZNF46/Kup (2), ZNF76 (7), ZNF91 (36), ZNF133 (3).

In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al.*, *J. Biomol. Struct. Dyn.* (1993) *11*:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue.

The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

u) <u>Zinc Finger, CCHC Class.</u> SEQ ID NO:322 corresponds to a polynucleotide encoding a novel member of the zinc finger CCHC family. The CCHC zinc finger protein family to date has been mostly composed of retroviral gag proteins (nucleocapsid). The prototype structure of this family is from HIV. The family also contains members involved in eukaryotic gene regulation, such as C. elegans GLH-1. The consensus sequence of this family is based upon the common structure of an 18-residue zinc finger.

v) Zinc-Binding Metalloprotease Domain. SEQ ID NO:306 and 395 represent polynucleotides encoding novel members of the zinc-binding metalloprotease domain protein family. The majority of zinc-dependent metallopeptidases (with the notable exception of the carboxypeptidases) share a common pattern of primary structure (Jongeneel *et al.*, *FEBS Lett.* (1989) *242*:211; Murphy *et al.*, *FEBS Lett.* (1991) *289*:4; and Bode *et al.*, *Zoology* (1996) *99*:237) in the part of their sequence involved in the binding of zinc, and can be grouped together as a superfamily, known as the metzincins, on the basis of this sequence similarity. Examples of these proteins include: 1) Angiotensin-converting enzyme (EC 3.4.15.1) (dipeptidyl carboxypeptidase I) (ACE), the enzyme responsible for hydrolyzing angiotensin I to angiotensin II. 2) Mammalian extracellular matrix metalloproteinases (known as matrixins) (Woessner, *FASEB J.* (1991) *5*:2145): MMP-1 (EC 3.4.24.7) (interstitial collagenase), MMP-2 (EC 3.4.24.24) (72 Kd gelatinase), MMP-9 (EC 3.4.24.35) (92 Kd gelatinase), MMP-7 (EC 3.4.24.23) (matrylisin), MMP-8 (EC 3.4.24.34) (neutrophil collagenase), MMP-3 (EC 3.4.24.17) (stromelysin-1), MMP-10 (EC 3.4.24.22) (stromelysin-2), and MMP-11 (stromelysin-3), MMP-12 (EC 3.4.24.65) (macrophage metalloelastase). 3) Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1), which processes the precursor of endothelin to release the active peptide.

A signature pattern which includes the two histidine and the glutamic acid residues is sufficient to detect this superfamily of proteins, having the consensus pattern: [GSTALIVN]-x(2)-H-E-[LIVMFYW]-{DEHRKP}-H-x-[LIVMFYWGSPQ]. The two H's are zinc ligands, and E is the active site residue.

Example 4: Differential Expression of Polynucleotides of the Invention : Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 4 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Table 4 Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – bFGF treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – VEGF treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library "High Colon Tumor Tissue"	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	30956

The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) *53*:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, *e.g.*, Chandrasekaran *et al.*, *Cancer Res.* (1979) *39*:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) *41*:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) *77*:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) *26*:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) *40*:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) *11*:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) *10*:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) *15*:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) *8*:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3).

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) *37*(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the

highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1^{st}), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2^{nd}). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5 , where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Tables 5 to 7 (inserted before the claims) show the number of clones in each of the above libraries that were analyzed for differential expression. Examples of differentially expressed polynucleotides of particular interest are described in more detail below.

Example 5: Polynucleotides Differentially Expressed in High Metastatic Potential Breast Cancer Cells Versus Low Metastatic Breast Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential breast cancer tissue and low

metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

Table 8. Differentially expressed polynucleotides: High metastatic potential breast cancer vs. low metastatic breast cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
65	High Breast > Low Breast (Lib3 > Lib4)	5749	9	0	8.780930
66	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
68	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
114	High Breast > Low Breast (Lib3 > Lib4)	2030	32	4	7.805271
123	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
144	High Breast > Low Breast (Lib3 > Lib4)	4623	12	2	5.853953
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
178	High Breast > Low Breast (Lib3 > Lib4)	3681	10	1	9.756589
214	High Breast > Low Breast (Lib3 > Lib4)	3900	8	1	7.805271
219	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
223	High Breast > Low Breast (Lib3 > Lib4)	1399	19	7	2.648217
258	High Breast > Low Breast (Lib3 > Lib4)	4837	10	0	9.756589
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
4	Low Breast > High Breast (Lib4 > Lib3)	3706	22	4	5.637215
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
74	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
81	Low Breast > High Breast (Lib4 > Lib3)	40392	8	1	8.199586
130	Low Breast > High Breast (Lib4 > Lib3)	13183	7	0	7.174638
157	Low Breast > High Breast (Lib4 > Lib3)	5417	9	0	9.224535
162	Low Breast > High Breast (Lib4 > Lib3)	9685	7	0	7.174638
183	Low Breast > High Breast (Lib4 > Lib3)	7337	16	3	5.466391
202	Low Breast > High Breast (Lib4 > Lib3)	6124	9	1	9.224535
298	Low Breast > High Breast (Lib4 > Lib3)	1037	22	4	5.637215
338	Low Breast > High Breast (Lib4 > Lib3)	689	36	17	2.170478
384	Low Breast > High Breast (Lib4 > Lib3)	697	72	30	2.459876
386	Low Breast > High Breast (Lib4 > Lib3)	4568	9	0	9.224535
388	Low Breast > High Breast (Lib4 > Lib3)	5622	13	2	6.662164

Example 6: Polynucleotides Differentially Expressed in High Metastatic Potential Lung Cancer Cells Versus Low Metastatic Lung Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential lung cancer tissue and low metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these

polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

Table 9 Differentially expressed polynucleotides: High metastatic potential lung cancer vs. low metastatic lung cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
400	High Lung > Low Lung (Lib8 > Lib 9)	14929	23	16	2.008868
9	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
34	High Lung > Low Lung (Lib8 > Lib9)	5832	5	0	6.987366
42	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
62	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
106	High Lung > Low Lung (Lib8 > Lib9)	10717	8	0	11.17978
119	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
361	High Lung > Low Lung (Lib8 > Lib9)	1120	5	0	6.987366
369	High Lung > Low Lung (Lib8 > Lib9)	2790	6	0	8.384840
371	High Lung > Low Lung (Lib8 > Lib9)	8847	6	1	8.384840
379	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210
395	High Lung > Low Lung (Lib8 > Lib9)	13538	9	1	12.57726
135	Low Lung > High Lung (Lib9 > Lib8)	36313	30	1	21.46731
154	Low Lung > High Lung (Lib9 > Lib8)	5345	27	6	3.220097
160	Low Lung > High Lung (Lib9 > Lib8)	4386	21	3	5.009039
260	Low Lung > High Lung (Lib9 > Lib8)	4141	27	4	4.830145
308	Low Lung > High Lung (Lib9 > Lib8)	15855	213	12	12.70149
323	Low Lung > High Lung (Lib9 > Lib8)	5257	25	5	3.577885
349	Low Lung > High Lung (Lib9 > Lib8)	2797	14	1	10.01807
381	Low Lung > High Lung (Lib9 > Lib8)	2428	19	2	6.797982

Example 7: Polynucleotides Differentially Expressed in High Metastatic Potential Colon Cancer Cells Versus Low Metastatic Colon Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and low

metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

Table 11: Differentially expressed polynucleotides: High metastatic potential colon cancer vs. low metastatic colon cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
1	High Colon > Low Colon (Lib1 > Lib2)	6660	7	0	6.489973
176	High Colon > Low Colon (Lib1 > Lib2)	3765	19	6	2.935940
241	High Colon > Low Colon (Lib1 > Lib2)	4275	11	2	5.099264
362	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
374	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
39	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
97	Low Colon > High Colon (Lib2 > Lib1)	945	21	9	2.516702
134	Low Colon > High Colon (Lib2 > Lib1)	2464	19	5	4.098630
317	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
357	Low Colon > High Colon (Lib2 > Lib1)	4309	13	4	3.505407

Example 8: Polynucleotides Differentially Expressed at Higher Levels in High Metastatic Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be

indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

Table 11: Differentially expressed polynucleotides: High metastatic potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
52	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
52	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
172	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930

Example 9: Polynucleotides Differentially Expressed at Higher Levels in High Colon Tumor Potential Patient Tissue Versus Metastasized Colon Cancer Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

Table 12: Differentially expressed polynucleotides: High tumor potential colon tissue vs. metastatic colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
52	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
172	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	102	43	10	3.216168

Example 10: Polynucleotides Differentially Expressed at Higher Levels in High Tumor Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

Table 13: Differentially expressed polynucleotides: High tumor potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
52	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
288	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	1267	7	0	6.125253
52	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
119	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
172	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222

Example 11: Polynucleotides Differentially Expressed Across Multiple Libraries

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across all three tissue types tested (*i.e.*, breast, colon, and lung). Expression of these sequences in a tissue or any origin can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following table summarizes identified polynucleotides that were differentially expressed but without tissue type-specificity in the breast, colon, and lung libraries tested.

Table 14: Polynucleotides Differentially Expressed Across Multiple Library Comparisons

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930
	High Colon Tumor Tissue > Metastasis	102	43	10	3.216168

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1st Library	Clones in 2nd Library	Ratio
	Tissue of UC#3 (Lib19 > Lib20)				
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210

Example 12: Polynucleotides Exhibiting Colon-Specific Expression

The cDNA libraries described herein were also analyzed to identify those polynucleotides that were specifically expressed in colon cells or tissue, *i.e.*, the polynucleotides were identified in libraries prepared from colon cell lines or tissue, but not in libraries of breast or lung origin. The polynucleotides that were expressed in a colon cell line and/or in colon tissue, but were present in the breast or lung cDNA libraries described herein, are shown in Table 15.

Table 15 Polynucleotides specifically expressed in colon cells.

SEQ ID NO.	Cluster	Clones in 1st Library	Clones in 2nd Library	SEQ ID NO.	Cluster	Clones in 1st Library	Clones in 2nd Library
5	36535	2	0	229	39648	2	0
13	27250	2	0	231	85064	1	0
19	16283	3	0	234	39391	2	0
24	16918	4	0	236	39498	2	0
26	40108	2	0	242	22113	3	0
32	32663	1	1	247	19255	2	0
43	39833	2	0	252	22814	3	0
47	18957	3	0	253	39563	2	0
48	39508	2	0	254	39420	2	0
56	7005	8	2	257	39412	2	0
58	18957	3	0	261	38085	2	0
59	18957	3	0	265	40054	1	0
60	16283	3	0	266	39423	2	0
64	13238	4	1	267	39453	2	0
70	39442	2	0	270	78091	1	0
71	17036	4	0	276	39168	2	0
73	7005	8	2	277	39458	2	0
83	11476	6	0	278	14391	3	1
86	39425	2	0	279	39195	2	0
94	21847	2	1	282	12977	5	0
100	16731	3	1	284	14391	3	1
101	12439	4	0	290	16347	4	0
113	17055	4	0	293	39478	2	0
120	67907	1	0	294	39392	2	0
121	12081	4	0	297	39180	2	0
124	39174	2	0	299	6867	7	3

SEQ ID NO.	Cluster	Clones in 1st Library	Clones in 2nd Library	SEQ ID NO.	Cluster	Clones in 1st Library	Clones in 2nd Library
126	8210	2	6	301	41633	1	1
128	40455	2	0	302	23218	3	0
139	22195	3	0	303	39380	2	0
143	86859	1	0	309	84328	1	0
150	8672	4	4	314	14367	3	0
153	16977	4	0	320	39886	2	0
156	17036	4	0	324	9061	5	2
159	40044	2	0	327	16653	3	1
161	40044	2	0	328	16985	4	0
163	22155	3	0	329	12977	5	0
166	15066	4	0	330	9061	5	2
170	11465	5	0	333	16392	3	0
176	3765	19	6	342	39486	2	0
181	86110	1	0	344	6874	6	3
182	39648	2	0	345	6874	6	3
185	17076	4	0	353	11494	4	0
186	22794	2	0	354	17062	3	0
187	39171	2	0	355	16245	4	0
194	40455	2	0	356	83103	1	0
199	16317	3	0	358	13072	4	1
210	39186	2	0	366	14364	1	0
211	40122	2	0	368	84182	1	0
218	26295	2	0	372	56020	1	0
222	4665	5	9	389	7514	5	3
226	82498	1	0	391	7570	5	3
227	35702	2	0	393	23210	3	0

In addition to the above, SEQ ID NOS:159 and 161 were each present in one clone in each of Lib16 (Normal Colon Tumor Tissue), and SEQ ID NOS:344 and 345 were each present in one clone in Lib17 (High Colon Metastasis Tissue). No clones corresponding to the colon-specific polynucleotides in the table above were present in any of Libraries 3, 4, 8, or 9. The polynucleotide provided above can be used as markers of cells of colon origin, and find particular use in reference arrays, as described above.

Example 13: Identification of Contiguous Sequences Having a Polynucleotide of the Invention

The novel polynucleotides were used to screen publicly available and proprietary databases to determine if any of the polynucleotides of SEQ ID NOS:1-404 would facilitate identification of a contiguous sequence, *e.g.*, the polynucleotides would provide sequence that would result in 5' extension of another DNA sequence, resulting in production of a longer contiguous sequence composed of the provided polynucleotide and the other DNA sequence(s). Contiging was performed using the AssemblyLign program with the following

parameters: 1) Overlap: Minimum Overlap Length: 30; % Stringency: 50; Minimum Repeat Length: 30; Alignment: gap creation penalty: 1.00, gap extension penalty: 1.00; 2) Consensus: % Base designation threshold: 80.

Using these parameters, 44 polynucleotides provided contiged sequences. These contiged sequences are provided as SEQ ID NOS:801-844. The contiged sequences can be correlated with the sequences of SEQ ID NOS:1-404 upon which the contiged sequences are based by identifying those sequences of SEQ ID NOS:1-404 and the contiged sequences of SEQ ID NOS:801-844 that share the same clone name in Table 1. It should be noted that of these 44 sequences that provided a contiged sequence, the following members of that group of 44 did not contig using the overlap settings indicated in parentheses (Stringency/Overlap): SEQ ID NO:804 (30%/10); SEQ ID NO:810 (20%/20); SEQ ID NO:812 (30%/10); SEQ ID NO:814 (40%/20); SEQ ID NO:816 (30%/10); SEQ ID NO:832 (30%/10); SEQ ID NO:840 (20%/20); SEQ ID NO:841 (40%/20). To generalize, the indicated polynucleotides did not contig using a minimum 20% stringency, 10 overlap. There was a corresponding increase in the number of degenerate codons in these sequences.

The contiged sequences (SEQ ID NO:801-844) thus represent longer sequences that encompass a polynucleotide sequence of the invention. The contiged sequences were then translated in all three reading frames to determine the best alignment with individual sequences using the BLAST programs as described above for SEQ ID NOS:1-404 and the validation sequences SEQ ID NOS:405-800. Again the sequences were masked using the XBLAST profram for masking low complexity as described above in Example 1 (Table 2). Several of the contiged sequences were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 16). Thus the invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Table 16. Profile hits using contiged sequences

SEQ ID NO.	Sequence Name	Profile	Start (Stop)	Score
809	Contig_RTA00000177AF.n.18.3. Seq_THC123051	ATPases	778 (1612)	6040
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	homeobox	531 (707)	12080
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	MAP kinase kinase	769 (1494)	5784
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027

All stop/start sequences are provided in the forward direction.

The profiles for the ATPases (AAA) and protein kinase families are described above in Example 2. The homeobox and MAP kinase kinase protein families are described further below.

Homeobox domain. The 'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerglin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) *17*:277-280; Gehring *et al Annu. Rev. Genet.* (1986) *20*:147-173; Schofield *Trends Neurosci.* (1987) *10*:3-6; http://copan.bioz.unibas.ch/ homeo.html) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

```
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxHHHHHHHHtttHHHHHHHHHxxxxxxxxxx
1                                                            60
```

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

MAP kinase kinase (MAPKK). MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic module activated in distinct pathways in yeast and in vertebrates. MAPKK regulation studies have led to the discovery of at least four MAPKK convergent pathways in higher organisms. One of these is similar to the yeast pheromone response pathway which includes the ste11 protein kinase. Two other pathways require the activation of either one or both of the serine/threonine kinase-encoded oncogenes c-Raf-1 and c-Mos. Additionally, several studies suggest a possible effect of the cell cycle control regulator cyclin-dependent kinase 1 (cdc2) on MAPKK activity. Finally, MAPKKs are apparently essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, Biologique *Biol Cell* (1993) *79*:193-207; Nishida *et al.*, *Trends Biochem Sci* (1993) *18*:128-31; Ruderman *Curr Opin Cell Biol* (1993) *5*:207-13; Dhanasekaran *et al.*, *Oncogene* (1998) *17*:1447-55; Kiefer *et al.*, *Biochem Soc Trans* (1997) *25*:491-8; and Hill, *Cell Signal* (1996) *8*:533-44.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection: CMCC = (Chiron Master Culture Collection)

Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

CDNA Library Deposits

cDNA Library ES1 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001395A:C03	4016	79.A1.sp6:130016.Seq
M00001395A:C03	4016	RTA00000118A.c.4.1
M00001449A:D12	3681	RTA00000131A.g.15.2
M00001449A:D12	3681	79.E1.sp6:130064.Seq
M00001452A:D08	1120	79.C2.sp6:130041.Seq
M00001452A:D08	1120	RTA00000118A.p.15.3
M00001513A:B06	4568	79.D4.sp6:130055.Seq
M00001513A:B06	4568	RTA00000122A.d.15.3
M00001517A:B07	4313	79.F4.sp6:130079.Seq
M00001517A:B07	4313	RTA00000122A.n.3.1
M00001533A:C11	2428	RTA00000123A.l.21.1
M00001533A:C11	2428	79.A5.sp6:130020.Seq
M00001533A:C11	2428	RTA00000123A.l.21.1.Seq_THC205063
M00001542A:A09	22113	79.F5.sp6:130080.Seq
M00001542A:A09	22113	RTA00000125A.c.7.1

cDNA Library ES2 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001343C:F10	2790	80.E1.sp6:130256.Seq
M00001343C:F10	2790	RTA00000177AF.e.2.1.Seq_THC229461
M00001343C:F10	2790	RTA00000177AF.e.2.1
M00001343D:H07	23255	100.C1.sp6:131446.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3.Seq_THC228776
M00001343D:H07	23255	80.F1.sp6:130268.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3
M00001345A:E01	6420	172.E1.sp6:133925.Seq
M00001345A:E01	6420	RTA00000177AF.f.10.3
M00001345A:E01	6420	RTA00000177AF.f.10.3.Seq_THC226443
M00001345A:E01	6420	80.G1.sp6:130280.Seq
M00001347A:B10	13576	80.D2.sp6:130245.Seq
M00001347A:B10	13576	100.E1.sp6:131470.Seq
M00001347A:B10	13576	RTA00000177AF.g.16.1
M00001353A:G12	8078	80.E3.sp6:130258.Seq
M00001353A:G12	8078	RTA00000177AR.l.13.1
M00001353A:G12	8078	172.C3.sp6:133903.Seq
M00001353D:D10	14929	RTA00000177AF.m.1.2
M00001353D:D10	14929	80.F3.sp6:130270.Seq
M00001353D:D10	14929	172.D3.sp6:133915.Seq
M00001361A:A05	4141	80.B4.sp6:130223.Seq
M00001361A:A05	4141	RTA00000177AF.p.20.3
M00001362B:D10	5622	80.D4.sp6:130247.Seq
M00001362B:D10	5622	RTA00000178AF.a.11.1

cDNA Library ES3 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001362C:H11	945	RTA00000178AR.a.20.1
M00001362C:H11	945	100.E4.sp6:131473.Seq
M00001362C:H11	945	80.E4.sp6:130259.Seq
M00001362C:H11	945	180.C2.sp6:135940.Seq
M00001376B:G06	17732	RTA00000178AR.i.2.2
M00001376B:G06	17732	80.B5.sp6:130224.Seq
M00001387A:C05	2464	80.D6.sp6:130249.Seq
M00001387A:C05	2464	RTA00000178AF.n.18.1
M00001412B:B10	8551	RTA00000179AF.p.21.1
M00001412B:B10	8551	80.G7.sp6:130286.Seq
M00001415A:H06	13538	80.B8.sp6:130227.Seq
M00001415A:H06	13538	RTA00000180AF.a.24.1
M00001416B:H11	8847	80.C8.sp6:130239.Seq
M00001416B:H11	8847	RTA00000180AF.b.16.1
M00001429D:D07	40392	RTA00000180AF.j.8.1
M00001429D:D07	40392	80.H9.sp6:130300.Seq
M00001448D:H01	36313	80.A11.sp6:130218.Seq
M00001448D:H01	36313	RTA00000181AF.e.23.1

cDNA Library ES4 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001463C:B11	19	RTA00000182AF.b.7.1
M00001463C:B11	19	89.D1.sp6:130703.Seq
M00001470A:B10	1037	89.F2.sp6:130728.Seq
M00001470A:B10	1037	RTA00000121A.f.8.1
M00001497A:G02	2623	89.F3.sp6:130729.Seq
M00001497A:G02	2623	RTA00000183AF.a.6.1
M00001500A:E11	2623	RTA00000183AF.b.14.1
M00001500A:E11	2623	89.A4.sp6:130670.Seq
M00001501D:C02	9685	RTA00000183AF.c.11.1.Seq_THC109544
M00001501D:C02	9685	RTA00000183AF.c.11.1
M00001501D:C02	9685	89.C4.sp6:130694.Seq
M00001504C:H06	6974	89.F4.sp6:130730.Seq
M00001504C:H06	6974	RTA00000183AF.d.9.1
M00001504C:H06	6974	RTA00000183AF.d.9.1.Seq_THC223129
M00001504D:G06	6420	173.F5.SP6:134133.Seq
M00001504D:G06	6420	89.G4.sp6:130742.Seq
M00001504D:G06	6420	RTA00000183AF.d.11.1.Seq_THC226443
M00001504D:G06	6420	RTA00000183AF.d.11.1
M00001528A:C04	35555	89.B6.sp6:130684.Seq
M00001528A:C04	7337	RTA00000123A.b.17.1
M00001528A:C04	35555	184.A5.sp6:135530.Seq

cDNA Library ES5 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001537B:G07	3389	RTA00000183AF.m.19.1
M00001537B:G07	3389	89.A8.sp6:130674.Seq
M00001541A:D02	3765	89.C8.sp6:130698.Seq
M00001541A:D02	3765	RTA00000135A.d.1.1
M00001544B:B07	6974	89.A9.sp6:130675.Seq
M00001544B:B07	6974	RTA00000184AF.a.15.1
M00001546A:G11	1267	89.D9.sp6:130711.Seq
M00001546A:G11	1267	RTA00000125A.o.5.1
M00001549B:F06	4193	89.G9.sp6:130747.Seq
M00001549B:F06	4193	RTA00000184AF.e.13.1
M00001556A:F11	1577	173.C9.SP6:134101.Seq
M00001556A:F11	1577	89.F11.sp6:130737.Seq
M00001556A:F11	1577	RTA00000184AF.i.23.1
M00001556B:C08	4386	RTA00000184AF.j.4.1
M00001556B:C08	4386	89.H11.sp6:130761.Seq

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Clone Name	Cluster ID	Sequence Name
M00001563B:F06	102	RTA00000184AF.o.5.1
M00001563B:F06	102	90.B1.sp6:130871.Seq
M00001571C:H06	5749	90.E1.sp6:130907.Seq
M00001571C:H06	5749	RTA00000185AF.a.19.1
M00001594B:H04	260	90.D2.sp6:130896.Seq
M00001594B:H04	260	RTA00000185AR.i.12.2
M00001597C:H02	4837	90.E2.sp6:130908.Seq
M00001597C:H02	4837	RTA00000185AR.k.3.2
M00001624C:F01	4309	90.C4.sp6:130886.Seq
M00001624C:F01	4309	RTA00000186AF.e.22.1
M00001679A:A06	6660	90.F6.sp6:130924.Seq
M00001679A:A06	6660	122.B5.sp6:132089.Seq
M00001679A:A06	6660	RTA00000187AF.h.15.1
M00003759B:B09	697	90.G8.sp6:130938.Seq
M00003759B:B09	697	RTA00000188AF.d.6.1
M00003759B:B09	697	RTA00000188AF.d.6.1.Seq_THC178884
M00003844C:B11	6539	176.D9.sp6:134556.Seq
M00003844C:B11	6539	RTA00000189AF.d.22.1
M00003844C:B11	6539	90.B10.sp6:130880.Seq
M00003857A:G10	3389	90.A11.sp6:130869.Seq
M00003857A:G10	3389	RTA00000189AF.g.3.1

cDNA Library ES7 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003914C:F05	3900	99.E1.sp6:131278.Seq
M00003914C:F05	3900	RTA00000190AF.g.13.1
M00003922A:E06	23255	RTA00000190AF.j.4.1
M00003922A:E06	23255	99.F1.sp6:131290.Seq
M00003922A:E06	23255	RTA00000190AF.j.4.1.Seq_THC228776
M00003983A:A05	9105	99.C3.sp6:131256.Seq
M00003983A:A05	9105	RTA00000191AF.a.21.2
M00004028D:A06	6124	RTA00000191AR.e.2.3
M00004028D:A06	6124	99.D3.sp6:131268.Seq
M00004031A:A12	9061	RTA00000191AR.e.11.2
M00004031A:A12	9061	RTA00000191AR.e.11.3
M00004087D:A01	6880	RTA00000191AF.m.20.1
M00004087D:A01	6880	99.A5.sp6:131234.Seq
M00004108A:E06	4937	99.E5.sp6:131282.Seq
M00004108A:E06	4937	RTA00000191AF.p.21.1
M00004114C:F11	13183	123.D5.sp6:132305.Seq
M00004114C:F11	13183	RTA00000192AF.a.24.1
M00004114C:F11	13183	99.G5.sp6:131306.Seq

cDNA Library ES8 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004146C:C11	5257	99.B6.sp6:131247.Seq
M00004146C:C11	5257	177.F5.sp6:134768.Seq
M00004146C:C11	5257	RTA00000192AF.f.3.1
M00004146C:C11	5257	RTA00000192AF.f.3.1.Seq_THC213833
M00004157C:A09	6455	RTA00000192AF.g.23.1
M00004157C:A09	6455	99.D6.sp6:131271.Seq
M00004157C:A09	6455	123.E7.sp6:132319.Seq
M00004172C:D08	11494	RTA00000192AF.j.6.1
M00004172C:D08	11494	99.G6.sp6:131307.Seq
M00004172C:D08	11494	177.E6.sp6:134757.Seq
M00004229B:F08	6455	RTA00000193AF.b.9.1
M00004229B:F08	6455	99.C8.sp6:131261.Seq

cDNA Library ES9 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001466A:E07	4275	RTA00000120A.j.14.1
M00001531A:H11		89.F6.sp6:130732.Seq
M00001531A:H11		RTA00000123A.g.19.1
M00001551A:B10	6268	79.G9.sp6:130096.Seq
M00001551A:B10	6268	184.C12.sp6:135561.Seq
M00001551A:B10	6268	RTA00000126A.o.23.1
M00001552A:B12	307	RTA00000136A.o.4.2
M00001552A:B12	307	79.C7.sp6:130046.Seq
M00001556A:H01	15855	RTA00000184AF.j.1.1
M00001586C:C05	4623	RTA00000185AF.f.4.1
M00001604A:B10	1399	79.G8.sp6:130095.Seq
M00001604A:B10	1399	RTA00000129A.o.10.1
M00003879B:C11	5345	RTA00000189AF.l.19.1
M00003879B:C11	5345	90.B12.sp6:130882.Seq

cDNA Library ES10 - ATCC#
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Clone Name	Cluster ID	Sequence Name
M00001358C:C06		RTA00000177AF.o.4.3
M00001388D:G05	5832	80.F6.sp6:130273.Seq
M00001388D:G05	5832	RTA00000178AF.o.23.1
M00001394A:F01	6583	RTA00000179AF.d.13.1
M00001394A:F01	6583	172.B8.sp6:133896.Seq
M00001394A:F01	6583	80.H6.sp6:130297.Seq
M00001429A:H04	2797	RTA00000180AF.i.19.1
M00001447A:G03	10717	RTA00000181AF.d.10.1
M00001448D:C09	8	80.H10.sp6:130301.Seq
M00001448D:C09	8	RTA00000181AF.e.17.1
M00001448D:C09	8	100.B11.sp6:131444.Seq
M00001454D:G03	689	RTA00000181AR.l.22.1

cDNA Library ES11 - ATCC#
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Clone Name	Cluster ID	Sequence Name
M00003975A:G11	12439	RTA00000190AF.o.24.1
M00003978B:G05	5693	RTA00000190AF.p.17.2.Seq_THC173318
M00003978B:G05	5693	RTA00000190AF.p.17.2
M00004059A:D06	5417	RTA00000191AF.h.19.1
M00004068B:A01	3706	99.C4.sp6:131257.Seq
M00004068B:A01	3706	RTA00000191AF.i.17.2
M00004205D:F06		99.E7.sp6:131284.Seq
M00004205D:F06		177.G7.sp6:134782.Seq
M00004205D:F06		RTA00000192AF.o.11.1
M00004212B:C07	2379	RTA00000192AF.p.8.1
M00004223A:G10	16918	RTA00000193AF.a.16.1

cDNA Library ES12 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004223B:D09	7899	RTA00000193AF.a.17.1
M00004249D:G12		RTA00000193AF.c.22.1
M00004251C:G07		RTA00000193AF.d.2.1
M00004372A:A03	2030	RTA00000193AF.m.20.1

cDNA Library ES13 - ATCC#
Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001340B:A06	17062	80.A1.sp6:130208.Seq
M00001340B:A06	17062	RTA00000177AF.b.8.4
M00001340D:F10	11589	80.B1.sp6:130220.Seq
M00001340D:F10	11589	RTA00000177AF.b.17.4
M00001341A:E12	4443	80.C1.sp6:130232.Seq
M00001341A:E12	4443	RTA00000177AF.b.20.4
M00001342B:E06	39805	80.D1.sp6:130244.Seq
M00001342B:E06	39805	RTA00000177AF.c.21.3
M00001346A:F09	5007	RTA00000177AF.g.2.1
M00001346A:F09	5007	80.H1.sp6:130292.Seq
M00001346D:G06	5779	RTA00000177AF.g.14.3
M00001346D:G06	5779	RTA00000177AF.g.14.1
M00001348B:B04	16927	80.E2.sp6:130257.Seq
M00001348B:B04	16927	RTA00000177AF.h.9.3
M00001348B:G06	16985	RTA00000177AF.h.10.1
M00001348B:G06	16985	80.F2.sp6:130269.Seq
M00001349B:B08	3584	RTA00000177AF.h.20.1
M00001349B:B08	3584	80.G2.sp6:130281.Seq
M00001350A:H01	7187	100.C2.sp6:131447.Seq
M00001350A:H01	7187	80.A3.sp6:130210.Seq
M00001350A:H01	7187	RTA00000177AF.i.8.2
M00001352A:E02	16245	RTA00000177AF.k.9.3
M00001352A:E02	16245	172.D2.sp6:133914.Seq
M00001352A:E02	16245	80.D3.sp6:130246.Seq
M00001355B:G10	14391	RTA00000177AF.m.17.3
M00001355B:G10	14391	80.G3.sp6:130282.Seq
M00001355B:G10	14391	172.H3.sp6:133963.Seq
M00001355B:G10	14391	100.E3.sp6:131472.Seq
M00001361D:F08	2379	80.C4.sp6:130235.Seq
M00001361D:F08	2379	RTA00000178AF.a.6.1
M00001365C:C10	40132	RTA00000178AF.c.7.1
M00001365C:C10	40132	80.F4.sp6:130271.Seq
M00001368D:E03		80.G4.sp6:130283.Seq
M00001368D:E03		RTA00000178AF.d.20.1
M00001370A:C09	6867	80.H4.sp6:130295.Seq
M00001370A:C09	6867	RTA00000178AF.e.12.1
M00001371C:E09	7172	100.A5.sp6:131426.Seq
M00001371C:E09	7172	RTA00000178AF.f.9.1
M00001371C:E09	7172	80.A5.sp6:130212.Seq
M00001378B:B02	39833	80.C5.sp6:130236.Seq
M00001378B:B02	39833	RTA00000178AF.i.23.1
M00001379A:A05	1334	80.D5.sp6:130248.Seq
M00001379A:A05	1334	RTA00000178AF.j.7.1
M00001380D:B09	39886	RTA00000178AF.j.24.1
M00001380D:B09	39886	80.E5.sp6:130260.Seq
M00001381D:E06		80.F5.sp6:130272.Seq
M00001381D:E06		RTA00000178AF.k.16.1
M00001382C:A02	22979	80.G5.sp6:130284.Seq
M00001382C:A02	22979	RTA00000178AF.k.22.1
M00001384B:A11		80.B6.sp6:130225.Seq
M00001384B:A11		RTA00000178AF.m.13.1
M00001386C:B12	5178	80.C6.sp6:130237.Seq

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Clone Name	Cluster ID	Sequence Name
M00001386C:B12	5178	RTA00000178AF.n.10.1
M00001387B:G03	7587	80.E6.sp6:130261.Seq
M00001387B:G03	7587	RTA00000178AF.n.24.1
M00001389A:C08	16269	RTA00000178AF.p.1.1
M00001389A:C08	16269	80.G6.sp6:130285.Seq
M00001396A:C03	4009	172.D8.sp6:133920.Seq
M00001396A:C03	4009	80.A7.sp6:130214.Seq
M00001396A:C03	4009	RTA00000179AF.e.20.1
M00001400B:H06		172.B9.sp6:133897.Seq
M00001400B:H06		80.B7.sp6:130226.Seq
M00001400B:H06		RTA00000179AF.j.13.1
M00001400B:H06		RTA00000179AF.j.13.1.Seq_THC105720
M00001402A:E08	39563	80.C7.sp6:130238.Seq
M00001402A:E08	39563	RTA00000179AF.k.20.1
M00001407B:D11	5556	RTA00000179AF.n.10.1
M00001407B:D11	5556	80.D7.sp6:130250.Seq
M00001410A:D07	7005	180.H5.sp6:136003.Seq
M00001410A:D07	7005	RTA00000179AF.o.22.1
M00001410A:D07	7005	80.F7.sp6:130274.Seq
M00001414A:B01		RTA00000180AF.a.9.1
M00001414A:B01		80.H7.sp6:130298.Seq
M00001414C:A07		80.A8.sp6:130215.Seq
M00001414C:A07		RTA00000180AF.a.11.1
M00001416A:H01	7674	79.C1.sp6:130040.Seq
M00001416A:H01	7674	RTA00000118A.g.9.1
M00001417A:E02	36393	RTA00000180AF.c.2.1
M00001417A:E02	36393	80.D8.sp6:130251.Seq
M00001423B:E07	15066	RTA00000180AF.e.24.1
M00001423B:E07	15066	80.H8.sp6:130299.Seq
M00001424B:G09	10470	80.A9.sp6:130216.Seq
M00001424B:G09	10470	RTA00000180AF.f.18.1
M00001425B:H08	22195	RTA00000180AF.g.7.1
M00001425B:H08	22195	80.B9.sp6:130228.Seq
M00001426B:D12		RTA00000180AF.g.22.1
M00001426B:D12		80.C9.sp6:130240.Seq
M00001426D:C08	4261	80.D9.sp6:130252.Seq
M00001426D:C08	4261	RTA00000180AF.h.5.1
M00001428A:H10	84182	100.G9.sp6:131502.Seq
M00001428A:H10	84182	RTA00000180AF.h.19.1
M00001428A:H10	84182	80.E9.sp6:130264.Seq
M00001449A:A12	5857	80.B11.sp6:130230.Seq
M00001449A:A12	5857	RTA00000118A.g.14.1
M00001449A:B12	41633	80.C11.sp6:130242.Seq
M00001449A:B12	41633	RTA00000118A.g.16.1
M00001449A:G10	36535	RTA00000181AF.f.5.1
M00001449A:G10	36535	80.D11.sp6:130254.Seq
M00001449A:G10	36535	100.D11.sp6:131468.Seq
M00001449C:D06	86110	RTA00000181AF.f.12.1
M00001449C:D06	86110	80.E11.sp6:130266.Seq
M00001450A:A02	39304	RTA00000118A.j.21.1.Seq_THC151859
M00001450A:A02	39304	RTA00000118A.j.21.1
M00001450A:A02	39304	79.F1.sp6:130076.Seq

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Clone Name	Cluster ID	Sequence Name
M00001450A:A02	39304	180.G9.sp6:135995.Seq
M00001450A:A11	32663	80.F11.sp6:130278.Seq
M00001450A:A11	32663	RTA00000118A.l.8.1
M00001450A:B12	82498	100.F11.sp6:131492.Seq
M00001450A:B12	82498	RTA00000118A.m.10.1
M00001450A:B12	82498	79.G1.sp6:130088.Seq
M00001450A:D08	27250	80.G11.sp6:130290.Seq
M00001450A:D08	27250	180.B10.sp6:135936.Seq
M00001450A:D08	27250	RTA00000181AF.g.10.1
M00001452A:B04	84328	RTA00000118A.p.10.1
M00001452A:B04	84328	79.A2.sp6:130017.Seq
M00001452A:B12	86859	RTA00000118A.p.8.1
M00001452A:B12	86859	79.B2.sp6:130029.Seq
M00001452A:F05	85064	RTA00000131A.m.23.1
M00001452A:F05	85064	79.D2.sp6:130053.Seq
M00001452C:B06	16970	80.H11.sp6:130302.Seq
M00001452C:B06	16970	100.C12.sp6:131457.Seq
M00001452C:B06	16970	RTA00000181AR.i.18.2
M00001453A:E11	16130	80.A12.sp6:130219.Seq
M00001453A:E11	16130	100.D12.sp6:131469.Seq
M00001453A:E11	16130	RTA00000119A.c.13.1
M00001453C:F06	16653	80.B12.sp6:130231.Seq
M00001453C:F06	16653	RTA00000181AF.k.5.3
M00001454A:A09	83103	RTA00000119A.e.24.2
M00001454A:A09	83103	79.G2.sp6:130089.Seq
M00001454B:C12	7005	121.D1.sp6:131917.Seq
M00001454B:C12	7005	RTA00000181AF.k.24.1
M00001454B:C12	7005	80.C12.sp6:130243.Seq
M00001455B:E12	13072	80.F12.sp6:130279.Seq
M00001455B:E12	13072	RTA00000181AR.m.5.2
M00001460A:F06	2448	89.A1.sp6:130667.Seq
M00001460A:F06	2448	RTA00000119A.j.21.1
M00001461A:D06	1531	89.C1.sp6:130691.Seq
M00001461A:D06	1531	RTA00000119A.o.3.1
M00001465A:B11	10145	79.F3.sp6:130078.Seq
M00001465A:B11	10145	RTA00000120A.g.12.1
M00001467A:B07	38759	89.F1.sp6:130727.Seq
M00001467A:B07	38759	RTA00000120A.m.12.3
M00001467A:D04	39508	RTA00000120A.o.2.1
M00001467A:D04	39508	89.G1.sp6:130739.Seq
M00001467A:E10	39442	89.A2.sp6:130668.Seq
M00001467A:E10	39442	RTA00000120A.o.21.1
M00001468A:F05	7589	RTA00000120A.p.23.1
M00001468A:F05	7589	89.B2.sp6:130680.Seq
M00001469A:A01		RTA00000121A.c.10.1
M00001469A:A01		89.C2.sp6:130692.Seq
M00001469A:C10	12081	89.D2.sp6:130704.Seq
M00001469A:C10	12081	RTA00000133A.d.14.2
M00001469A:H12	19105	89.E2.sp6:130716.Seq
M00001469A:H12	19105	RTA00000133A.e.15.1
M00001470A:C04	39425	89.G2.sp6:130740.Seq
M00001470A:C04	39425	RTA00000133A.f.1.1

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Clone Name	Cluster ID	Sequence Name
M00001471A:B01	39478	89.H2.sp6:130752.Seq
M00001471A:B01	39478	RTA00000133A.i.5.1
M00001487B:H06		RTA00000182AF.l.15.1
M00001487B:H06		89.B3.sp6:130681.Seq
M00001488B:F12		RTA00000182AF.l.20.1
M00001488B:F12		89.C3.sp6:130693.Seq
M00001494D:F06	7206	RTA00000182AF.o.15.1
M00001494D:F06	7206	89.E3.sp6:130717.Seq
M00001499B:A11	10539	RTA00000183AF.a.24.1
M00001499B:A11	10539	89.G3.sp6:130741.Seq
M00001499B:A11	10539	173.B5.SP6:134085.Seq
M00001500A:C05	5336	RTA00000183AF.b.13.1
M00001500A:C05	5336	89.H3.sp6:130753.Seq
M00001504A:E01		RTA00000183AF.c.24.1
M00001504A:E01		89.D4.sp6:130706.Seq
M00001504A:E01		RTA00000183AF.c.24.1.Seq_THC125912
M00001504C:A07	10185	RTA00000183AF.d.5.1
M00001504C:A07	10185	89.E4.sp6:130718.Seq
M00001505C:C05		89.H4.sp6:130754.Seq
M00001505C:C05		RTA00000183AF.e.1.1
M00001506D:A09		89.A5.sp6:130671.Seq
M00001506D:A09		RTA00000183AF.e.23.1
M00001506D:A09		121.G6.sp6:131958.Seq
M00001507A:H05	39168	RTA00000121A.l.10.1
M00001507A:H05	39168	89.B5.sp6:130683.Seq
M00001535A:F10	39423	79.C5.sp6:130044.Seq
M00001535A:F10	39423	RTA00000134A.k.22.1
M00001541A:H03	39174	79.E5.sp6:130068.Seq
M00001541A:H03	39174	RTA00000124A.n.13.1
M00001544A:G02	19829	79.H5.sp6:130104.Seq
M00001544A:G02	19829	RTA00000125A.h.24.4
M00001545A:D08	13864	RTA00000125A.m.9.1
M00001545A:D08	13864	79.B6.sp6:130033.Seq
M00001551A:F05	39180	RTA00000126A.n.8.2
M00001551A:F05	39180	79.A7.sp6:130022.Seq
M00001552A:D11	39458	RTA00000126A.p.15.2
M00001552A:D11	39458	79.D7.sp6:130058.Seq
M00001557A:F03	39490	RTA00000128A.b.4.1

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Clone Name	Cluster ID	Sequence Name
M00001511A:H06	39412	RTA00000133A.k.17.1
M00001511A:H06	39412	89.C5.sp6:130695.Seq
M00001512A:A09	39186	89.D5.sp6:130707.Seq
M00001512A:A09	39186	RTA00000121A.p.15.1
M00001512D:G09	3956	89.E5.sp6:130719.Seq
M00001512D:G09	3956	173.H5.SP6:134157.Seq
M00001512D:G09	3956	RTA00000183AF.g.3.1
M00001513B:G03		RTA00000183AF.g.9.1
M00001513B:G03		89.F5.sp6:130731.Seq
M00001513B:G03		RTA00000183AF.g.9.1.Seq_THC198280
M00001513C:E08	14364	RTA00000183AF.g.12.1
M00001513C:E08	14364	89.G5.sp6:130743.Seq
M00001514C:D11	40044	RTA00000183AF.g.22.1
M00001514C:D11	40044	RTA00000183AF.g.22.1.Seq_THC232899
M00001514C:D11	40044	89.H5.sp6:130755.Seq
M00001518C:B11	8952	89.A6.sp6:130672.Seq
M00001518C:B11	8952	RTA00000183AF.h.15.1
M00001528B:H04	8358	89.D6.sp6:130708.Seq
M00001528B:H04	8358	RTA00000183AF.i.5.1
M00001531A:D01	38085	RTA00000123A.e.15.1
M00001531A:D01	38085	89.E6.sp6:130720.Seq
M00001534A:C04	16921	RTA00000183AF.k.6.1
M00001534A:C04	16921	89.H6.sp6:130756.Seq
M00001534A:D09	5097	RTA00000134A.k.1.1
M00001534A:D09	5097	RTA00000134A.k.1.1.Seq_THC215869
M00001534C:A01	4119	RTA00000183AF.k.16.1
M00001534C:A01	4119	89.C7.sp6:130697.Seq
M00001535A:C06	20212	89.E7.sp6:130721.Seq
M00001535A:C06	20212	RTA00000134A.l.22.1.Seq_THC128232
M00001535A:C06	20212	RTA00000134A.l.22.1
M00001536A:B07	2696	RTA00000134A.m.13.1
M00001536A:B07	2696	89.F7.sp6:130733.Seq
M00001537A:F12	39420	89.H7.sp6:130757.Seq
M00001537A:F12	39420	RTA00000134A.o.23.1
M00001540A:D06	8286	89.B8.sp6:130686.Seq
M00001540A:D06	8286	RTA00000183AF.o.1.1
M00001542A:E06	39453	89.E8.sp6:130722.Seq
M00001542A:E06	39453	RTA00000135A.g.11.1
M00001544A:E06		RTA00000184AF.a.8.1
M00001544A:E06		173.G7.SP6:134147.Seq
M00001544A:E06		89.H8.sp6:130758.Seq
M00001545A:B02		89.B9.sp6:130687.Seq
M00001545A:B02		RTA00000135A.l.2.2
M00001548A:E10	5892	89.E9.sp6:130723.Seq
M00001548A:E10	5892	RTA00000184AF.d.11.1
M00001548A:E10	5892	RTA00000184AF.d.11.1.Seq_THC161896
M00001549C:E06	16347	89.H9.sp6:130759.Seq
M00001549C:E06	16347	RTA00000184AF.e.15.1
M00001550A:A03	7239	89.A10.sp6:130676.Seq
M00001550A:A03	7239	RTA00000126A.m.4.2
M00001550A:G01	5175	RTA00000184AF.f.3.1
M00001550A:G01	5175	89.B10.sp6:130688.Seq

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Clone Name	Cluster ID	Sequence Name
M00001551A:G06	22390	RTA00000136A.j.13.1
M00001551A:G06	22390	89.C10.sp6:130700.Seq
M00001551C:G09	3266	RTA00000184AR.g.1.1
M00001551C:G09	3266	89.D10.sp6:130712.Seq
M00001553A:H06	8298	RTA00000127A.d.19.1
M00001553A:H06	8298	89.G10.sp6:130748.Seq
M00001553B:F12	4573	89.H10.sp6:130760.Seq
M00001553B:F12	4573	RTA00000184AF.h.9.1
M00001555A:B02	39539	RTA00000127A.i.21.1
M00001555A:B02	39539	89.B11.sp6:130689.Seq
M00001555A:C01	39195	89.C11.sp6:130701.Seq
M00001555A:C01	39195	RTA00000137A.c.16.1
M00001555D:G10	4561	RTA00000184AF.i.21.1
M00001555D:G10	4561	89.D11.sp6:130713.Seq
M00001556A:C09	9244	89.E11.sp6:130725.Seq
M00001556A:C09	9244	RTA00000127A.l.3.1
M00001556B:G02	11294	RTA00000184AF.j.6.1
M00001556B:G02	11294	89.A12.sp6:130678.Seq
M00001557B:H10	5192	173.E9.SP6:134125.Seq
M00001557B:H10	5192	RTA00000184AF.k.2.1
M00001557B:H10	5192	89.D12.sp6:130714.Seq
M00001557D:D09	8761	RTA00000184AF.k.12.1
M00001557D:D09	8761	89.E12.sp6:130726.Seq
M00001558B:H11	7514	RTA00000184AF.k.21.1
M00001558B:H11	7514	89.G12.sp6:130750.Seq
M00001559B:F01		89.H12.sp6:130762.Seq
M00001559B:F01		RTA00000184AF.l.11.1
M00001560D:F10	6558	90.A1.sp6:130859.Seq
M00001560D:F10	6558	RTA00000184AF.m.21.1
M00001566B:D11		RTA00000184AF.p.3.1
M00001566B:D11		90.D1.sp6:130895.Seq
M00001583D:A10	6293	RTA00000185AF.e.11.1
M00001583D:A10	6293	90.A2.sp6:130860.Seq
M00001590B:F03		RTA00000185AF.g.11.1
M00001590B:F03		90.C2.sp6:130884.Seq
M00001597D:C05	10470	RTA00000185AF.k.6.1
M00001597D:C05	10470	90.F2.sp6:130920.Seq
M00001598A:G03	16999	90.G2.sp6:130932.Seq
M00001598A:G03	16999	RTA00000185AF.k.9.1
M00001601A:D08	22794	RTA00000138A.b.5.1
M00001601A:D08	22794	90.H2.sp6:130944.Seq
M00001607A:E11	11465	RTA00000185AF.m.19.1
M00001607A:E11	11465	90.A3.sp6:130861.Seq
M00001608A:B03	7802	RTA00000185AF.n.5.1
M00001608A:B03	7802	90.B3.sp6:130873.Seq
M00001608B:E03	22155	RTA00000185AF.n.9.1
M00001608B:E03	22155	90.C3.sp6:130885.Seq
M00001608D:A11		RTA00000185AF.n.12.1
M00001608D:A11		90.D3.sp6:130897.Seq
M00001614C:F10	13157	RTA00000186AF.a.6.1
M00001614C:F10	13157	90.E3.sp6:130909.Seq
M00001617C:E02	17004	RTA00000186AF.b.21.1

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Clone Name	Cluster ID	Sequence Name
M00001617C:E02	17004	90.F3.sp6:130921.Seq
M00001619C:F12	40314	90.G3.sp6:130933.Seq
M00001619C:F12	40314	RTA00000186AF.c.15.1
M00001621C:C08	40044	RTA00000186AF.d.1.1
M00001621C:C08	40044	RTA00000186AF.d.1.1.Seq_THC232899
M00001621C:C08	40044	90.H3.sp6:130945.Seq
M00001621C:C08	40044	122.E1.sp6:132121.Seq
M00001623D:F10	13913	RTA00000186AF.e.6.1
M00001623D:F10	13913	90.A4.sp6:130862.Seq
M00001632D:H07		RTA00000186AF.h.14.1.Seq_THC112525
M00001632D:H07		RTA00000186AF.h.14.1
M00001632D:H07		90.E4.sp6:130910.Seq
M00001632D:H07		176.A3.sp6:134514.Seq
M00001644C:B07	39171	RTA00000186AF.l.7.1
M00001644C:B07	39171	90.F4.sp6:130922.Seq
M00001644C:B07	39171	217.A12.sp6:139369.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1.Seq_THC178183
M00001645A:C12	19267	176.G3.sp6:134586.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1
M00001645A:C12	19267	90.G4.sp6:130934.Seq
M00001648C:A01	4665	90.H4.sp6:130946.Seq
M00001648C:A01	4665	RTA00000186AF.m.3.1
M00001657D:C03	23201	RTA00000187AF.a.14.1
M00001657D:C03	23201	90.B5.sp6:130875.Seq
M00001657D:F08	76760	90.C5.sp6:130887.Seq
M00001657D:F08	76760	RTA00000187AF.a.15.1
M00001662C:A09	23218	RTA00000187AR.c.5.2
M00001662C:A09	23218	90.D5.sp6:130899.Seq
M00001663A:E04	35702	90.E5.sp6:130911.Seq
M00001663A:E04	35702	RTA00000187AR.c.15.2
M00001669B:F02	6468	90.F5.sp6:130923.Seq
M00001669B:F02	6468	RTA00000187AF.d.15.1
M00001670C:H02	14367	90.G5.sp6:130935.Seq
M00001670C:H02	14367	RTA00000187AF.e.8.1
M00001673C:H02	7015	90.H5.sp6:130947.Seq
M00001673C:H02	7015	RTA00000187AF.f.18.1
M00001675A:C09	8773	RTA00000187AF.f.24.1
M00001675A:C09	8773	90.A6.sp6:130864.Seq
M00001675A:C09	8773	RTA00000187AF.f.24.1.Seq_THC220002
M00001676B:F05	11460	RTA00000187AF.g.12.1
M00001676B:F05	11460	90.B6.sp6:130876.Seq
M00001676B:F05	11460	219.F2.sp6:139035.Seq
M00001677D:A07	7570	90.D6.sp6:130900.Seq
M00001677D:A07	7570	RTA00000187AF.g.24.1
M00001677D:A07	7570	RTA00000187AF.g.24.1.Seq_THC168636
M00001678D:F12	4416	90.E6.sp6:130912.Seq
M00001678D:F12	4416	RTA00000187AF.h.13.1
M00001679A:F10	26875	RTA00000187AF.i.1.1
M00001679A:F10	26875	90.A7.sp6:130865.Seq
M00001679B:F01	6298	90.B7.sp6:130877.Seq
M00001679B:F01	6298	RTA00000187AR.i.10.2
M00001680D:F08	10539	90.F7.sp6:130925.Seq

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Clone Name	Cluster ID	Sequence Name
M00001680D:F08	10539	219.F6.sp6:139039.Seq
M00001680D:F08	10539	RTA00000187AF.l.7.1
M00001682C:B12	17055	90.G7.sp6:130937.Seq
M00001682C:B12	17055	RTA00000187AF.m.3.1
M00001682C:B12	17055	176.D6.sp6:134553.Seq
M00001688C:F09	5382	90.A8.sp6:130866.Seq
M00001688C:F09	5382	RTA00000187AF.m.23.2
M00001693C:G01	4393	RTA00000187AF.n.17.1
M00001693C:G01	4393	90.B8.sp6:130878.Seq
M00001716D:H05	67252	RTA00000187AF.o.6.1
M00001716D:H05	67252	90.C8.sp6:130890.Seq
M00003741D:C09	40108	90.D8.sp6:130902.Seq
M00003741D:C09	40108	RTA00000187AF.o.24.1
M00003747D:C05	11476	RTA00000187AF.p.19.1
M00003747D:C05	11476	90.E8.sp6:130914.Seq
M00003747D:C05	11476	RTA00000187AF.p.19.1.Seq_THC108482
M00003747D:C05	11476	219.H8.sp6:139065.Seq
M00003754C:E09		90.F8.sp6:130926.Seq
M00003754C:E09		RTA00000188AF.b.12.1
M00003761D:A09		RTA00000188AF.d.11.1
M00003761D:A09		90.H8.sp6:130950.Seq
M00003761D:A09		RTA00000188AF.d.11.1.Seq_THC212094
M00003762C:B08	17076	RTA00000188AF.d.21.1.Seq_THC208760
M00003762C:B08	17076	90.A9.sp6:130867.Seq
M00003762C:B08	17076	RTA00000188AF.d.21.1
M00003763A:F06	3108	RTA00000188AF.d.24.1
M00003763A:F06	3108	90.B9.sp6:130879.Seq
M00003774C:A03	67907	RTA00000188AF.g.11.1.Seq_THC123222
M00003774C:A03	67907	RTA00000188AF.g.11.1
M00003774C:A03	67907	90.C9.sp6:130891.Seq
M00003784D:D12		RTA00000188AF.i.8.1
M00003784D:D12		90.D9.sp6:130903.Seq
M00003839A:D08	7798	RTA00000189AF.c.18.1
M00003839A:D08	7798	90.A10.sp6:130868.Seq
M00003851B:D08		90.D10.sp6:130904.Seq
M00003851B:D08		RTA00000189AF.f.7.1
M00003851B:D10	13595	90.E10.sp6:130916.Seq
M00003851B:D10	13595	RTA00000189AF.f.8.1
M00003853A:D04	5619	90.F10.sp6:130928.Seq
M00003853A:D04	5619	RTA00000189AF.f.17.1
M00003853A:F12	10515	90.G10.sp6:130940.Seq
M00003853A:F12	10515	RTA00000189AF.f.18.1
M00003856B:C02	4622	90.H10.sp6:130952.Seq
M00003856B:C02	4622	RTA00000189AF.g.1.1
M00003857A:H03	4718	90.B11.sp6:130881.Seq
M00003857A:H03	4718	RTA00000189AF.g.5.1.Seq_THC196102
M00003857A:H03	4718	RTA00000189AF.g.5.1

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Clone Name	Cluster ID	Sequence Name
M00003867A:D10		90.C11.sp6:130893.Seq
M00003867A:D10		RTA00000189AF.h.17.1
M00003871C:E02	4573	RTA00000189AF.j.12.1
M00003875C:G07	8479	90.G11.sp6:130941.Seq
M00003875C:G07	8479	RTA00000189AF.j.22.1
M00003875D:D11		90.H11.sp6:130953.Seq
M00003875D:D11		RTA00000189AF.j.23.1
M00003876D:E12	7798	90.A12.sp6:130870.Seq
M00003876D:E12	7798	RTA00000189AF.k.12.1
M00003906C:E10	9285	90.H12.sp6:130954.Seq
M00003906C:E10	9285	RTA00000190AF.d.7.1
M00003907D:A09	39809	99.A1.sp6:131230.Seq
M00003907D:A09	39809	RTA00000190AF.e.3.1.Seq_THC150217
M00003907D:A09	39809	RTA00000190AF.e.3.1
M00003907D:H04	16317	99.B1.sp6:131242.Seq
M00003907D:H04	16317	RTA00000190AF.e.6.1
M00003909D:C03	8672	RTA00000190AF.f.11.1
M00003909D:C03	8672	99.C1.sp6:131254.Seq
M00003968B:F06	24488	RTA00000190AF.n.16.1
M00003968B:F06	24488	99.C2.sp6:131255.Seq
M00003970C:B09	40122	RTA00000190AF.n.23.1
M00003970C:B09	40122	RTA00000190AF.n.23.1.Seq_THC109227
M00003970C:B09	40122	99.D2.sp6:131267.Seq
M00003974D:E07	23210	RTA00000190AF.o.20.1
M00003974D:E07	23210	RTA00000190AF.o.20.1.Seq_THC207240
M00003974D:E07	23210	99.E2.sp6:131279.Seq
M00003974D:H02	23358	RTA00000190AF.o.21.1.Seq_THC207240
M00003974D:H02	23358	RTA00000190AF.o.21.1
M00003974D:H02	23358	99.F2.sp6:131291.Seq
M00003981A:E10	3430	99.A3.sp6:131232.Seq
M00003981A:E10	3430	RTA00000191AF.a.9.1
M00003982C:C02	2433	RTA00000191AF.a.15.2
M00003982C:C02	2433	99.B3.sp6:131244.Seq
M00003982C:C02	2433	RTA00000191AF.a.15.2.Seq_THC79498
M00004028D:C05	40073	RTA00000191AF.e.3.1
M00004028D:C05	40073	99.E3.sp6:131280.Seq
M00004035C:A07	37285	99.H3.sp6:131316.Seq
M00004035C:A07	37285	RTA00000191AF.f.11.1
M00004035D:B06	17036	RTA00000191AF.f.13.1
M00004035D:B06	17036	99.A4.sp6:131233.Seq
M00004072A:C03		RTA00000191AF.j.9.1
M00004072A:C03		99.D4.sp6:131269.Seq
M00004081C:D10	15069	99.F4.sp6:131293.Seq
M00004081C:D10	15069	RTA00000191AF.l.6.1
M00004086D:G06	9285	99.H4.sp6:131317.Seq
M00004086D:G06	9285	RTA00000191AF.m.18.1
M00004105C:A04	7221	99.D5.sp6:131270.Seq
M00004105C:A04	7221	RTA00000191AF.p.9.1
M00004171D:B03	4908	RTA00000192AF.j.2.1
M00004171D:B03	4908	99.F6.sp6:131295.Seq
M00004185C:C03	11443	RTA00000192AF.l.13.2
M00004185C:C03	11443	123.A8.sp6:132272.Seq

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Clone Name	Cluster ID	Sequence Name
M00004185C:C03	11443	99.A7.sp6:131236.Seq
M00004191D:B11		RTA00000192AF.m.12.1
M00004191D:B11		99.B7.sp6:131248.Seq
M00004191D:B11		123.C8.sp6:132296.Seq
M00004197D:H01	8210	99.C7.sp6:131260.Seq
M00004197D:H01	8210	123.E8.sp6:132320.Seq
M00004197D:H01	8210	RTA00000192AF.n.13.1
M00004203B:C12	14311	99.D7.sp6:131272.Seq
M00004203B:C12	14311	RTA00000192AF.o.2.1
M00004214C:H05	11451	177.D8.sp6:134747.Seq
M00004214C:H05	11451	RTA00000192AF.p.17.1
M00004223D:E04	12971	RTA00000193AF.a.20.1
M00004223D:E04	12971	99.B8.sp6:131249.Seq
M00004269D:D06	4905	99.H8.sp6:131321.Seq
M00004269D:D06	4905	RTA00000193AF.e.14.1
M00004295D:F12	16921	99.D9.sp6:131274.Seq
M00004295D:F12	16921	RTA00000193AF.h.15.1
M00004296C:H07	13046	99.E9.sp6:131286.Seq
M00004296C:H07	13046	RTA00000193AF.h.19.1
M00004307C:A06	9457	RTA00000193AF.i.14.2
M00004307C:A06	9457	99.F9.sp6:131298.Seq
M00004307C:A06	9457	123.D11.sp6:132311.Seq
M00004312A:G03	26295	RTA00000193AF.i.24.2
M00004312A:G03	26295	99.G9.sp6:131310.Seq
M00004312A:G03	26295	RTA00000193AF.i.24.2.Seq_THC197345
M00004318C:D10	21847	RTA00000193AF.j.9.1
M00004318C:D10	21847	99.H9.sp6:131322.Seq
M00004359B:G02		RTA00000193AF.m.5.1.Seq_THC173318
M00004359B:G02		RTA00000193AF.m.5.1
M00004505D:F08		RTA00000194AF.b.19.1
M00004505D:F08		99.H10.sp6:131323.Seq
M00004692A:H08		99.B11.sp6:131252.Seq
M00004692A:H08		RTA00000194AF.c.24.1
M00004692A:H08		377.F4.sp6:141957.Seq
M00005180C:G03		RTA00000194AF.f.4.1

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Clone Name	Cluster ID	Sequence Name
M00001346D:E03	6806	RTA00000177AF.g.13.3
M00001350A:B08		80.H2.sp6:130293.Seq
M00001350A:B08		RTA00000177AF.i.6.2
M00001357D:D11	4059	RTA00000177AF.n.18.3.Seq_THC123051
M00001357D:D11	4059	RTA00000177AF.n.18.3
M00001409C:D12	9577	RTA00000179AF.o.17.1
M00001409C:D12	9577	80.E7.sp6:130262.Seq
M00001418B:F03	9952	RTA00000180AF.c.20.1
M00001418B:F03	9952	RTA00000180AF.c.20.1.Seq_THC162284
M00001418B:F03	9952	80.E8.sp6:130263.Seq
M00001418D:B06	8526	RTA00000180AF.d.1.1
M00001421C:F01	9577	RTA00000180AF.d.23.1
M00001421C:F01	9577	80.G8.sp6:130287.Seq
M00001429B:A11	4635	RTA00000180AF.i.20.1
M00001432C:F06		RTA00000180AF.k.24.1
M00001439C:F08	40054	RTA00000180AF.p.10.1
M00001442C:D07	16731	RTA00000181AF.a.20.1
M00001442C:D07	16731	80.C10.sp6:130241.Seq
M00001443B:F01		80.D10.sp6:130253.Seq
M00001443B:F01		RTA00000181AF.b.7.1
M00001445A:F05	13532	80.E10.sp6:130265.Seq
M00001445A:F05	13532	RTA00000181AF.c.4.1
M00001446A:F05	7801	RTA00000181AF.c.21.1
M00001455A:E09	13238	RTA00000181AF.m.4.1
M00001455A:E09	13238	RTA00000181AF.m.4.1.Seq_THC140691
M00001460A:F12	39498	RTA00000119A.j.20.1
M00001481D:A05	7985	RTA00000182AR.j.2.1
M00001490B:C04	18699	RTA00000182AF.m.16.1
M00001490B:C04	18699	89.D3.sp6:130705.Seq
M00001500C:E04	9443	89.B4.sp6:130682.Seq
M00001500C:E04	9443	RTA00000183AF.c.1.1
M00001532B:A06	3990	89.G6.sp6:130744.Seq
M00001532B:A06	3990	RTA00000183AF.j.11.1
M00001534A:F09	5321	89.B7.sp6:130685.Seq
M00001534A:F09	5321	RTA00000183AF.k.8.1
M00001535A:B01	7665	RTA00000134A.l.19.1
M00001536A:C08	39392	89.G7.sp6:130745.Seq
M00001536A:C08	39392	RTA00000134A.m.16.1
M00001541A:F07	22085	RTA00000135A.e.5.2
M00001542B:B01		RTA00000183AF.p.4.1
M00001542B:B01		89.F8.sp6:130734.Seq
M00001544A:E03	12170	RTA00000125A.h.18.4
M00001545A:C03	19255	RTA00000135A.m.18.1
M00001545A:C03	19255	184.B10.sp6:135547.Seq
M00001545A:C03	19255	89.C9.sp6:130699.Seq
M00001548A:H09	1058	RTA00000126A.e.20.3.Seq_THC217534
M00001548A:H09	1058	RTA00000126A.e.20.3
M00001548A:H09	1058	79.F6.sp6:130081.Seq
M00001549A:B02	4015	RTA00000136A.e.12.1
M00001549A:B02	4015	79.G6.sp6:130093.Seq
M00001549A:D08	10944	RTA00000126A.h.17.2
M00001552B:D04	5708	RTA00000184AF.g.12.1

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Clone Name	Cluster ID	Sequence Name
M00001552B:D04	5708	89.E10.sp6:130724.Seq
M00001552D:A01		89.F10.sp6:130736.Seq
M00001552D:A01		RTA00000184AF.g.22.1
M00001553D:D10	22814	RTA00000184AF.h.14.1
M00001553D:D10	22814	89.A11.sp6:130677.Seq
M00001558A:H05		RTA00000128A.c.20.1
M00001558A:H05		89.F12.sp6:130738.Seq
M00001561A:C05	39486	RTA00000128A.m.22.2
M00001561A:C05	39486	79.B8.sp6:130035.Seq
M00001564A:B12	5053	RTA00000184AF.o.12.1
M00001578B:E04	23001	RTA00000185AF.c.24.1
M00001579D:C03	6539	90.G1.sp6:130931.Seq
M00001579D:C03	6539	173.A12.SP6:134080.Seq
M00001579D:C03	6539	RTA00000185AF.d.11.1
M00001582D:F05		RTA00000185AF.d.24.1
M00001587A:B11	39380	RTA00000129A.e.24.1
M00001587A:B11	39380	79.E8.sp6:130071.Seq
M00001604A:F05	39391	RTA00000138A.c.3.1
M00001604A:F05	39391	79.A9.sp6:130024.Seq
M00001624A:B06	3277	RTA00000138A.l.5.1
M00001624A:B06	3277	217.E1.sp6:139406.Seq
M00001624A:B06	3277	90.B4.sp6:130874.Seq
M00001630B:H09	5214	90.D4.sp6:130898.Seq
M00001630B:H09	5214	122.C2.sp6:132098.Seq
M00001630B:H09	5214	RTA00000186AF.g.11.1
M00001651A:H01		RTA00000186AF.n.7.1
M00001651A:H01		90.A5.sp6:130863.Seq
M00001677C:E10	14627	RTA00000187AF.g.23.1
M00001679C:F01	78091	90.C7.sp6:130889.Seq
M00001679C:F01	78091	RTA00000187AF.j.6.1
M00001679C:F01	78091	176.G5.sp6:134588.Seq
M00001686A:E06	4622	RTA00000187AF.m.15.2
M00003796C:D05	5619	RTA00000188AF.l.9.1.Seq_THC167845
M00003796C:D05	5619	RTA00000188AF.l.9.1
M00003826B:A06	11350	RTA00000189AF.a.24.2
M00003826B:A06	11350	90.F9.sp6:130927.Seq
M00003833A:E05	21877	RTA00000189AF.b.21.1
M00003837D:A01	7899	90.H9.sp6:130951.Seq
M00003837D:A01	7899	RTA00000189AF.c.10.1
M00003846B:D06	6874	RTA00000189AF.e.9.1
M00003846B:D06	6874	90.C10.sp6:130892.Seq
M00003879B:D10	31587	RTA00000189AF.l.20.1
M00003879B:D10	31587	90.C12.sp6:130894.Seq
M00003879D:A02	14507	90.D12.sp6:130906.Seq
M00003879D:A02	14507	RTA00000189AR.l.23.2
M00003891C:H09		90.G12.sp6:130942.Seq
M00003891C:H09		RTA00000189AF.p.8.1
M00003912B:D01	12532	99.D1.sp6:131266.Seq
M00003912B:D01	12532	RTA00000190AF.g.2.1
M00004072B:B05	17036	RTA00000191AF.j.10.1
M00004081C:D12	14391	RTA00000191AF.l.7.1
M00004111D:A08	6874	RTA00000192AF.a.14.1

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Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004111D:A08	6874	99.F5.sp6:131294.Seq
M00004121B:G01		177.H4.sp6:134791.Seq
M00004121B:G01		99.H5.sp6:131318.Seq
M00004121B:G01		RTA00000192AF.c.2.1
M00004138B:H02	13272	99.A6.sp6:131235.Seq
M00004138B:H02	13272	RTA00000192AF.e.3.1
M00004151D:B08	16977	RTA00000192AF.g.3.1
M00004169C:C12	5319	99.E6.sp6:131283.Seq
M00004169C:C12	5319	RTA00000192AF.i.12.1
M00004169C:C12	5319	123.F7.sp6:132331.Seq
M00004183C:D07	16392	RTA00000192AF.l.1.1
M00004183C:D07	16392	RTA00000192AF.l.1.1.Seq_THC202071
M00004230B:C07	7212	RTA00000193AF.b.14.1
M00004230B:C07	7212	99.D8.sp6:131273.Seq
M00004249D:F10		RTA00000193AF.c.21.1.Seq_THC222602
M00004249D:F10		RTA00000193AF.c.21.1
M00004275C:C11	16914	99.A9.sp6:131238.Seq
M00004275C:C11	16914	RTA00000193AF.f.5.1
M00004283B:A04	14286	RTA00000193AF.f.22.1
M00004285B:E08	56020	RTA00000193AF.g.2.1
M00004327B:H04		RTA00000193AF.j.20.1
M00004377C:F05	2102	RTA00000193AF.n.7.1
M00004384C:D02		RTA00000193AF.n.15.1
M00004384C:D02		RTA00000193AF.n.15.1.Seq_THC215687
M00004461A:B08		RTA00000194AR.a.10.2
M00004461A:B09		RTA00000194AF.a.11.1
M00004691D:A05		RTA00000194AF.c.23.1
M00004896A:C07		RTA00000194AF.d.13.1

The above material has been deposited with the American Type Culture Collection, Rockville, Maryland, under the accession number indicated. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for purposes of Patent Procedure. The deposit will be maintained for a period of 30 years following issuance of this patent, or for the enforceable life of the patent, whichever is greater. Upon issuance of the patent, the deposit will be available to the public from the ATCC without restriction.

This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may

be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 1. Sequence identification numbers, cluster ID, sequence name, and clone name

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
1	4635	RTA00000180AF.i.20.1	M00001429B:A11
2		RTA00000185AF.n.12.1	M00001608D:A11
3	4622	RTA00000187AF.m.15.2	M00001686A:E06
4	3706	RTA00000191AF.i.17.2	M00004068B:A01
5	36535	RTA00000181AF.f.5.1	M00001449A:G10
6	3990	RTA00000183AF.j.11.1	M00001532B:A06
7	5319	RTA00000192AF.i.12.1	M00004169C:C12
8	36393	RTA00000180AF.c.2.1	M00001417A:E02
9	2623	RTA00000183AF.a.6.1	M00001497A:G02
10	7587	RTA00000178AF.n.24.1	M00001387B:G03
11	7065	RTA00000137A.g.6.1	M00001557A:D02
12	10539	RTA00000187AF.l.7.1	M00001680D:F08
13	27250	RTA00000181AF.g.10.1	M00001450A:D08
14	5556	RTA00000179AF.n.10.1	M00001407B:D11
15		RTA00000192AF.m.12.1	M00004191D:B11
16	8761	RTA00000184AF.k.12.1	M00001557D:D09
17	4622	RTA00000189AF.g.1.1	M00003856B:C02
18	11460	RTA00000187AF.g.12.1	M00001676B:F05
19	16283	RTA00000120A.o.20.1	M00001467A:D08
20	3430	RTA00000191AF.a.9.1	M00003981A:E10
21	7065	RTA00000184AF.j.21.1	M00001557A:D02
22		RTA00000182AF.l.20.1	M00001488B:F12
23		RTA00000123A.g.19.1	M00001531A:H11
24	16918	RTA00000193AF.a.16.1	M00004223A:G10
25	16914	RTA00000193AF.f.5.1	M00004275C:C11
26	40108	RTA00000187AF.o.24.1	M00003741D:C09
27	14286	RTA00000193AF.f.22.1	M00004283B:A04
28	17004	RTA00000186AF.b.21.1	M00001617C:E02
29		RTA00000180AF.g.22.1	M00001426B:D12
30	13272	RTA00000192AF.e.3.1	M00004138B:H02
31		RTA00000194AF.f.4.1	M00005180C:G03
32	32663	RTA00000118A.l.8.1	M00001450A:A11
33		RTA00000180AF.a.9.1	M00001414A:B01
34	5832	RTA00000178AF.o.23.1	M00001388D:G05
35	7801	RTA00000181AF.c.21.1	M00001446A:F05
36	76760	RTA00000187AF.a.15.1	M00001657D:F08
37	40132	RTA00000178AF.c.7.1	M00001365C:C10
38		RTA00000183AF.e.1.1	M00001505C:C05
39	4016	RTA00000118A.c.4.1	M00001395A:C03
40	5382	RTA00000187AF.m.23.2	M00001688C:F09

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
41	5693	RTA00000190AF.p.17.2	M00003978B:G05
42	307	RTA00000136A.o.4.2	M00001552A:B12
43	39833	RTA00000178AF.i.23.1	M00001378B:B02
44		RTA00000193AF.m.5.1	M00004359B:G02
45	5325	RTA00000191AF.o.6.1	M00004093D:B12
46	5325	RTA00000191AF.o.6.2	M00004093D:B12
47	18957	RTA00000190AR.m.9.1	M00003958A:H02
48	39508	RTA00000120A.o.2.1	M00001467A:D04
49	22390	RTA00000136A.j.13.1	M00001551A:G06
50	12170	RTA00000125A.h.18.4	M00001544A:E03
51	4393	RTA00000187AF.n.17.1	M00001693C:G01
52	19	RTA00000182AF.b.7.1	M00001463C:B11
53		RTA00000193AF.c.21.1	M00004249D:F10
54	7899	RTA00000189AF.c.10.1	M00003837D:A01
55	40073	RTA00000191AF.e.3.1	M00004028D:C05
56	7005	RTA00000179AF.o.22.1	M00001410A:D07
57		RTA00000187AF.h.22.1	M00001679A:F06
58	18957	RTA00000190AF.m.9.2	M00003958A:H02
59	18957	RTA00000183AF.h.23.1	M00001528A:F09
60	16283	RTA00000182AF.c.22.1	M00001467A:D08
61	6974	RTA00000183AF.d.9.1	M00001504C:H06
62	2623	RTA00000183AF.b.14.1	M00001500A:E11
63	9105	RTA00000191AF.a.21.2	M00003983A:A05
64	13238	RTA00000181AF.m.4.1	M00001455A:E09
65	5749	RTA00000185AF.a.19.1	M00001571C:H06
66	6455	RTA00000193AF.b.9.1	M00004229B:F08
67	23001	RTA00000185AF.c.24.1	M00001578B:E04
68	6455	RTA00000192AF.g.23.1	M00004157C:A09
69	13595	RTA00000189AF.f.8.1	M00003851B:D10
70	39442	RTA00000120A.o.21.1	M00001467A:E10
71	17036	RTA00000191AF.f.13.1	M00004035D:B06
72		RTA00000183AF.g.9.1	M00001513B:G03
73	7005	RTA00000181AF.k.24.1	M00001454B:C12
74	6268	RTA00000126A.o.23.1	M00001551A:B10
75	16130	RTA00000119A.c.13.1	M00001453A:E11
76	23201	RTA00000187AF.a.14.1	M00001657D:C03
77	5321	RTA00000183AF.k.8.1	M00001534A:F09
78	13157	RTA00000186AF.a.6.1	M00001614C:F10
79	2102	RTA00000193AF.n.7.1	M00004377C:F05
80	1058	RTA00000126A.e.20.3	M00001548A:H09
81	40392	RTA00000180AF.j.8.1	M00001429D:D07
82		RTA00000183AF.e.23.1	M00001506D:A09
83	11476	RTA00000187AF.p.19.1	M00003747D:C05

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84	3584	RTA00000177AF.h.20.1	M00001349B:B08
85	10470	RTA00000180AF.f.18.1	M00001424B:G09
86	39425	RTA00000133A.f.1.1	M00001470A:C04
87	5175	RTA00000184AF.f.3.1	M00001550A:G01
88	13576	RTA00000189AF.o.13.1	M00003885C:A02
89	7665	RTA00000134A.l.19.1	M00001535A:B01
90	16927	RTA00000177AF.h.9.3	M00001348B:B04
91	6660	RTA00000187AF.h.15.1	M00001679A:A06
92	2433	RTA00000191AF.a.15.2	M00003982C:C02
93	5097	RTA00000134A.k.1.1	M00001534A:D09
94	21847	RTA00000193AF.j.9.1	M00004318C:D10
95	3277	RTA00000138A.l.5.1	M00001624A:B06
96	5708	RTA00000184AF.g.12.1	M00001552B:D04
97	945	RTA00000178AR.a.20.1	M00001362C:H11
98	16269	RTA00000178AF.p.1.1	M00001389A:C08
99		RTA00000183AF.c.24.1	M00001504A:E01
100	16731	RTA00000181AF.a.20.1	M00001442C:D07
101	12439	RTA00000190AF.o.24.1	M00003975A:G11
102	3162	RTA00000177AF.j.12.3	M00001351B:A08
103		RTA00000194AF.b.19.1	M00004505D:F08
104		RTA00000193AF.n.15.1	M00004384C:D02
105		RTA00000186AF.n.7.1	M00001651A:H01
106	10717	RTA00000181AF.d.10.1	M00001447A:G03
107	4573	RTA00000189AF.j.12.1	M00003871C:E02
108		RTA00000186AF.h.14.1	M00001632D:H07
109	11443	RTA00000192AF.l.13.2	M00004185C:C03
110	5892	RTA00000184AF.d.11.1	M00001548A:E10
111	3162	RTA00000177AF.j.12.1	M00001351B:A08
112	10470	RTA00000185AF.k.6.1	M00001597D:C05
113	17055	RTA00000187AF.m.3.1	M00001682C:B12
114	2030	RTA00000193AF.m.20.1	M00004372A:A03
115	6558	RTA00000184AF.m.21.1	M00001560D:F10
116	23255	RTA00000190AF.j.4.1	M00003922A:E06
117	9577	RTA00000179AF.o.17.1	M00001409C:D12
118		RTA00000180AF.a.11.1	M00001414C:A07
119	8	RTA00000181AF.e.17.1	M00001448D:C09
120	67907	RTA00000188AF.g.11.1	M00003774C:A03
121	12081	RTA00000133A.d.14.2	M00001469A:C10
122	2448	RTA00000119A.j.21.1	M00001460A:F06
123	3389	RTA00000189AF.g.3.1	M00003857A:G10
124	39174	RTA00000124A.n.13.1	M00001541A:H03
125	24488	RTA00000190AF.n.16.1	M00003968B:F06
126	8210	RTA00000192AF.n.13.1	M00004197D:H01

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
127		RTA00000135A.l.2.2	M00001545A:B02
128	40455	RTA00000190AF.m.10.2	M00003958C:G10
129	9577	RTA00000180AF.d.23.1	M00001421C:F01
130	13183	RTA00000192AF.a.24.1	M00004114C:F11
131	5214	RTA00000186AF.g.11.1	M00001630B:H09
132	67252	RTA00000187AF.o.6.1	M00001716D:H05
133	3108	RTA00000188AF.d.24.1	M00003763A:F06
134	2464	RTA00000178AF.n.18.1	M00001387A:C05
135	36313	RTA00000181AF.e.23.1	M00001448D:H01
136	23255	RTA00000177AF.e.14.3	M00001343D:H07
137	7985	RTA00000182AR.j.2.1	M00001481D:A05
138	8286	RTA00000183AF.o.1.1	M00001540A:D06
139	22195	RTA00000180AF.g.7.1	M00001425B:H08
140	4573	RTA00000184AF.h.9.1	M00001553B:F12
141	26875	RTA00000187AF.i.1.1	M00001679A:F10
142	7187	RTA00000177AF.i.8.2	M00001350A:H01
143	86859	RTA00000118A.p.8.1	M00001452A:B12
144	4623	RTA00000185AF.f.4.1	M00001586C:C05
145		RTA00000121A.c.10.1	M00001469A:A01
146	10185	RTA00000183AF.d.5.1	M00001504C:A07
147		RTA00000183AF.p.4.1	M00001542B:B01
148	15069	RTA00000191AF.l.6.1	M00004081C:D10
149	39304	RTA00000118A.j.21.1	M00001450A:A02
150	8672	RTA00000190AF.f.11.1	M00003909D:C03
151	13576	RTA00000177AF.g.16.1	M00001347A:B10
152	6293	RTA00000185AF.e.11.1	M00001583D:A10
153	16977	RTA00000192AF.g.3.1	M00004151D:B08
154	5345	RTA00000189AF.l.19.1	M00003879B:C11
155	4905	RTA00000193AF.e.14.1	M00004269D:D06
156	17036	RTA00000191AF.j.10.1	M00004072B:B05
157	5417	RTA00000191AF.h.19.1	M00004059A:D06
158	7172	RTA00000178AF.f.9.1	M00001371C:E09
159	40044	RTA00000186AF.d.1.1	M00001621C:C08
160	4386	RTA00000184AF.j.4.1	M00001556B:C08
161	40044	RTA00000183AF.g.22.1	M00001514C:D11
162	9685	RTA00000183AF.c.11.1	M00001501D:C02
163	22155	RTA00000185AF.n.9.1	M00001608B:E03
164	10515	RTA00000189AF.f.18.1	M00003853A:F12
165	6539	RTA00000185AF.d.11.1	M00001579D:C03
166	15066	RTA00000180AF.e.24.1	M00001423B:E07
167	4261	RTA00000180AF.h.5.1	M00001426D:C08
168	13864	RTA00000125A.m.9.1	M00001545A:D08
169	6539	RTA00000189AF.d.22.1	M00003844C:B11

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
170	11465	RTA00000185AF.m.19.1	M00001607A:E11
171	3266	RTA00000184AR.g.1.1	M00001551C:G09
172	102	RTA00000184AF.o.5.1	M00001563B:F06
173	16970	RTA00000181AR.i.18.2	M00001452C:B06
174	12971	RTA00000193AF.a.20.1	M00004223D:E04
175	5007	RTA00000177AF.g.2.1	M00001346A:F09
176	3765	RTA00000135A.d.1.1	M00001541A:D02
177	11294	RTA00000184AF.j.6.1	M00001556B:G02
178	3681	RTA00000131A.g.15.2	M00001449A:D12
179	9283	RTA00000181AR.m.21.2	M00001455D:F09
180	18699	RTA00000182AF.m.16.1	M00001490B:C04
181	86110	RTA00000181AF.f.12.1	M00001449C:D06
182	39648	RTA00000178AR.l.8.2	M00001383A:C03
183	7337	RTA00000123A.b.17.1	M00001528A:C04
184	1334	RTA00000178AF.j.7.1	M00001379A:A05
185	17076	RTA00000188AF.d.21.1	M00003762C:B08
186	22794	RTA00000138A.b.5.1	M00001601A:D08
187	39171	RTA00000186AF.l.7.1	M00001644C:B07
188	8551	RTA00000179AF.p.21.1	M00001412B:B10
189	5857	RTA00000118A.g.14.1	M00001449A:A12
190	9443	RTA00000183AF.c.1.1	M00001500C:E04
191	9457	RTA00000193AF.i.14.2	M00004307C:A06
192	7206	RTA00000182AF.o.15.1	M00001494D:F06
193	22979	RTA00000178AF.k.22.1	M00001382C:A02
194	40455	RTA00000190AR.m.10.1	M00003958C:G10
195	7221	RTA00000191AF.p.9.1	M00004105C:A04
196		RTA00000191AF.j.9.1	M00004072A:C03
197	7239	RTA00000126A.m.4.2	M00001550A:A03
198	31587	RTA00000189AF.l.20.1	M00003879B:D10
199	16317	RTA00000190AF.e.6.1	M00003907D:H04
200	13576	RTA00000189AR.o.13.1	M00003885C:A02
201	5779	RTA00000177AF.g.14.3	M00001346D:G06
202	6124	RTA00000191AR.e.2.3	M00004028D:A06
203	9952	RTA00000180AF.c.20.1	M00001418B:F03
204		RTA00000188AF.i.8.1	M00003784D:D12
205	5779	RTA00000177AF.g.14.1	M00001346D:G06
206	39490	RTA00000128A.b.4.1	M00001557A:F03
207	4416	RTA00000187AF.h.13.1	M00001678D:F12
208	4009	RTA00000179AF.e.20.1	M00001396A:C03
209	5336	RTA00000183AF.b.13.1	M00001500A:C05
210	39186	RTA00000121A.p.15.1	M00001512A:A09
211	40122	RTA00000190AF.n.23.1	M00003970C:B09
212	12532	RTA00000190AF.g.2.1	M00003912B:D01

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
213	8078	RTA00000177AR.l.13.1	M00001353A:G12
214	3900	RTA00000190AF.g.13.1	M00003914C:F05
215	7589	RTA00000120A.p.23.1	M00001468A:F05
216	8298	RTA00000127A.d.19.1	M00001553A:H06
217	4443	RTA00000177AF.b.20.4	M00001341A:E12
218	26295	RTA00000193AF.i.24.2	M00004312A:G03
219	3389	RTA00000183AF.m.19.1	M00001537B:G07
220	7015	RTA00000187AF.f.18.1	M00001673C:H02
221	8526	RTA00000180AF.d.1.1	M00001418D:B06
222	4665	RTA00000186AF.m.3.1	M00001648C:A01
223	1399	RTA00000129A.o.10.1	M00001604A:B10
224	9244	RTA00000127A.l.3.1	M00001556A:C09
225		RTA00000179AF.j.13.1	M00001400B:H06
226	82498	RTA00000118A.m.10.1	M00001450A:B12
227	35702	RTA00000187AR.c.15.2	M00001663A:E04
228	38759	RTA00000120A.m.12.3	M00001467A:B07
229	39648	RTA00000178AF.l.8.1	M00001383A:C03
230	19105	RTA00000133A.e.15.1	M00001469A:H12
231	85064	RTA00000131A.m.23.1	M00001452A:F05
232	9285	RTA00000191AF.m.18.1	M00004086D:G06
233	9285	RTA00000190AF.d.7.1	M00003906C:E10
234	39391	RTA00000138A.c.3.1	M00001604A:F05
235		RTA00000178AF.d.20.1	M00001368D:E03
236	39498	RTA00000119A.j.20.1	M00001460A:F12
237	7798	RTA00000189AF.k.12.1	M00003876D:E12
238	7798	RTA00000189AF.c.18.1	M00003839A:D08
239	19829	RTA00000125A.h.24.4	M00001544A:G02
240		RTA00000188AF.d.11.1	M00003761D:A09
241	4275	RTA00000120A.j.14.1	M00001466A:E07
242	22113	RTA00000125A.c.7.1	M00001542A:A09
243	40314	RTA00000186AF.c.15.1	M00001619C:F12
244	10944	RTA00000126A.h.17.2	M00001549A:D08
245	39809	RTA00000190AF.e.3.1	M00003907D:A09
246	22085	RTA00000135A.e.5.2	M00001541A:F07
247	19255	RTA00000135A.m.18.1	M00001545A:C03
248	14311	RTA00000192AF.o.2.1	M00004203B:C12
249	8479	RTA00000189AF.j.22.1	M00003875C:G07
250		RTA00000189AF.j.23.1	M00003875D:D11
251	4193	RTA00000184AF.e.13.1	M00001549B:F06
252	22814	RTA00000184AF.h.14.1	M00001553D:D10
253	39563	RTA00000179AF.k.20.1	M00001402A:E08
254	39420	RTA00000134A.o.23.1	M00001537A:F12
255	11589	RTA00000177AF.b.17.4	M00001340D:F10

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
256	4937	RTA00000191AF.p.21.1	M00004108A:E06
257	39412	RTA00000133A.k.17.1	M00001511A:H06
258	4837	RTA00000185AR.k.3.2	M00001597C:H02
259	13046	RTA00000193AF.h.19.1	M00004296C:H07
260	4141	RTA00000177AF.p.20.3	M00001361A:A05
261	38085	RTA00000123A.e.15.1	M00001531A:D01
262		RTA00000189AF.p.8.1	M00003891C:H09
263	11451	RTA00000192AF.p.17.1	M00004214C:H05
264	14507	RTA00000189AR.l.23.2	M00003879D:A02
265	40054	RTA00000180AF.p.10.1	M00001439C:F08
266	39423	RTA00000134A.k.22.1	M00001535A:F10
267	39453	RTA00000135A.g.11.1	M00001542A:E06
268	10751	RTA00000187AF.k.7.1	M00001679D:D03
269	10751	RTA00000187AF.k.6.1	M00001679D:D03
270	78091	RTA00000187AF.j.6.1	M00001679C:F01
271	39539	RTA00000127A.i.21.1	M00001555A:B02
272		RTA00000182AF.l.15.1	M00001487B:H06
273		RTA00000194AF.d.13.1	M00004896A:C07
274		RTA00000128A.c.20.1	M00001558A:H05
275	9283	RTA00000181AR.m.22.2	M00001455D:F09
276	39168	RTA00000121A.l.10.1	M00001507A:H05
277	39458	RTA00000126A.p.15.2	M00001552A:D11
278	14391	RTA00000177AF.m.17.3	M00001355B:G10
279	39195	RTA00000137A.c.16.1	M00001555A:C01
280	7212	RTA00000193AF.b.14.1	M00004230B:C07
281	4015	RTA00000136A.e.12.1	M00001549A:B02
282	12977	RTA00000189AF.j.19.1	M00003875B:F04
283		RTA00000178AF.m.13.1	M00001384B:A11
284	14391	RTA00000191AF.l.7.1	M00004081C:D12
285		RTA00000194AF.c.23.1	M00004691D:A05
286		RTA00000181AF.b.7.1	M00001443B:F01
287	8358	RTA00000183AF.i.5.1	M00001528B:H04
288	1267	RTA00000125A.o.5.1	M00001546A:G11
289		RTA00000189AF.f.7.1	M00003851B:D08
290	16347	RTA00000184AF.e.15.1	M00001549C:E06
291	7899	RTA00000193AF.a.17.1	M00004223B:D09
292	2379	RTA00000178AF.a.6.1	M00001361D:F08
293	39478	RTA00000133A.i.5.1	M00001471A:B01
294	39392	RTA00000134A.m.16.1	M00001536A:C08
295	5053	RTA00000184AF.o.12.1	M00001564A:B12
296	16999	RTA00000185AF.k.9.1	M00001598A:G03
297	39180	RTA00000126A.n.8.2	M00001551A:F05
298	1037	RTA00000121A.f.8.1	M00001470A:B10

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
299	6867	RTA00000178AF.e.12.1	M00001370A:C09
300	10539	RTA00000183AF.a.24.1	M00001499B:A11
301	41633	RTA00000118A.g.16.1	M00001449A:B12
302	23218	RTA00000187AR.c.5.2	M00001662C:A09
303	39380	RTA00000129A.e.24.1	M00001587A:B11
304		RTA00000185AF.d.24.1	M00001582D:F05
305		RTA00000177AF.o.4.3	M00001358C:C06
306	6974	RTA00000184AF.a.15.1	M00001544B:B07
307		RTA00000185AF.g.11.1	M00001590B:F03
308	15855	RTA00000184AF.j.1.1	M00001556A:H01
309	84328	RTA00000118A.p.10.1	M00001452A:B04
310	10145	RTA00000120A.g.12.1	M00001465A:B11
311	39805	RTA00000177AF.c.21.3	M00001342B:E06
312		RTA00000187AF.h.23.1	M00001679A:F06
313	6298	RTA00000187AR.i.10.2	M00001679B:F01
314	14367	RTA00000187AF.e.8.1	M00001670C:H02
315		RTA00000193AF.c.22.1	M00004249D:G12
316	16921	RTA00000183AF.k.6.1	M00001534A:C04
317	1577	RTA00000184AF.i.23.1	M00001556A:F11
318	8773	RTA00000187AF.f.24.1	M00001675A:C09
319		RTA00000194AF.a.11.1	M00004461A:B09
320	39886	RTA00000178AF.j.24.1	M00001380D:B09
321	13532	RTA00000181AF.c.4.1	M00001445A:F05
322		RTA00000193AF.d.2.1	M00004251C:G07
323	5257	RTA00000192AF.f.3.1	M00004146C:C11
324	9061	RTA00000191AR.e.11.2	M00004031A:A12
325	19267	RTA00000186AF.l.12.1	M00001645A:C12
326	20212	RTA00000134A.l.22.1	M00001535A:C06
327	16653	RTA00000181AF.k.5.3	M00001453C:F06
328	16985	RTA00000177AF.h.10.1	M00001348B:G06
329	12977	RTA00000189AR.j.19.1	M00003875B:F04
330	9061	RTA00000191AR.e.11.3	M00004031A:A12
331		RTA00000194AR.a.10.2	M00004461A:B08
332	6468	RTA00000187AF.d.15.1	M00001669B:F02
333	16392	RTA00000192AF.l.1.1	M00004183C:D07
334	14627	RTA00000187AF.g.23.1	M00001677C:E10
335	6583	RTA00000179AF.d.13.1	M00001394A:F01
336	6806	RTA00000177AF.g.13.3	M00001346D:E03
337	9635	RTA00000137A.e.23.4	M00001557A:F01
338	689	RTA00000181AR.l.22.1	M00001454D:G03
339	4119	RTA00000183AF.k.16.1	M00001534C:A01
340	8952	RTA00000183AF.h.15.1	M00001518C:B11
341	2379	RTA00000192AF.p.8.1	M00004212B:C07

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
342	39486	RTA00000128A.m.22.2	M00001561A:C05
343	21877	RTA00000189AF.b.21.1	M00003833A:E05
344	6874	RTA00000192AF.a.14.1	M00004111D:A08
345	6874	RTA00000189AF.e.9.1	M00003846B:D06
346	37285	RTA00000191AF.f.11.1	M00004035C:A07
347		RTA00000193AF.j.20.1	M00004327B:H04
348	7674	RTA00000118A.g.9.1	M00001416A:H01
349	2797	RTA00000180AF.i.19.1	M00001429A:H04
350		RTA00000184AF.g.22.1	M00001552D:A01
351	7802	RTA00000185AF.n.5.1	M00001608A:B03
352	16921	RTA00000193AF.h.15.1	M00004295D:F12
353	11494	RTA00000192AF.j.6.1	M00004172C:D08
354	17062	RTA00000177AF.b.8.4	M00001340B:A06
355	16245	RTA00000177AF.k.9.3	M00001352A:E02
356	83103	RTA00000119A.e.24.2	M00001454A:A09
357	4309	RTA00000186AF.e.22.1	M00001624C:F01
358	13072	RTA00000181AR.m.5.2	M00001455B:E12
359	4059	RTA00000177AF.n.18.3	M00001357D:D11
360	5178	RTA00000178AF.n.10.1	M00001386C:B12
361	1120	RTA00000118A.p.15.3	M00001452A:D08
362	6420	RTA00000183AF.d.11.1	M00001504D:G06
363	13913	RTA00000186AF.e.6.1	M00001623D:F10
364		RTA00000192AF.c.2.1	M00004121B:G01
365	3956	RTA00000183AF.g.3.1	M00001512D:G09
366	14364	RTA00000183AF.g.12.1	M00001513C:E08
367	6880	RTA00000191AF.m.20.1	M00004087D:A01
368	84182	RTA00000180AF.h.19.1	M00001428A:H10
369	2790	RTA00000177AF.e.2.1	M00001343C:F10
370	4561	RTA00000184AF.i.21.1	M00001555D:G10
371	8847	RTA00000180AF.b.16.1	M00001416B:H11
372	56020	RTA00000193AF.g.2.1	M00004285B:E08
373	1531	RTA00000119A.o.3.1	M00001461A:D06
374	6420	RTA00000177AF.f.10.3	M00001345A:E01
375		RTA00000188AF.b.12.1	M00003754C:E09
376		RTA00000180AF.k.24.1	M00001432C:F06
377		RTA00000184AF.a.8.1	M00001544A:E06
378	2696	RTA00000134A.m.13.1	M00001536A:B07
379	260	RTA00000185AR.i.12.2	M00001594B:H04
380	11350	RTA00000189AF.a.24.2	M00003826B:A06
381	2428	RTA00000123A.l.21.1	M00001533A:C11
382	4313	RTA00000122A.n.3.1	M00001517A:B07
383		RTA00000184AF.p.3.1	M00001566B:D11
384	697	RTA00000188AF.d.6.1	M00003759B:B09

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
385	5619	RTA00000188AF.l.9.1	M00003796C:D05
386	4568	RTA00000122A.d.15.3	M00001513A:B06
387		RTA00000177AF.i.6.2	M00001350A:B08
388	5622	RTA00000178AF.a.11.1	M00001362B:D10
389	7514	RTA00000184AF.k.21.1	M00001558B:H11
390	5619	RTA00000189AF.f.17.1	M00003853A:D04
391	7570	RTA00000187AF.g.24.1	M00001677D:A07
392	23358	RTA00000190AF.o.21.1	M00003974D:H02
393	23210	RTA00000190AF.o.20.1	M00003974D:E07
394	5192	RTA00000184AF.k.2.1	M00001557B:H10
395	13538	RTA00000180AF.a.24.1	M00001415A:H06
396		RTA00000189AF.h.17.1	M00003867A:D10
397		RTA00000192AF.o.11.1	M00004205D:F06
398		RTA00000184AF.l.11.1	M00001559B:F01
399	4718	RTA00000189AF.g.5.1	M00003857A:H03
400	14929	RTA00000177AF.m.1.2	M00001353D:D10
401	4908	RTA00000192AF.j.2.1	M00004171D:B03
402		RTA00000178AF.k.16.1	M00001381D:E06
403		RTA00000194AF.c.24.1	M00004692A:H08
404	17732	RTA00000178AR.i.2.2	M00001376B:G06
405	17062	80.A1.sp6:130208.Seq	M00001340B:A06
406	11589	80.B1.sp6:130220.Seq	M00001340D:F10
407	4443	80.C1.sp6:130232.Seq	M00001341A:E12
408	39805	80.D1.sp6:130244.Seq	M00001342B:E06
409	2790	80.E1.sp6:130256.Seq	M00001343C:F10
410	23255	80.F1.sp6:130268.Seq	M00001343D:H07
411	6420	80.G1.sp6:130280.Seq	M00001345A:E01
412	5007	80.H1.sp6:130292.Seq	M00001346A:F09
413	13576	80.D2.sp6:130245.Seq	M00001347A:B10
414	16927	80.E2.sp6:130257.Seq	M00001348B:B04
415	16985	80.F2.sp6:130269.Seq	M00001348B:G06
416	3584	80.G2.sp6:130281.Seq	M00001349B:B08
417		80.H2.sp6:130293.Seq	M00001350A:B08
418	7187	80.A3.sp6:130210.Seq	M00001350A:H01
419	16245	80.D3.sp6:130246.Seq	M00001352A:E02
420	8078	80.E3.sp6:130258.Seq	M00001353A:G12
421	14929	80.F3.sp6:130270.Seq	M00001353D:D10
422	14391	80.G3.sp6:130282.Seq	M00001355B:G10
423	4141	80.B4.sp6:130223.Seq	M00001361A:A05
424	2379	80.C4.sp6:130235.Seq	M00001361D:F08
425	5622	80.D4.sp6:130247.Seq	M00001362B:D10
426	945	80.E4.sp6:130259.Seq	M00001362C:H11
427	40132	80.F4.sp6:130271.Seq	M00001365C:C10

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
428		80.G4.sp6:130283.Seq	M00001368D:E03
429	6867	80.H4.sp6:130295.Seq	M00001370A:C09
430	7172	80.A5.sp6:130212.Seq	M00001371C:E09
431	17732	80.B5.sp6:130224.Seq	M00001376B:G06
432	39833	80.C5.sp6:130236.Seq	M00001378B:B02
433	1334	80.D5.sp6:130248.Seq	M00001379A:A05
434	39886	80.E5.sp6:130260.Seq	M00001380D:B09
435		80.F5.sp6:130272.Seq	M00001381D:E06
436	22979	80.G5.sp6:130284.Seq	M00001382C:A02
437	39648	80.H5.sp6:130296.Seq	M00001383A:C03
438		80.B6.sp6:130225.Seq	M00001384B:A11
439	5178	80.C6.sp6:130237.Seq	M00001386C:B12
440	2464	80.D6.sp6:130249.Seq	M00001387A:C05
441	7587	80.E6.sp6:130261.Seq	M00001387B:G03
442	5832	80.F6.sp6:130273.Seq	M00001388D:G05
443	16269	80.G6.sp6:130285.Seq	M00001389A:C08
444	6583	80.H6.sp6:130297.Seq	M00001394A:F01
445	4009	80.A7.sp6:130214.Seq	M00001396A:C03
446		80.B7.sp6:130226.Seq	M00001400B:H06
447	39563	80.C7.sp6:130238.Seq	M00001402A:E08
448	5556	80.D7.sp6:130250.Seq	M00001407B:D11
449	9577	80.E7.sp6:130262.Seq	M00001409C:D12
450	7005	80.F7.sp6:130274.Seq	M00001410A:D07
451	8551	80.G7.sp6:130286.Seq	M00001412B:B10
452		80.H7.sp6:130298.Seq	M00001414A:B01
453		80.A8.sp6:130215.Seq	M00001414C:A07
454	13538	80.B8.sp6:130227.Seq	M00001415A:H06
455	8847	80.C8.sp6:130239.Seq	M00001416B:H11
456	36393	80.D8.sp6:130251.Seq	M00001417A:E02
457	9952	80.E8.sp6:130263.Seq	M00001418B:F03
458	9577	80.G8.sp6:130287.Seq	M00001421C:F01
459	15066	80.H8.sp6:130299.Seq	M00001423B:E07
460	10470	80.A9.sp6:130216.Seq	M00001424B:G09
461	22195	80.B9.sp6:130228.Seq	M00001425B:H08
462		80.C9.sp6:130240.Seq	M00001426B:D12
463	4261	80.D9.sp6:130252.Seq	M00001426D:C08
464	84182	80.E9.sp6:130264.Seq	M00001428A:H10
465	40392	80.H9.sp6:130300.Seq	M00001429D:D07
466	16731	80.C10.sp6:130241.Seq	M00001442C:D07
467		80.D10.sp6:130253.Seq	M00001443B:F01
468	13532	80.E10.sp6:130265.Seq	M00001445A:F05
469	8	80.H10.sp6:130301.Seq	M00001448D:C09
470	36313	80.A11.sp6:130218.Seq	M00001448D:H01

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
471	5857	80.B11.sp6:130230.Seq	M00001449A:A12
472	41633	80.C11.sp6:130242.Seq	M00001449A:B12
473	36535	80.D11.sp6:130254.Seq	M00001449A:G10
474	86110	80.E11.sp6:130266.Seq	M00001449C:D06
475	32663	80.F11.sp6:130278.Seq	M00001450A:A11
476	27250	80.G11.sp6:130290.Seq	M00001450A:D08
477	16970	80.H11.sp6:130302.Seq	M00001452C:B06
478	16130	80.A12.sp6:130219.Seq	M00001453A:E11
479	16653	80.B12.sp6:130231.Seq	M00001453C:F06
480	7005	80.C12.sp6:130243.Seq	M00001454B:C12
481	13072	80.F12.sp6:130279.Seq	M00001455B:E12
482	9283	80.G12.sp6:130291.Seq	M00001455D:F09
483	23255	100.C1.sp6:131446.Seq	M00001343D:H07
484	13576	100.E1.sp6:131470.Seq	M00001347A:B10
485	7187	100.C2.sp6:131447.Seq	M00001350A:H01
486	14391	100.E3.sp6:131472.Seq	M00001355B:G10
487	945	100.E4.sp6:131473.Seq	M00001362C:H11
488	7172	100.A5.sp6:131426.Seq	M00001371C:E09
489	39648	100.A6.sp6:131427.Seq	M00001383A:C03
490	84182	100.G9.sp6:131502.Seq	M00001428A:H10
491	8	100.B11.sp6:131444.Seq	M00001448D:C09
492	36535	100.D11.sp6:131468.Seq	M00001449A:G10
493	82498	100.F11.sp6:131492.Seq	M00001450A:B12
494	16970	100.C12.sp6:131457.Seq	M00001452C:B06
495	16130	100.D12.sp6:131469.Seq	M00001453A:E11
496	7005	121.D1.sp6:131917.Seq	M00001454B:C12
497		121.G6.sp6:131958.Seq	M00001506D:A09
498	18957	121.F7.sp6:131947.Seq	M00001528A:F09
499	40044	122.E1.sp6:132121.Seq	M00001621C:C08
500	5214	122.C2.sp6:132098.Seq	M00001630B:H09
501	6660	122.B5.sp6:132089.Seq	M00001679A:A06
502	13183	123.D5.sp6:132305.Seq	M00004114C:F11
503	6455	123.E7.sp6:132319.Seq	M00004157C:A09
504	5319	123.F7.sp6:132331.Seq	M00004169C:C12
505	11443	123.A8.sp6:132272.Seq	M00004185C:C03
506		123.C8.sp6:132296.Seq	M00004191D:B11
507	8210	123.E8.sp6:132320.Seq	M00004197D:H01
508	9457	123.D11.sp6:132311.Seq	M00004307C:A06
509	6420	172.E1.sp6:133925.Seq	M00001345A:E01
510	16245	172.D2.sp6:133914.Seq	M00001352A:E02
511	8078	172.C3.sp6:133903.Seq	M00001353A:G12
512	14929	172.D3.sp6:133915.Seq	M00001353D:D10
513	14391	172.H3.sp6:133963.Seq	M00001355B:G10

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514	6583	172.B8.sp6:133896.Seq	M00001394A:F01
515	4009	172.D8.sp6:133920.Seq	M00001396A:C03
516		172.B9.sp6:133897.Seq	M00001400B:H06
517		176.A3.sp6:134514.Seq	M00001632D:H07
518	19267	176.G3.sp6:134586.Seq	M00001645A:C12
519	78091	176.G5.sp6:134588.Seq	M00001679C:F01
520	17055	176.D6.sp6:134553.Seq	M00001682C:B12
521	6539	176.D9.sp6:134556.Seq	M00003844C:B11
522		177.H4.sp6:134791.Seq	M00004121B:G01
523	5257	177.F5.sp6:134768.Seq	M00004146C:C11
524	11494	177.E6.sp6:134757.Seq	M00004172C:D08
525		177.G7.sp6:134782.Seq	M00004205D:F06
526	11451	177.D8.sp6:134747.Seq	M00004214C:H05
527	9283	173.D2.SP6:134106.Seq	M00001455D:F09
528	16283	173.F3.SP6:134131.Seq	M00001467A:D08
529	10539	173.B5.SP6:134085.Seq	M00001499B:A11
530	6420	173.F5.SP6:134133.Seq	M00001504D:G06
531	3956	173.H5.SP6:134157.Seq	M00001512D:G09
532		173.G7.SP6:134147.Seq	M00001544A:E06
533	1577	173.C9.SP6:134101.Seq	M00001556A:F11
534	9635	173.D9.SP6:134113.Seq	M00001557A:F01
535	5192	173.E9.SP6:134125.Seq	M00001557B:H10
536	6539	173.A12.SP6:134080.Seq	M00001579D:C03
537	945	180.C2.sp6:135940.Seq	M00001362C:H11
538	7005	180.H5.sp6:136003.Seq	M00001410A:D07
539	39304	180.G9.sp6:135995.Seq	M00001450A:A02
540	27250	180.B10.sp6:135936.Seq	M00001450A:D08
541	35555	184.A5.sp6:135530.Seq	M00001528A:C04
542	19255	184.B10.sp6:135547.Seq	M00001545A:C03
543	6268	184.C12.sp6:135561.Seq	M00001551A:B10
544	3277	217.E1.sp6:139406.Seq	M00001624A:B06
545	39171	217.A12.sp6:139369.Seq	M00001644C:B07
546	11460	219.F2.sp6:139035.Seq	M00001676B:F05
547	10539	219.F6.sp6:139039.Seq	M00001680D:F08
548	11476	219.H8.sp6:139065.Seq	M00003747D:C05
549	4016	79.A1.sp6:130016.Seq	M00001395A:C03
550	7674	79.C1.sp6:130040.Seq	M00001416A:H01
551	3681	79.E1.sp6:130064.Seq	M00001449A:D12
552	39304	79.F1.sp6:130076.Seq	M00001450A:A02
553	82498	79.G1.sp6:130088.Seq	M00001450A:B12
554	84328	79.A2.sp6:130017.Seq	M00001452A:B04
555	86859	79.B2.sp6:130029.Seq	M00001452A:B12
556	1120	79.C2.sp6:130041.Seq	M00001452A:D08

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557	85064	79.D2.sp6:130053.Seq	M00001452A:F05
558	83103	79.G2.sp6:130089.Seq	M00001454A:A09
559	10145	79.F3.sp6:130078.Seq	M00001465A:B11
560	16283	79.H3.sp6:130102.Seq	M00001467A:D08
561	4568	79.D4.sp6:130055.Seq	M00001513A:B06
562	4313	79.F4.sp6:130079.Seq	M00001517A:B07
563	2428	79.A5.sp6:130020.Seq	M00001533A:C11
564	39423	79.C5.sp6:130044.Seq	M00001535A:F10
565	39174	79.E5.sp6:130068.Seq	M00001541A:H03
566	22113	79.F5.sp6:130080.Seq	M00001542A:A09
567	19829	79.H5.sp6:130104.Seq	M00001544A:G02
568	13864	79.B6.sp6:130033.Seq	M00001545A:D08
569	1058	79.F6.sp6:130081.Seq	M00001548A:H09
570	4015	79.G6.sp6:130093.Seq	M00001549A:B02
571	39180	79.A7.sp6:130022.Seq	M00001551A:F05
572	307	79.C7.sp6:130046.Seq	M00001552A:B12
573	39458	79.D7.sp6:130058.Seq	M00001552A:D11
574	39490	79.G7.sp6:130094.Seq	M00001557A:F03
575	39486	79.B8.sp6:130035.Seq	M00001561A:C05
576	39380	79.E8.sp6:130071.Seq	M00001587A:B11
577	1399	79.G8.sp6:130095.Seq	M00001604A:B10
578	39391	79.A9.sp6:130024.Seq	M00001604A:F05
579	6268	79.G9.sp6:130096.Seq	M00001551A:B10
580		377.F4.sp6:141957.Seq	M00004692A:H08
581	2448	89.A1.sp6:130667.Seq	M00001460A:F06
582	1531	89.C1.sp6:130691.Seq	M00001461A:D06
583	19	89.D1.sp6:130703.Seq	M00001463C:B11
584	38759	89.F1.sp6:130727.Seq	M00001467A:B07
585	39508	89.G1.sp6:130739.Seq	M00001467A:D04
586	16283	89.H1.sp6:130751.Seq	M00001467A:D08
587	39442	89.A2.sp6:130668.Seq	M00001467A:E10
588	7589	89.B2.sp6:130680.Seq	M00001468A:F05
589		89.C2.sp6:130692.Seq	M00001469A:A01
590	12081	89.D2.sp6:130704.Seq	M00001469A:C10
591	19105	89.E2.sp6:130716.Seq	M00001469A:H12
592	1037	89.F2.sp6:130728.Seq	M00001470A:B10
593	39425	89.G2.sp6:130740.Seq	M00001470A:C04
594	39478	89.H2.sp6:130752.Seq	M00001471A:B01
595		89.B3.sp6:130681.Seq	M00001487B:H06
596		89.C3.sp6:130693.Seq	M00001488B:F12
597	18699	89.D3.sp6:130705.Seq	M00001490B:C04
598	7206	89.E3.sp6:130717.Seq	M00001494D:F06
599	2623	89.F3.sp6:130729.Seq	M00001497A:G02

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
600	10539	89.G3.sp6:130741.Seq	M00001499B:A11
601	5336	89.H3.sp6:130753.Seq	M00001500A:C05
602	2623	89.A4.sp6:130670.Seq	M00001500A:E11
603	9443	89.B4.sp6:130682.Seq	M00001500C:E04
604	9685	89.C4.sp6:130694.Seq	M00001501D:C02
605		89.D4.sp6:130706.Seq	M00001504A:E01
606	10185	89.E4.sp6:130718.Seq	M00001504C:A07
607	6974	89.F4.sp6:130730.Seq	M00001504C:H06
608	6420	89.G4.sp6:130742.Seq	M00001504D:G06
609		89.H4.sp6:130754.Seq	M00001505C:C05
610		89.A5.sp6:130671.Seq	M00001506D:A09
611	39168	89.B5.sp6:130683.Seq	M00001507A:H05
612	39412	89.C5.sp6:130695.Seq	M00001511A:H06
613	39186	89.D5.sp6:130707.Seq	M00001512A:A09
614	3956	89.E5.sp6:130719.Seq	M00001512D:G09
615		89.F5.sp6:130731.Seq	M00001513B:G03
616	14364	89.G5.sp6:130743.Seq	M00001513C:E08
617	40044	89.H5.sp6:130755.Seq	M00001514C:D11
618	8952	89.A6.sp6:130672.Seq	M00001518C:B11
619	35555	89.B6.sp6:130684.Seq	M00001528A:C04
620	18957	89.C6.sp6:130696.Seq	M00001528A:F09
621	8358	89.D6.sp6:130708.Seq	M00001528B:H04
622	38085	89.E6.sp6:130720.Seq	M00001531A:D01
623		89.F6.sp6:130732.Seq	M00001531A:H11
624	3990	89.G6.sp6:130744.Seq	M00001532B:A06
625	16921	89.H6.sp6:130756.Seq	M00001534A:C04
626	5321	89.B7.sp6:130685.Seq	M00001534A:F09
627	4119	89.C7.sp6:130697.Seq	M00001534C:A01
628	20212	89.E7.sp6:130721.Seq	M00001535A:C06
629	2696	89.F7.sp6:130733.Seq	M00001536A:B07
630	39392	89.G7.sp6:130745.Seq	M00001536A:C08
631	39420	89.H7.sp6:130757.Seq	M00001537A:F12
632	3389	89.A8.sp6:130674.Seq	M00001537B:G07
633	8286	89.B8.sp6:130686.Seq	M00001540A:D06
634	3765	89.C8.sp6:130698.Seq	M00001541A:D02
635	39453	89.E8.sp6:130722.Seq	M00001542A:E06
636		89.F8.sp6:130734.Seq	M00001542B:B01
637		89.H8.sp6:130758.Seq	M00001544A:E06
638	6974	89.A9.sp6:130675.Seq	M00001544B:B07
639		89.B9.sp6:130687.Seq	M00001545A:B02
640	19255	89.C9.sp6:130699.Seq	M00001545A:C03
641	1267	89.D9.sp6:130711.Seq	M00001546A:G11
642	5892	89.E9.sp6:130723.Seq	M00001548A:E10

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643	4193	89.G9.sp6:130747.Seq	M00001549B:F06
644	16347	89.H9.sp6:130759.Seq	M00001549C:E06
645	7239	89.A10.sp6:130676.Seq	M00001550A:A03
646	5175	89.B10.sp6:130688.Seq	M00001550A:G01
647	22390	89.C10.sp6:130700.Seq	M00001551A:G06
648	3266	89.D10.sp6:130712.Seq	M00001551C:G09
649	5708	89.E10.sp6:130724.Seq	M00001552B:D04
650		89.F10.sp6:130736.Seq	M00001552D:A01
651	8298	89.G10.sp6:130748.Seq	M00001553A:H06
652	4573	89.H10.sp6:130760.Seq	M00001553B:F12
653	22814	89.A11.sp6:130677.Seq	M00001553D:D10
654	39539	89.B11.sp6:130689.Seq	M00001555A:B02
655	39195	89.C11.sp6:130701.Seq	M00001555A:C01
656	4561	89.D11.sp6:130713.Seq	M00001555D:G10
657	9244	89.E11.sp6:130725.Seq	M00001556A:C09
658	1577	89.F11.sp6:130737.Seq	M00001556A:F11
659	4386	89.H11.sp6:130761.Seq	M00001556B:C08
660	11294	89.A12.sp6:130678.Seq	M00001556B:G02
661	5192	89.D12.sp6:130714.Seq	M00001557B:H10
662	8761	89.E12.sp6:130726.Seq	M00001557D:D09
663		89.F12.sp6:130738.Seq	M00001558A:H05
664	7514	89.G12.sp6:130750.Seq	M00001558B:H11
665		89.H12.sp6:130762.Seq	M00001559B:F01
666	6558	90.A1.sp6:130859.Seq	M00001560D:F10
667	102	90.B1.sp6:130871.Seq	M00001563B:F06
668		90.D1.sp6:130895.Seq	M00001566B:D11
669	5749	90.E1.sp6:130907.Seq	M00001571C:H06
670	6539	90.G1.sp6:130931.Seq	M00001579D:C03
671	6293	90.A2.sp6:130860.Seq	M00001583D:A10
672		90.C2.sp6:130884.Seq	M00001590B:F03
673	260	90.D2.sp6:130896.Seq	M00001594B:H04
674	4837	90.E2.sp6:130908.Seq	M00001597C:H02
675	10470	90.F2.sp6:130920.Seq	M00001597D:C05
676	16999	90.G2.sp6:130932.Seq	M00001598A:G03
677	22794	90.H2.sp6:130944.Seq	M00001601A:D08
678	11465	90.A3.sp6:130861.Seq	M00001607A:E11
679	7802	90.B3.sp6:130873.Seq	M00001608A:B03
680	22155	90.C3.sp6:130885.Seq	M00001608B:E03
681		90.D3.sp6:130897.Seq	M00001608D:A11
682	13157	90.E3.sp6:130909.Seq	M00001614C:F10
683	17004	90.F3.sp6:130921.Seq	M00001617C:E02
684	40314	90.G3.sp6:130933.Seq	M00001619C:F12
685	40044	90.H3.sp6:130945.Seq	M00001621C:C08

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686	13913	90.A4.sp6:130862.Seq	M00001623D:F10
687	3277	90.B4.sp6:130874.Seq	M00001624A:B06
688	4309	90.C4.sp6:130886.Seq	M00001624C:F01
689	5214	90.D4.sp6:130898.Seq	M00001630B:H09
690		90.E4.sp6:130910.Seq	M00001632D:H07
691	39171	90.F4.sp6:130922.Seq	M00001644C:B07
692	19267	90.G4.sp6:130934.Seq	M00001645A:C12
693	4665	90.H4.sp6:130946.Seq	M00001648C:A01
694		90.A5.sp6:130863.Seq	M00001651A:H01
695	23201	90.B5.sp6:130875.Seq	M00001657D:C03
696	76760	90.C5.sp6:130887.Seq	M00001657D:F08
697	23218	90.D5.sp6:130899.Seq	M00001662C:A09
698	35702	90.E5.sp6:130911.Seq	M00001663A:E04
699	6468	90.F5.sp6:130923.Seq	M00001669B:F02
700	14367	90.G5.sp6:130935.Seq	M00001670C:H02
701	7015	90.H5.sp6:130947.Seq	M00001673C:H02
702	8773	90.A6.sp6:130864.Seq	M00001675A:C09
703	11460	90.B6.sp6:130876.Seq	M00001676B:F05
704	7570	90.D6.sp6:130900.Seq	M00001677D:A07
705	4416	90.E6.sp6:130912.Seq	M00001678D:F12
706	6660	90.F6.sp6:130924.Seq	M00001679A:A06
707		90.H6.sp6:130948.Seq	M00001679A:F06
708	26875	90.A7.sp6:130865.Seq	M00001679A:F10
709	6298	90.B7.sp6:130877.Seq	M00001679B:F01
710	78091	90.C7.sp6:130889.Seq	M00001679C:F01
711	10751	90.D7.sp6:130901.Seq	M00001679D:D03
712	10539	90.F7.sp6:130925.Seq	M00001680D:F08
713	17055	90.G7.sp6:130937.Seq	M00001682C:B12
714	5382	90.A8.sp6:130866.Seq	M00001688C:F09
715	4393	90.B8.sp6:130878.Seq	M00001693C:G01
716	67252	90.C8.sp6:130890.Seq	M00001716D:H05
717	40108	90.D8.sp6:130902.Seq	M00003741D:C09
718	11476	90.E8.sp6:130914.Seq	M00003747D:C05
719		90.F8.sp6:130926.Seq	M00003754C:E09
720	697	90.G8.sp6:130938.Seq	M00003759B:B09
721		90.H8.sp6:130950.Seq	M00003761D:A09
722	17076	90.A9.sp6:130867.Seq	M00003762C:B08
723	3108	90.B9.sp6:130879.Seq	M00003763A:F06
724	67907	90.C9.sp6:130891.Seq	M00003774C:A03
725		90.D9.sp6:130903.Seq	M00003784D:D12
726	11350	90.F9.sp6:130927.Seq	M00003826B:A06
727	7899	90.H9.sp6:130951.Seq	M00003837D:A01
728	7798	90.A10.sp6:130868.Seq	M00003839A:D08

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731		90.D10.sp6:130904.Seq	M00003851B:D08
732	13595	90.E10.sp6:130916.Seq	M00003851B:D10
733	5619	90.F10.sp6:130928.Seq	M00003853A:D04
734	10515	90.G10.sp6:130940.Seq	M00003853A:F12
735	4622	90.H10.sp6:130952.Seq	M00003856B:C02
736	3389	90.A11.sp6:130869.Seq	M00003857A:G10
737	4718	90.B11.sp6:130881.Seq	M00003857A:H03
738		90.C11.sp6:130893.Seq	M00003867A:D10
739	12977	90.F11.sp6:130929.Seq	M00003875B:F04
740	8479	90.G11.sp6:130941.Seq	M00003875C:G07
741		90.H11.sp6:130953.Seq	M00003875D:D11
742	7798	90.A12.sp6:130870.Seq	M00003876D:E12
743	5345	90.B12.sp6:130882.Seq	M00003879B:C11
744	31587	90.C12.sp6:130894.Seq	M00003879B:D10
745	14507	90.D12.sp6:130906.Seq	M00003879D:A02
746	13576	90.F12.sp6:130930.Seq	M00003885C:A02
747		90.G12.sp6:130942.Seq	M00003891C:H09
748	9285	90.H12.sp6:130954.Seq	M00003906C:E10
749	39809	99.A1.sp6:131230.Seq	M00003907D:A09
750	16317	99.B1.sp6:131242.Seq	M00003907D:H04
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758	23358	99.F2.sp6:131291.Seq	M00003974D:H02
759	3430	99.A3.sp6:131232.Seq	M00003981A:E10
760	2433	99.B3.sp6:131244.Seq	M00003982C:C02
761	9105	99.C3.sp6:131256.Seq	M00003983A:A05
762	6124	99.D3.sp6:131268.Seq	M00004028D:A06
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764	37285	99.H3.sp6:131316.Seq	M00004035C:A07
765	17036	99.A4.sp6:131233.Seq	M00004035D:B06
766	3706	99.C4.sp6:131257.Seq	M00004068B:A01
767		99.D4.sp6:131269.Seq	M00004072A:C03
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770	6880	99.A5.sp6:131234.Seq	M00004087D:A01
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772	7221	99.D5.sp6:131270.Seq	M00004105C:A04
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774	6874	99.F5.sp6:131294.Seq	M00004111D:A08
775	13183	99.G5.sp6:131306.Seq	M00004114C:F11
776		99.H5.sp6:131318.Seq	M00004121B:G01
777	13272	99.A6.sp6:131235.Seq	M00004138B:H02
778	5257	99.B6.sp6:131247.Seq	M00004146C:C11
779	6455	99.D6.sp6:131271.Seq	M00004157C:A09
780	5319	99.E6.sp6:131283.Seq	M00004169C:C12
781	4908	99.F6.sp6:131295.Seq	M00004171D:B03
782	11494	99.G6.sp6:131307.Seq	M00004172C:D08
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785	8210	99.C7.sp6:131260.Seq	M00004197D:H01
786	14311	99.D7.sp6:131272.Seq	M00004203B:C12
787		99.E7.sp6:131284.Seq	M00004205D:F06
788	12971	99.B8.sp6:131249.Seq	M00004223D:E04
789	6455	99.C8.sp6:131261.Seq	M00004229B:F08
790	7212	99.D8.sp6:131273.Seq	M00004230B:C07
791	4905	99.H8.sp6:131321.Seq	M00004269D:D06
792	16914	99.A9.sp6:131238.Seq	M00004275C:C11
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803	1058	RTA00000126A.e.20.3.Seq_THC217534	
804	5097	RTA00000134A.k.1.1.Seq_THC215869	
805	20212	RTA00000134A.l.22.1.Seq_THC128232	
806	23255	RTA00000177AF.e.14.3.Seq_THC228776	
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809	4059	RTA00000177AF.n.18.3.Seq_THC123051	
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818		RTA00000183AF.g.9.1.Seq_THC198280	
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820	40044	RTA00000186AF.d.1.1.Seq_THC232899	
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822	19267	RTA00000186AF.l.12.1.Seq_THC178183	
823	8773	RTA00000187AF.f.24.1.Seq_THC220002	
824	7570	RTA00000187AF.g.24.1.Seq_THC168636	
825	11476	RTA00000187AF.p.19.1.Seq_THC108482	
826		RTA00000188AF.d.11.1.Seq_THC212094	
827	17076	RTA00000188AF.d.21.1.Seq_THC208760	
828	697	RTA00000188AF.d.6.1.Seq_THC178884	
829	67907	RTA00000188AF.g.11.1.Seq_THC123222	
830	5619	RTA00000188AF.l.9.1.Seq_THC167845	
831	4718	RTA00000189AF.g.5.1.Seq_THC196102	
832	39809	RTA00000190AF.e.3.1.Seq_THC150217	
833	23255	RTA00000190AF.j.4.1.Seq_THC228776	
834	40122	RTA00000190AF.n.23.1.Seq_THC109227	
835	23210	RTA00000190AF.o.20.1.Seq_THC207240	
836	23358	RTA00000190AF.o.21.1.Seq_THC207240	
837	5693	RTA00000190AF.p.17.2.Seq_THC173318	
838	2433	RTA00000191AF.a.15.2.Seq_THC79498	
839	5257	RTA00000192AF.f.3.1.Seq_THC213833	
840	16392	RTA00000192AF.l.1.1.Seq_THC202071	
841		RTA00000193AF.c.21.1.Seq_THC222602	
842	26295	RTA00000193AF.i.24.2.Seq_THC197345	
843		RTA00000193AF.m.5.1.Seq_THC173318	
844		RTA00000193AF.n.15.1.Seq_THC215687	

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
1	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
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3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	BAR3_CHITE	BALBIANI RING PROTEIN 3 PRECURSOR>PIR2:S08167 Balbiani ring 3 protein - midge (Chironomus tentans)>GP:CTBR3_1 C;tentans balbiani ring 3 (BR3) gene	1
5	<NONE>	<NONE>	<NONE>	CYAA_PODAN	ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)>PIR2:JC4747 adenylate cyclase (EC 4.6.1.1) - Podospora anserina>GP:PANADCY_1 Podospora anserina adenyl cyclase gene, exons 1-4	1
6	<NONE>	<NONE>	<NONE>	VP03_HSVSA	PROBABLE MEMBRANE ANTIGEN 3 (TEGUMENT PROTEIN)>PIR2:C36806 hypothetical protein ORF3 - saimiriine herpesvirus 1 (strain 11)>GP:HSGEND_3 Herpesvirus saimiri complete genome DNA; ORF 03; similarity to ORF 75 and EBV BNRF1	0.97

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
7	<NONE>	<NONE>	<NONE>	ATFCA2_18	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 2; Hydroxyproline-rich glycoprotein homolog; Similarity to hydroxyproline-rich glycoprotein precursor-common tobacco	0.93
8	<NONE>	<NONE>	<NONE>	DHAL_ASPNG	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDDH)>GP:ASNALDAA_1 Aspergillus niger aldehyde dehydrogenase (aldA) gene, complete cds	0.9
9	<NONE>	<NONE>	<NONE>	NCU50264_1	Neurospora crassa two-component histidine kinase (nik-1) gene, 5' region and partial cds	0.86
10	<NONE>	<NONE>	<NONE>	NEUG_BOVIN	NEUROGRANIN (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)>PIR2: A39034 neurogranin - bovine (fragment)	0.82
11	<NONE>	<NONE>	<NONE>	HUMBYSTIN_1	Homo sapiens bystin mRNA, complete cds	0.81
12	<NONE>	<NONE>	<NONE>	BTBMP1_1	Bos taurus BMP1 gene, partial sequence; Bone morphogenetic protein 1	0.69
13	<NONE>	<NONE>	<NONE>	TCCYSPROT_1	T;congolense mRNA for (prepro) cysteine proteinase	0.56
14	<NONE>	<NONE>	<NONE>	P60_LISIV	PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN)>GP:LISIAPRELB_1 Listeria	0.15

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ivanovii extracellular protein homologue (iap) gene, complete cds	
15	<NONE>	<NONE>	<NONE>	HEX_ADE31	HEXON PROTEIN (LATE PROTEIN 2) (FRAGMENT)>PIR2: S37217 hexon protein - human adenovirus 31 (fragment)>GP:HSAT31H_1 H;sapiens adenovirus type 31 hexon gene; Hexon protein; Internal fragment containing hypervariable regions	0.15
16	<NONE>	<NONE>	<NONE>	HSU77493_1	Human Notch2 mRNA, partial cds; Transmembrane protein; hN	0.13
17	<NONE>	<NONE>	<NONE>	CYB_PARTE	CYTOCHROME B (EC 1.10.2.2)>PIR2:S07743 cytochrome b - Paramecium tetraurelia mitochondrion (SGC6)>GP:MIPAGEN_19 Paramecium aurelia mitochondrial complete genome; Apocytochrome b (AA 1-391)	0.078
18	<NONE>	<NONE>	<NONE>	HUMERB27_1	Human c-erbB-2 gene, exon 7; C-erb-2 protein	0.054
19	<NONE>	<NONE>	<NONE>	DMTRXIII_2	D;melanogaster DNA for trxI and trxII genes; Trithorax protein trxI; Trithorax; putative>GP:DMTTHORAX_2 D;melanogaster DNA for (putative) trithorax protein; Predicted trithorax protein	0.047

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
20	<NONE>	<NONE>	<NONE>	CELB0281_5	Caenorhabditis elegans cosmid B0281; Similar to reverse transcriptases	0.043
21	<NONE>	<NONE>	<NONE>	MOTY_VIBPA	SODIUM-TYPE FLAGELLAR PROTEIN MOTY PRECURSOR>GP:VPU06949_4 Vibrio parahaemolyticus BB22 RNase T (rnt) gene and flagellar motor component (motY) gene, complete cds	0.041
22	<NONE>	<NONE>	<NONE>	A56263	beta-galactosidase (EC 3.2.1.23) isozyme 12 - Arthrobacter sp. (strain B7)>GP:ASU17417_1 Arthrobacter sp; beta-galactosidase gene, complete cds	0.04
23	<NONE>	<NONE>	<NONE>	GSA_PSEAE	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8) (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)>PIR2:S57898 glutamate 1-semialdehyde 2,1-aminomutase - Pseudomonas aeruginosa>GP:PAHEML_1 P;aeruginosa hemL gene; Glutamate 1-sem	0.038
24	<NONE>	<NONE>	<NONE>	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1 A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.035

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
25	<NONE>	<NONE>	<NONE>	IRS1_RAT	INSULIN RECEPTOR SUBSTRATE-1>PIR2:S16948 hypothetical protein IRS-1 - rat>GP:RNIRS1IRM_1 R;Norvegicus IRS-1 mRNA for insulin-receptor; During insulin stimulation, undergoes tyrosine phosphorylation and binds phosphatidylinositol 3-kinase	0.027
26	<NONE>	<NONE>	<NONE>	CEM02G9_2	Caenorhabditis elegans cosmid M02G9; M02G9;1; Similar to keratin like protein; cDNA EST yk308g11;5 comes from this gene; cDNA EST yk208e11;5 comes from this gene; cDNA EST yk208e11;3 comes	0.0088
27	<NONE>	<NONE>	<NONE>	S75490_3	competence region: iga=IgA protease, comA=transformation competence [Neisseria gonorrhoeae, MS11, Genomic, 3 genes, 2664 nt]	0.0041
28	<NONE>	<NONE>	<NONE>	EXTN_TOBAC	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)>PIR2:S06733 hydroxyproline-rich glycoprotein precursor - common tobacco>GP:NTEXT_1 Tobacco HRGPnt3 gene for extensin; Extensin (AA 1-620)	0.0025

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
29	<NONE>	<NONE>	<NONE>	HPCEGS_1	Hepatitis C virus complete genome sequence; Polyprotein	0.0014
30	<NONE>	<NONE>	<NONE>	HHVBC_4	Human hepatitis virus (genotype C, HMA) preS1, preS2, S, C, X, antigens, core antigen, X protein and polymerase	0.00093
31	<NONE>	<NONE>	<NONE>	HSLTGFBP4_1	Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4; Latent TGF-beta binding protein-4	0.00061
32	<NONE>	<NONE>	<NONE>	S74909	transposase - Synechocystis sp. (PCC 6803)>GP:D90909_108 Synechocystis sp; PCC6803 complete genome, 11/27, 1311235- 1430418; Transposase; ORF_ID:slr2062	0.00051
33	<NONE>	<NONE>	<NONE>	GRN_MOUSE	GRANULINS PRECURSOR (ACROGRANIN)>GP: MUSAP_1 Mouse gene for acrogranin precursor, complete cds	0.00022
34	<NONE>	<NONE>	<NONE>	CA21_MOUSE	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR>PIR2:A43291 collagen alpha 2(I) chain precursor - mouse>GP:MMCOL1A2_1 Mouse COL1A2 mRNA for pro-alpha-2(I) collagen	0.00016
35	<NONE>	<NONE>	<NONE>	MMMHC29N7_2	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-	8.00E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					alpha, palmitoyl-	
36	<NONE>	<NONE>	<NONE>	NFH_RAT	NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT)	2.40E-05
37	<NONE>	<NONE>	<NONE>	HUMVWFM_1	Human von Willebrand factor mRNA, 3' end; Von Willebrand factor prepropeptide	1.70E-05
38	<NONE>	<NONE>	<NONE>	CGHU2E	collagen alpha 2(XI) chain - human (fragment)	2.00E-06
39	<NONE>	<NONE>	<NONE>	A61183	hypothetical protein (sdsB region) - Pseudomonas sp.	4.90E-08
40	<NONE>	<NONE>	<NONE>	YM8L_YEAST	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION>PIR2:S54585 hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae)>GP:SC8021X_4 S;cerevisiae chromosome XIII cosmid 8021; Unknown; YM8021;04, unknown, len: 622, CAI: 0;16,	1.50E-09
41	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210;31, unknown, len: 299 aa, slight similarity to carboxykinases	3.10E-10

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
42	<NONE>	<NONE>	<NONE>	CEC01G10_5	Caenorhabditis elegans cosmid C01G10, complete sequence; C01G10;8; CDNA EST CEMSC45R comes from this gene>GP:CEC01G10_5 Caenorhabditis elegans cosmid C01G10; C01G10;8; CDNA EST CEMSC45R comes from this gene	2.30E-12
43	<NONE>	<NONE>	<NONE>	HSU15779_1	Human p70 (ST5) mRNA, alternatively spliced, complete cds; Differentially expressed; alternatively spliced	9.50E-14
44	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210;31, unknown, len: 299 aa, slight similarity to carboxykinases	1.70E-17
45	U61403	Dictyostelium discoideum PrlA (prlA) mRNA, partial cds.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.95
46	Z92832	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone F31D4; HTGS phase 1.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.94
47	L36557	Oryza sativa (clone pRG3) repetitive element.	1	HSU61262_1	Human neogenin mRNA, complete cds	0.89

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
48	AF005898	Homo sapiens Na,K-ATPase beta-3 subunit pseudogene, complete sequence.	1	LRP1_CHICK	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR)>PIR2:A53102 LDL receptor-related protein / alpha-2-macroglobulin receptor precursor - chicken>GP:GGLRPA 2MR_1 G;gallus mRNA for LRP/alp	0.85
49	U18795	Saccharomyces cerevisiae chromosome V cosmids 9669, 8334, 8199, and lambda clone 1160.	1	NKC1_SQUAC	BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 2 (NA-K-CL SYMPORTER)>PIR2: A53491 bumetanide-sensitive Na-K-C1 cotransporter - spiny dogfish>GP:SANKCC 1_1 Squalus acanthias bumetanide-sensitive Na-K-Cl cotransport protein (NKCC	0.73
50	AC002523	Homo sapiens; HTGS phase 1, 54 unordered pieces.	1	BXEN_CLOBO	BOTULINUM NEUROTOXIN TYPE E, NONTOXIC COMPONENT>GP:C LOENT120_1 C;botulinum gene for nontoxic component of progenitor toxin, complete cds	0.71

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
51	AC002345	*** SEQUENCING IN PROGRESS *** Genomic sequence from Human 17; HTGS phase 1, 10 unordered pieces.	1	P3K2_DICDI	PHOSPHATIDYLINOSITOL 3-KINASE 2 (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)>GP:DDU23477_1 Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK2) mRNA, complete cds	0.58
52	X14253	Human mRNA for cripto protein.	1	I55651	noradrenaline transporter - bovine>GP:BTU09198_1 Bos taurus noradrenaline transporter mRNA, complete cds	0.55
53	U23516	Caenorhabditis elegans cosmid B0416.	1	I69024	MHC sex-limited protein - mouse (fragment)>GP:MUSMHC4AD_1 Mouse class III H2-Slp sex-limited protein gene, exons 1, 2 and 3; MHC sex-limited protein	0.47
54	AB006698	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19.	1	S81293_1	L1 {insertion sequence, provirus} [human papillomavirus type 6b HPV6b, KP4, Genomic Mutant, 121 nt]; Authors note this reading frame results from a 454 bp deletion and resulting	0.25
55	K03458	Human immunodeficiency virus type 1, isolate Zaire 6, vif, tat, rev, env, nef genes and 3' LTR.	1	S13383	hydroxyproline-rich glycoprotein - sorghum	0.24

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
56	B26794	T1O16TR TAMU Arabidopsis thaliana genomic clone T1O16.	1	RK34_PORPU	CHLOROPLAST 50S RIBOSOMAL PROTEIN L34>PIR2:S73111 ribosomal protein L34 - red alga (Porphyra purpurea) chloroplast>GP:PPU38804_4 Porphyra purpurea chloroplast genome, complete sequence; 50S ribosomal protein L34	0.021
57	Z98950	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 507I15; HTGS phase 1.	1	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S21932 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
58	U57057	Human WD protein IR10 mRNA, complete cds.	1	DMU15602_1	Drosophila melanogaster (zeste-white 4) mRNA, complete cds; Similar to C; elegans B0464;4 gene product, Swiss-Prot Accession Number Q03562	0.019
59	U57057	Human WD protein IR10 mRNA, complete cds.	1	CR2_MOUSE	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)>PIR2:A43526 complement C3d/Epstein-Barr virus receptor 2 precursor - mouse>GP:MUSCR2AA_1 Murine complement receptor type 2 (CR2) mRNA, complete cds; Complement receptor type	0.0074

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
60	B65337	CIT-HSP-2021H21.TF CIT-HSP Homo sapiens genomic clone 2021H21.	1	A38096	perlecan precursor - human>GP:HUMHSPG2B_1 Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	0.0051
61	U84722	Human vascular endothelial cadherin mRNA, complete cds.	1	HSTAFII13_1	H;sapiens mRNA for TAFII135; Subunit of RNA polymerase II transcription factor TFIID	0.0012
62	L41493	Avian rotavirus (strain turkey 1) genomic segment 4 outer capsid protein (VP8*) gene.	1	Y328_MYCPN	HYPOTHETICAL PROTEIN MG328 HOMOLOG>PIR2:S73693 MG328 homolog P01_orf1033 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)>GP:MPAE000035_2 Mycoplasma pneumoniae from bases 442306 to 452472 (section 35 of 63) of the complete genome; MG328 homolog,	0.00015
63	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	1	MTCY16B7_3	Mycobacterium tuberculosis cosmid SCY16B7; Unknown; MTCY16B7;03, initiation factor, len: 900, similar at C-terminal half to eg IF2_BACSU P17889 initiation factor if-2 (716 aa), fasta	6.30E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
64	J04974	Human alpha-2 type XI collagen mRNA (COL11A2).	1	GDF6_BOVIN	GROWTH/DIFFERENTIATION FACTOR GDF-6 PRECURSOR (CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT)>PIR2: B55452 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)>GP:BTU13661_1 Bos taurus cartilage-derived morp	1.00E-05
65	AC002394	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-211C6 ~complete genomic sequence, complete sequence.	1	CELC14F11_6	Caenorhabditis elegans cosmid C14F11; Similar to aspartate aminotransferase; coded for by C; elegans cDNA CEMSF95FB; coded for by C; elegans cDNA yk41e4;3; coded for by C; elegans	4.60E-06
66	AB002312	Human mRNA for KIAA0314 gene, partial cds.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)	1.00E-09
67	AC003085	Human BAC clone RG094H21 from 7q21-q22, complete sequence.	1	DP19_CAEEL	DPY-19 PROTEIN>PIR2:S44629 f22b7.10 protein - Caenorhabditis elegans>GP:CELF22B7_9 C;aenorhabditis elegans (Bristol N2) cosmid F22B7; Putative	4.20E-11
68	X55026	P.anserina complete mitochondrial genome.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFER	8.40E-12

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
					ASE 1)	
69	Z95399	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6; HTGS phase 1.	1	CER06B9_5	Caenorhabditis elegans cosmid R06B9, complete sequence; R06B9;b; Protein predicted using Genefinder; preliminary prediction	1.50E-24
70	AC002339	Arabidopsis thaliana chromosome II BAC T11A07 genomic sequence, complete sequence.	0.99	POLG_BVDVS	GENOME POLYPROTEIN>PIR1:A44217 genome polyprotein - bovine viral diarrhea virus (strain SD-1)>GP:BVDPOLYPRO_1 Bovine viral diarrhea virus polyprotein RNA, complete cds; Putative	1
71	Y08559	B.subtilis urease operon and downstream DNA.	0.99	LRP_CAEEL	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN PRECURSOR (LRP)>PIR2:A47437 LDL-receptor-related protein - Caenorhabditis elegans>GP:CEF29D11_2 Caenorhabditis elegans cosmid F29D11, complete sequence; F29D11;1; Protein predicted using Genefi	1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
72	U67548	Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome.	0.99	YB60_YEAST	HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION>PIR2:S46084 probable membrane protein YBR210w - yeast (Saccharomyces cerevisiae)>GP:SCYBR210W_1 S;cerevisiae chromosome II reading frame ORF YBR210w	1
73	U51645	Plasmodium falciparum cytidine triphosphate synthetase gene, complete cds.	0.99	HPSVRPL_1	Sin Nombre virus (NM H10) RNA L segment encoding RNA polymerase (L protein), complete cds; Viral RNA polymerase (L protein); Putative>GP:HPSVRPLA_1 Sin Nombre virus (NM R11) RNA L segment encoding RNA polymerase (L protein), complete cds; Vir	0.99
74	Z49889	Caenorhabditis elegans cosmid T06H11, complete sequence.	0.99	MUSHDPROB_1	Mouse alternatively spliced HD protein mRNA, complete cds	0.021
75	Z69374	Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains a pair of ESTs.	0.99	NCPR_YEAST	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	0.017

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
76	Z35847	S.cerevisiae chromosome II reading frame ORF YBL086c.	0.99	CYPA_CAEEL	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10)>GP:CELB0252_4 Caenorhabditis elegans cosmid B0252; Similar to peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)>GP: CEU34954_1 Caenorhabditis el	0.0044
77	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.99	CELR148_1	Caenorhabditis elegans cosmid R148; Contains similarity to drosophila DNA-binding protein K10 (NID:g8148); coded for by C; elegans cDNA yk118e11;5; coded for by C; elegans cDNA	0.0032
78	Y00324	Chicken vitellogenin gene 3' flanking region.	0.99	A56922	transcription factor shn - fruit fly (Drosophila melanogaster)	0.0023
79	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.99	OMU25146_1	Oncorhynchus mykiss recombination activating protein 2 gene, partial cds	0.0017
80	Z69880	H.sapiens SERCA3 gene (partial).	0.99	M84D_DROME	MALE SPECIFIC SPERM PROTEIN MST84DD>PIR2:S25775 testis-specific protein Mst84Dd - fruit fly (Drosophila melanogaster)>GP:DMMST84D_4 D;melanogaster Mst84Da, Mst84Db, Mst84Dc and Mst84Dd genes for put; sperm protein	0.0011

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
81	M99166	Escherichia coli Trp repressor binding protein (wrbA) gene, complete cds.	0.99	MTU88962_1	Mycobacterium tuberculosis unknown protein gene, partial cds	6.50E-07
82	X99257	R.norvegicus mRNA for lamin C2.	0.99	MIU68729_1	Meloidogyne incognita cuticle preprocollagen (col-2) mRNA, complete cds; Putative	1.60E-09
83	AC002432	Human BAC clone RG317G18 from 7q31, complete sequence.	0.98	1FMDC	Foot and mouth disease virus type c-s8c1, chain C - foot and mouth disease virus type c-s8c1 expressed in hamster kidney cells	0.14
84	Z34799	Caenorhabditis elegans cosmid F34D10, complete sequence.	0.98	MMU57368_1	Mus musculus EGF repeat transmembrane protein mRNA, complete cds; Notch like repeats; notch 2	0.0028
85	B15207	344E15.TV CIT978SKA1 Homo sapiens genomic clone A-344E15.	0.98	POLG_HCVJ6	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5))>PI	0.00083

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
86	AC002412	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.98	KDG1_ARATH	DIACYLGLYCEROL KINASE 1 (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1)>PIR2:S71467 diacylglycerol kinase (EC 2.7.1.107) ATDGK1 - Arabidopsis thaliana>GP:ATHATDGK1_1 Arabidopsis thaliana mRNA for diacylglycerol kinase, complete c	0.00024
87	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15.	0.98	D80005_1	Human mRNA for KIAA0183 gene, partial cds	5.90E-10
88	M83093	Neurospora crassa cAMP-dependent protein kinase (cot-1) gene, complete cds.	0.98	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	3.00E-22
89	U96271	Helicobacter pylori heat shock protein 70 (hsp70) gene, complete cds.	0.97	SLMEN6_1	S;latifolia mRNA for Men-6 protein>GP:SLMEN6_1 S;latifolia mRNA for Men-6 protein	0.43
90	U49944	Caenorhabditis elegans cosmid C39E6.	0.97	RON_HUMAN	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (EC 2.7.1.112)>PIR2:I38185 protein-tyrosine kinase (EC 2.7.1.112), receptor type ron - human>GP:HSRON_1 H;sapiens RON mRNA for tyrosine kinase; Putative	0.034

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
91	Y09255	B.cereus dnaI gene, partial.	0.97	CELT05C1_5	Caenorhabditis elegans cosmid T05C1; Coded for by C; elegans cDNA yk30f6;3; coded for by C; elegans cDNA yk34f10;3	0.00043
92	AC002413	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.96	CELC44E4_5	Caenorhabditis elegans cosmid C44E4; Weak similarity to the drosophila hyperplastic disc protein (GB:L14644); coded for by C; elegans cDNA yk49h6;5; coded for by C; elegans cDNA	1
93	U41625	Caenorhabditis elegans cosmid K03A1.	0.96	HMGC_HUMAN	HIGH MOBILITY GROUP PROTEIN HMGI-C>PIR2:JC2232 high mobility group I-C phosphoprotein - human>GP:HSHMGICG5_1 Human high-mobility group phosphoprotein isoform I-C (HMGIC) gene, exon 5>GP:HSHMGICP_1 H;sapiens mRNA for HMGI-C protein>GP:HSHMGIC	1
94	Z82202	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34P24; HTGS phase 1.	0.96	YTH3_CAEEL	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II>GP:CEC14A4_3 Caenorhabditis elegans cosmid C14A4, complete sequence; C14A4;3; Weak similarity with a B; Flavum translocation protein (Swiss Prot accession number P38376)	0.73

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
95	AL008734	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8; HTGS phase 1.	0.96	S25299	extensin precursor (clone Tom L-4) - tomato>GP:TOMEXTENB_1 L;esculentum extensin (class II) gene, complete cds	0.0004
96	L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds.	0.96	HUMCOL7A1X_1	Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds	4.60E-06
97	X97384	A.thaliana atran3 gene.	0.95	<NONE>	<NONE>	<NONE>
98	M62505	Human C5a anaphylatoxin receptor mRNA, complete cds.	0.95	RIPB_BRYDI	RIBOSOME-INACTIVATING PROTEIN BRYODIN (RRNA N-GLYCOSIDASE) (EC 3.2.2.22) (FRAGMENT)>PIR2:S16491 rRNA N-glycosidase (EC 3.2.2.22) bryodin - red bryony (fragment)	0.83
99	D28778	Cucumber mosaic virus RNA 1 for 1a, complete sequence.	0.95	POLS_RUBVM	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2)>PIR1:GNWVR3 structural polyprotein - rubella virus (strain M33)>GP:TORUB24S_1 Rubella virus 24S subgenomic mRNA for structural proteins E1, E2 and C;	0.00037
100	AF016202	Homo sapiens immunoglobulin heavy chain CDR3 gene,	0.93	HSU79716_1	Human reelin (RELN) mRNA, complete cds	1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		partial cds.				
101	Z68303	Caenorhabditis elegans cosmid ZK809, complete sequence.	0.93	HS5HT4SAR_1	H;sapiens mRNA for serotonin 4SA receptor (5-HT4SA-R)	0.87
102	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.93	S37594	mucin - human (fragment)	0.0019
103	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.93	S38480	nonstructural protein - rubella virus>GP:RVM33NP_1 Rubella virus M33 RNA for a nonstructural protein; Nonstructural protein genes	2.30E-06
104	D88687	Human mRNA for KM-102-derived reductase-like factor, complete cds.	0.93	BAT3_HUMAN	LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3)>PIR2:A35098 MHC class III histocompatibility antigen HLA-B-associated transcript 3 - human>GP:HUMBAT3A_1 Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds>GP:HUMBAT3	8.70E-07
105	D16847	Mouse mRNA for stromal cell derived protein-1, complete cds.	0.93	S52796	prpL2 protein - human (fragment)>GP:HSPRPL2_1 H;sapiens mRNA for PRPL-2 protein	3.20E-08

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
106	D90915	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259.	0.92	YEK9_YEAST	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S50477 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE9537_20 Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898	5.90E-05
107	AJ001101	Mus musculus mRNA for gC1qBP gene.	0.92	DMU58282_1	Drosophila melanogaster Bowel (bowl) mRNA, complete cds; Transcription factor; C2H2 zinc finger protein; zinc fingers have extensive sequence similarity to Drosophila odd-skipped	3.50E-05
108	X57108	Human gene for cerebroside sulfate activator protein, exons 10-14.	0.92	S69032	hypothetical protein YPR144c - yeast (Saccharomyces cerevisiae)>GP:YSCP9659_17 Saccharomyces cerevisiae chromosome XVI cosmid 9659; Ypr144cp; Weak similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot; accession number P11213)	4.30E-21

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
109	D14635	Caenorhabditis elegans DNA for EMB-5.	0.91	YM13_YEAST	PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W>PIR2:S53058 probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae)>GP:SC9553_4 S;cerevisiae chromosome XIII cosmid 9553; Unknown; YM9553;04, probable ATP-dependent RNA helicase, len:	0.69
110	B55500	CIT-HSP-387J2.TFB CIT-HSP Homo sapiens genomic clone 387J2.	0.91	U97553_79	Murine herpesvirus 68 strain WUMS, complete genome; Unknown	0.00016
111	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.9	POL_MLVAV	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))>PIR1:GNMVGV pol polyprotein - AKV murine leukemia virus	0.0019
112	U91327	Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.	0.89	JC5568	serine protease (EC 3.4.-.-) h1 - Serratia marcescens	1
113	X13295	Rat mRNA for alpha-2u globulin-related protein.	0.89	MNGPOLY_1	Mengo virus polyprotein genome, complete cds withe repeats	1
114	Z78415	Caenorhabditis elegans cosmid C17G1, complete sequence.	0.89	AB000121_1	Mouse mRNA for TBPIP, complete cds; TBP1 interacting protein	0.39

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
115	AC002308	*** SEQUENCING IN PROGRESS *** Human Chromosome 22q11 BAC Clone 1000e4; HTGS phase 1, 26 unordered pieces.	0.88	YLK2_CAEEL	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0037
116	AC002073	Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.	0.88	S28499	probable finger protein - rat>GP:RNZFP_1 R;norvegicus mRNA for putative zinc finger protein	1.10E-31
117	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.	0.87	NDL_DROME	SERINE PROTEASE NUDEL PRECURSOR (EC 3.4.21.-)>PIR2:A57096 nudel protein precursor - fruit fly (Drosophila melanogaster)>GP:DMU29153_1 Drosophila melanogaster nudel (ndl) mRNA, complete cds; Serine protease; Soma dependent gene required matern	1
118	U23449	Caenorhabditis elegans cosmid K06A1.	0.87	AF023268_3	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3)	0.21
119	Z68181	H.vulgaris mRNA for elongation factor EF1-alpha.	0.87	RABCY450C_1	Rabbit cytochrome P-450 gene, clone pP-450PBc3, 3' end	0.14

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
120	AC000033	Homo sapiens chromosome 9, complete sequence.	0.87	VWF_CANFA	VON WILLEBRAND FACTOR PRECURSOR>GP:DOGVWG_1 Canis familiaris von Willebrand factor mRNA, complete cds	0.036
121	U23449	Caenorhabditis elegans cosmid K06A1.	0.86	S48988_1	CRP-1=cystatin-related protein [rats, Wistar albino, mRNA Partial, 213 nt]; Cystatin-related protein; Method: conceptual translation supplied by author; This sequence comes from Fig;	0.64
122	Z89651	F.rubripes GSS sequence, clone 090I24cD5.	0.86	CPU65981_1	Cryptosporidium parvum P-ATPase gene (CppA-E1) gene, complete cds; Putative calcium-ATPase	0.6
123	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	0.86	GLTB_SYNY3	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1 (EC 1.4.7.1) (FD-GOGAT)>PIR2:S60228 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803)>GP:D90902_66 Synechocystis sp; PCC6803 complete genome, 4/27, 402290-524345; Gluta	0.03
124	Z49250	Human DNA sequence from cosmid HW2, Huntington's Disease Region, chromosome 4p16.3.	0.86	TRSCAPSID_1	Tobacco ringspot virus capsid protein gene, complete cds	3.00E-06

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
125	Z92855	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48C3; HTGS phase 1.	0.84	AE000809_8	Methanobacterium thermoautotrophicum from bases 161632 to 172569 (section 15 of 148) of the complete genome; Aspartyl-. tRNA synthetase; Function Code:10;07 - Metabolism of	1
126	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	CET01E8_3	Caenorhabditis elegans cosmid T01E8, complete sequence; T01E8;3; Similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; cDNA EST CEESG02F comes from this gene;	0.86
127	AL008716	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 206C7; HTGS phase 1.	0.83	HIVU51189_5	HIV-1 clone 93th253 from Thailand, complete genome; Tat protein	0.86
128	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	S60257	meltrin alpha - mouse>GP:MUSMAB_1 Mouse mRNA for meltrin alpha, complete cds	0.0013

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
129	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.	0.82	ARO1_PNECA	PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3-DEHYDROQUINATE SYNTHASE (EC 4.6.1.3), 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE), SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25), SHIKIMATE KINASE (EC 2.7.1.71), AND EPSP SYNTHASE (E	0.0098
130	AF029308	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.	0.8	CELZK84_5	Caenorhabditis elegans cosmid ZK84; Final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein; coded for by C; elegans	2.00E-08
131	AC002458	Human BAC clone RG098M04 from 7q21-q22, complete sequence.	0.78	IGF2_PIG	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II)>GP:SSIGF2_1 S;scrofa mRNA IGF2 for insulin-like-growth factor 2; Insulin- like-growth factor 2 preproprotein	0.44
132	Z83843	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 368A4; HTGS phase 1.	0.78	PAR51A_1	P;tetraurelia 51A surface protein gene, complete cds	0.0014

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
133	X03021	Human gene for granulocyte-macrophage colony stimulating factor (GM-CSF).	0.78	CEF57B1_3	Caenorhabditis elegans cosmid F57B1, complete sequence; F57B1;3; Protein predicted using Genefinder; similar to collagen	2.20E-05
134	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.	0.77	SYLM_SCHPO	PUTATIVE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)>PIR2:S62486 hypothetical protein SPAC4G8.09 - fission yeast (Schizosaccharomyces pombe)>GP:SPAC4G8_9 S;pombe chromosome I cosmid c4G8; Unknown; SPAC	0.96
135	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.	0.77	RNU59809_1	Rattus norvegicus mannose 6-phosphate/insulin-like growth factor II receptor (M6P/IGF2r) mRNA, complete cds; Also termed IGF-II/Man 6-P receptor, MPR, CI-MPR	0.01
136	U80445	Caenorhabditis elegans cosmid C50F2.	0.76	S28499	probable finger protein - rat>GP:RNZFP_1 R;norvegicus mRNA for putative zinc finger protein	1.10E-31
137	Z78545	Caenorhabditis elegans cosmid M03B6, complete sequence.	0.75	RRU73586_1	Rattus norvegicus Fanconi anemia group C mRNA, complete cds; Fanconi anemia group C protein; Similar to human FAC protein, GenBank Accession Numbers X66893 and X66894	0.023

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
138	Z97630	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1; HTGS phase 1.	0.74	HSMSHRECA_1	H;sapiens mRNA for MSH receptor; Author-given protein sequence is in conflict with the conceptual translation	0.036
139	AF007269	Arabidopsis thaliana BAC IG002N01.	0.71	HSU95090_1	Homo sapiens chromosome 19 cosmid F19541, complete sequence; F19541_1; Hypothetical (partial) protein similar to proline oxidase	0.16
140	AC002393	Mouse BAC284H12 Chromosome 6, complete sequence.	0.7	RNLTBP2_1	Rattus norvegicus mRNA for LTBP-2 like protein; Latent TGF-beta binding protein-2 like protein	4.40E-05
141	B15232	344G8.TV CIT978SKA1 Homo sapiens genomic clone A-344G08.	0.67	DMSEVL2_2	Drosophila melanogaster sevenless mRNA; Put; sevenless protein (AA 1 - 2510)	0.41
142	D13748	Human mRNA for eukaryotic initiation factor 4AI.	0.66	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein	0.00016
143	S45791	band 3-related protein=renal anion exchanger AE2 homolog [rabbits, New Zealand White, ileal epithelial cells, mRNA, 3964 nt].	0.66	POLS_RUBVR	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2)>PIR1:GNWVRA structural polyprotein - rubella virus (strain RA27/3 vaccine)>GP:RUBCE21_1 Rubella virus RA27/3 RNA for capsid, E2 and E1 proteins; Poly	5.60E-05
144	M22462	Chicken protein p54 (ets-1)	0.66	HSHP8PROT_1	H;sapiens mRNA for HP8 protein; HP8	2.00E-06

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA, complete cds.			peptide	
145	U27999	Human clone pDEL52A11 HLA-C region cosmid 52 genomic survey sequence.	0.65	CA18_HUMAN	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)>PIR2:S15435 collagen alpha 1(VIII) chain precursor - human>GP:HSCOL8A1_1 Human COL8A1 mRNA for alpha 1(VIII) collagen	5.70E-06
146	M54787	N.crassa mating type a-1 protein (mt a-1) gene, exons 1-3.	0.64	I50717	vacuolar H+-ATPase A subunit - chicken (fragment)>GP:GGU22078_1 Gallus gallus vacuolar H+-ATPase A subunit gene, partial cds	0.0046
147	AC002094	Genomic sequence from Human 17, complete sequence.	0.63	PVPVA1_1	P;vivax pva1 gene	0.1
148	U32701	Haemophilus influenzae from bases 165345 to 176101 (section 16 of 163) of the complete genome.	0.63	FABG_HAEIN	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL- ACYL CARRIER PROTEIN REDUCTASE)>PIR2:D64051 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Haemophilus influenzae (strain Rd KW20)>GP:HIU32701_7 Haemophilus	2.00E-12
149	Z37159	T.brucei serum resistance associated (SRA) mRNA for VSG-like protein.	0.61	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
150	AF027865	Mus musculus Major Histocompatibility Locus class II region.	0.61	A56514	chromokinesin - chicken>GP:GGU18309_1 Gallus gallus chromokinesin mRNA, complete cds	0.045
151	U40938	Caenorhabditis elegans cosmid D1009.	0.61	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	1.90E-24
152	I16670	Sequence 1 from patent US 5476781.	0.59	CELF21F8_7	Caenorhabditis elegans cosmid F21F8; Similar to eukaryotic aspartyl proteases	0.39
153	Z84468	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 299D3; HTGS phase 1.	0.59	CLG1_YEAST	CYCLIN-LIKE PROTEIN CLG1>PIR2:S37607 cyclin-like protein YGL215w - yeast (Saccharomyces cerevisiae)>GP:SCYGL215W_1 S;cerevisiae chromosome VII reading frame ORF YGL215w>GP:YSCCLG1CPR_1 Saccharomyces cerevisiae cyclin-like protein (CLG1) gene	0.0015
154	U00054	Caenorhabditis elegans cosmid K07E12.	0.57	<NONE>	<NONE>	<NONE>
155	M21207	Synthetic SV40 T antigen mutant pseudogene, 3' end.	0.57	1CJL2	cathepsin L (EC 3.4.22.15) mutant (F(78P)L, C25S, T110A, E176G, D178G), fragment 2 - human	0.43

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
156	AF020282	Dictyostelium discoideum DG2033 gene, partial cds.	0.56	AC002125_4	Homo sapiens DNA from chromosome 19-cosmid F25965, genomic sequence, complete sequence; F25965_5; Hypothetical 35;3 kDa protein similar to GTPase-activating proteins and orf3 from	0.6
157	M86352	Stigmatella aurantiaca reverse transcriptase (163 RT) gene, complete cds.	0.56	AC002398_4	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence; F25965_3; Hypothetical 96 kDa human protein similar to alpha chimaerin; Hypothetical protein>GP:AC002398_4 Human DNA from chromosome 19-specific cosmi	4.50E-06
158	AC003101	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.54	<NONE>	<NONE>	<NONE>
159	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	CEF32H2_5	Caenorhabditis elegans cosmid F32H2, complete sequence; F32H2;5; Similarity to Chicken fatty acid synthase (SW:P12276); cDNA EST yk16c2;5 comes from this gene; cDNA EST yk113h6;5 comes	1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
160	AE000664	Mus musculus TCR beta locus from bases 250554 to 501917 (section 2 of 3) of the complete sequence.	0.54	CET01G9_6	Caenorhabditis elegans cosmid T01G9, complete sequence; T01G9;4; CDNA EST yk29b7;5 comes from this gene	0.84
161	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	A39718	nicotinic acetylcholine receptor alpha chain - marbled electric ray (fragments)	0.27
162	Z71261	Caenorhabditis elegans cosmid F21C3, complete sequence.	0.5	KDGE_DROME	EYE-SPECIFIC DIACYLGLYCEROL KINASE (EC 2.7.1.107) (RETINAL DEGENERATION A PROTEIN) (DIGLYCERIDE KINASE) (DGK)>GP:DRODAGK_1 Fruit fly mRNA for diacylglycerol kinase, complete cds	4.60E-05
163	M61831	Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds.	0.49	P2C2_ARATH	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)>PIR2:S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana>GP:ATHPP2CA_1 Arabidopsis thaliana mRNA for protein phosphatase 2C	5.60E-08
164	U42608	Glycine max clathrin heavy chain mRNA, complete cds.	0.48	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
165	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.47	PYRD_BACSU	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) (DHODEHASE)>PIR1:H39845 dihydroorotate oxidase (EC 1.3.3.1) - Bacillus subtilis>GPN:BSUB0009_25 Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200;	0.002
166	AC000044	Human Chromosome 22q13 Cosmid Clone p76e10, complete sequence.	0.47	MATK_MARPO	PROBABLE INTRON MATURASE>PIR2:A05034 hypothetical protein 370i - liverwort (Marchantia polymorpha) chloroplast>GP:CHMPXX_21 Liverwort Marchantia polymorpha chloroplast genome DNA; ORF370i	0.0011
167	X51508	Rabbit mRNA for aminopeptidase N (partial).	0.47	S45361	LRR47 protein - fruit fly (Drosophila melanogaster)>GP:DMLRR47_1 D;melanogaster mRNA for LRR47	5.30E-07
168	Z67035	H.sapiens DNA segment containing (CA) repeat; clone AFM323yf1; single read.	0.45	JQ2246	22.5K cathepsin D inhibitor protein precursor - potato>GP:POTCATHD_1 Potato cathepsin D inhibitor protein mRNA, complete cds	0.79
169	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.44	SMU31768_1	Schistosoma mansoni elastase gene, 3045 bp clone, complete cds	0.0022

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
170	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.43	HUMPKD1G08_1	Homo sapiens polycystic kidney disease (PKD1) gene, exons 43-46; Polycystic kidney disease 1 protein	1
171	Z95889	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 211A9; HTGS phase 1.	0.43	A09811_1	R;norvegicus mRNA for BRL-3A binding protein; Author-given protein sequence is in conflict with the conceptual translation	0.00083
172	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.43	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CELF37A4_8 Caenorhabditis elegans cosmid F37A4	2.50E-28
173	Z99281	Caenorhabditis elegans cosmid Y57G11C, complete sequence.	0.42	PTU19464_1	Paramecium tetraurelia outer arm dynein beta heavy chain gene, complete cds	1
174	X04571	Human mRNA for kidney epidermal growth factor (EGF) precursor.	0.42	YEK9_YEAST	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S50477 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE9537_20 Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898	0.99

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
175	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.41	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CELF37A4_8 Caenorhabditis elegans cosmid F37A4	7.80E-21
176	AC002053	Human Chromosome 9p22 Cosmid Clone 92f5, complete sequence.	0.4	HSU33837_1	Human glycoprotein receptor gp330 precursor, mRNA, complete cds	1
177	U88309	Caenorhabditis elegans cosmid T23B3.	0.4	DROMTTGNC_1	Drosophila melanogaster mitochondrial cytochrome c oxidase subunit I (COI) gene, 5' end, Trp-, Cys-, and Tyr-tRNA genes, NADH dehydrogenase subunit 2 (ND2) gene, 3' end	0.99
178	M34025	Human fetal Ig heavy chain variable region (clone M44) mRNA, partial cds.	0.39	DNA2_YEAST	DNA REPLICATION HELICASE DNA2>PIR2:S48904 probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae)>GPN:YSCH9986_3 Saccharomyces cerevisiae chromosome VIII cosmid 9986; Dna2p: DNA replication helicase; YHR164C>GP:	1
179	AC002395	Homo sapiens; HTGS phase 1, 127 unordered pieces.	0.39	VV_MUMPE	NONSTRUCTURAL PROTEIN V (NONSTRUCTURAL PROTEIN NS1)	0.11

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
180	AC003101	*** . SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.39	YLK2_CAEEL	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0001
181	Z54335	Human DNA sequence from cosmid L17A9, Huntington's Disease Region, chromosome 4p16.3. Contains VNTR and a CpG island.	0.39	HUMNFAT3A_1	Homo sapiens NF-AT3 mRNA, complete cds	1.60E-06
182	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	0.38	CEZC434_6	Caenorhabditis elegans cosmid ZC434, complete sequence; ZC434;6; CDNA EST CEESO02F comes from this gene; cDNA EST CEESS60F comes from this gene	0.18
183	AC001229	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence.	0.34	HSOCAM_1	H;sapiens mRNA for immunoglobulin-like domain-containing 1 protein	0.051
184	X01703	Human gene for alpha-tubulin (b alpha 1).	0.33	NTC3_MOUSE	NEUROGENIC LOCUS NOTCH 3 PROTEIN>PIR2:S45306 notch 3 protein - mouse>GP:MMNOTC_1 M;musculus mRNA for Notch 3	0.012

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
185	Z82189	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 170A21; HTGS phase 1.	0.31	LG106_3	Lemna gibba negatively light-regulated mRNA (Lg106); Second longest ORF (2)	0.27
186	Z98051	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4; HTGS phase 1.	0.3	S34960	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion (SGC6)>GP:MICOCNNR_3 Crithidia oncopelti mitochondrial ND4, ND5, COI, 12S ribosomal RNA genes for NADH dehydrogenase subunit 4/5, cytochrome oxidase subun	0.25
187	Z98749	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 449O17; HTGS phase 1.	0.3	SCKC_LEIQH	CHARYBDOTOXIN (CHTX) (CHTX-LQ1)>PIR2:A60963 charybdotoxin 1 - scorpion (Leiurus quinquestriatus)>3D:2CRD Charybdotoxin (nmr, 12 structures) - scorpion (Leiurus quinquestriatus)	0.12
188	X96763	C.albicans CDC4 gene.	0.29	CECC4_1	Caenorhabditis elegans cosmid CC4, complete sequence; CC4;a; Protein predicted using Genefinder; preliminary prediction	1.30E-17

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
189	U38804	Porphyra purpurea chloroplast genome, complete sequence.	0.28	HIVHCDR3C_1	Human immunodeficiency virus type 1 heavy-chain complemetarity-determining region 3 mRNA (clone 11), partial cds; Heavy-chain complementarity-determining region 3 (CDR3) from HIV gp120->GP:HIVHCDR3I_1 Human immunodeficiency virus type 1 he	1
190	U20657	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds.	0.28	HSU20657_1	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds	5.60E-12
191	AC002037	Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.	0.27	VRP1_YEAST	VERPROLIN>GP:SCVERPRL_1 S;cerevisiae (A364) gene for verprolin	2.00E-11
192	U58748	Caenorhabditis elegans cosmid ZK180.	0.27	EXLP_TOBAC	PISTIL-SECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)>PIR2:JQ1696 pistil extensin-like protein precursor (clone pMG15) - common tobacco>GP:NTPMG15_1 N;tabacum mRNA for pistil extensin like protein	4.10E-12
193	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence.	0.26	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
194	AF017042	Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 5' end.	0.26	SPBC31F10_14	S;pombe chromosome II cosmid c31F10; Hypothetical protein; SPBC31F10;14c, unknown, len:1586aa, some similarity eg; to YJR140C, YJ9H_YEAST, P47171, involved in cell cycle regulation	1
195	B03174	cSRL-16e2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-16e2.	0.26	CELC30E1_7	Caenorhabditis elegans cosmid C30E1	0.38
196	X70810	E.gracilis chloroplast complete genome.	0.25	CEK10H10_8	Caenorhabditis elegans cosmid K10H10, complete sequence; K10H10;k; Protein predicted using Genefinder; preliminary prediction	0.98
197	U80024	Caenorhabditis elegans cosmid C18B10.	0.25	MMAF001794_1	Mus musculus Treacher Collins Syndrome protein (Tcof1) mRNA, complete cds; Putative nucleolar phosphoprotein; similar to Homo sapiens Treacher Collins syndrome TCOF1 protein encoded>GP:MMAF001794_1 Mus musculus Treacher Collins Syndrome p	0.017

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
198	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOLI	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli , mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068
199	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOLI	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli , mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068
200	Z99571	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 388N15; HTGS phase 1.	0.24	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	0.017
201	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.24	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
202	AC003061	*** SEQUENCING IN PROGRESS *** Mouse Chromosome 6 BAC clone b245c12; HTGS phase 2, 8 ordered pieces.	0.23	CG1_HUMAN	CG1 PROTEIN>GP:HSU46023_1 Human Xq28 mRNA, complete cds; Orf	0.00078
203	AF009420	Homo sapiens microsatellite sequence in the HNF3a gene.	0.22	PN0675	collagen alpha 1(XVIII) chain - mouse (fragment)>GP:MUSCOLLAG_1 Mouse mRNA for collagen, partial cds	0.00072
204	B18861	F20C18-Sp6 IGF Arabidopsis thaliana genomic clone F20C18.	0.22	TFDP00659	- Polypeptides entry for factor PR	0.0003
205	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.22	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05
206	X52105	Dictyostelium discoideum SP60 gene for spore coat protein.	0.18	<NONE>	<NONE>	<NONE>
207	L07628	Saccharopolyspora erythraea insertion sequence IS1136, copy B, 3' end.	0.17	D88764_1	Rana catesbeiana mRNA for alpha 2 type I collagen, complete cds	0.00021
208	Z49631	S.cerevisiae chromosome X reading frame ORF YJR131w.	0.16	YSCDAL1A_1	Saccharomyces cerevisiae alantoinase (DAL1) gene, complete cds	1
209	Z87893	F.rubripes GSS sequence, clone 043C17aB8.	0.16	CELC27A12_8	Caenorhabditis elegans cosmid C27A12; Partial CDS; this gene begins in the neighboring clone; coded for by C; elegans cDNA yk127f1;3; coded for by C; elegans cDNA yk127f1;5	1.30E-07

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
210	U92852	Rhoiptelea chiliantha maturase (matK) gene, chloroplast gene encoding chloroplast protein, complete cds.	0.15	SEU40259_5	Staphyloccous epidermidis trimethoprim resistance plasmid pSK639; Orf53	0.95
211	X62620	B.mori Abd-A gene homeobox.	0.15	ATAP22_36	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No; 2; Hypothetical protein; Similarity to NADH dehydrogenase, Chondrus crispus; MNOS:S59107	0.75
212	J02079	epstein-barr virus simple repeat array (ir3).	0.15	A38346	ultra-high-sulfur keratin 1 - mouse>GP:MUSSER1_1 Mouse serine 1 ultra high sulfur protein gene, complete cds; Putative	7.50E-05
213	M35027	Vaccinia virus, complete genome.	0.14	MTF1_FUSNU	MODIFICATION METHYLASE FNUDI (EC 2.1.1.73) (CYTOSINE-SPECIFIC METHYLTRANSFERASE FNUDI) (M.FNUDI)	0.87
214	AC003058	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'IGF' BAC 'F27F23' genomic sequence near marker 'CIC06E08'; HTGS phase 1, 8 unordered pieces.	0.14	HEXA_DICDI	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE)>PIR2:A30766 beta-N-acetylhexosaminidase (EC 3.2.1.52) A precursor - slime mold (Dictyostelium	0.006

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					discoideum)>GP:DDINAGA_1 D;d	
215	AC001229	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence.	0.13	A49281	pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (isolate Bab34) (fragment)>GP:STVBABPOLA_1 Simian T-cell leukemia virus PCR derived (pol) gene, partial sequence BAB34POL; Bases 4779-4918 EMBL ATK numbering system; BAB34POL	0.77
216	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	0.12	S70663	lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)>GP:EHU33443_1 Entamoeba histolytica GalNAc lectin heavy subunit (hgl4) gene, partial cds; N-acetylgalactosamine adherence lectin heavy subunit	0.8
217	AC000380	*** SEQUENCING IN PROGRESS *** Human Chromosome 3 pac pDJ70i11; HTGS phase 1, 2 unordered pieces.	0.12	ATFCA8_19	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 8; Unnamed protein product	0.64

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	X61207	A.brasilense hisB, H, A, F and E genes for imidazole glycerolphosphate dehydratase, glutamine amidotransferase, phosphorybosilformimino-5-amino-phosphorybosil-4-imidazolecarboxamide isomerase, cyclase and phosphorybosil-AMP-cyclohydrolase.	0.12	OCCLO2_1	O;circumcincta colost-2 gene; Cuticular collagen	0.0074
219	AF014259	HIV-1 Patient 1088 from Edinburgh, MA-p17 (gag) gene, partial cds.	0.11	DMU88570_1	Drosophila melanogaster CREB-binding protein homolog mRNA, complete cds; CBP	1
220	AC000636	Drosophila melanogaster (subclone 2_c11 from P1 DS07660 (D44)) DNA sequence, complete sequence.	0.11	A64829	hypothetical protein in dmsC 3' region - Escherichia coli (strain K-12)>GP:ECAE000192_1 Escherichia coli , ycaD, ycaK, pflA, pflB, focA genes from bases 944908 to 955952 (section 82 of 400) of the complete genome; Hypothetical protein in dmsC	0.051
221	AC002428	Human BAC clone GS039E22 from 5q31, complete sequence.	0.11	HSNMYC2_1	Human N-myc gene exon 2; Put; N-myc protein (aa 1-263) (953 is 1st base in codon)	0.00014
222	L40949	Homo sapiens (clone AT7-5eu) opioid-receptor-like protein mRNA, 5' end.	0.11	CEUNC93_2	C;elegans unc-93 gene; Protein 2	1.20E-13

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
223	AL008636	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 722E9; HTGS phase 1.	0.1	XELCOL2A1A_1	Xenopus laevis alpha-1 collagen type II' mRNA, complete cds; Alpha-1 type II' collagen	2.60E-06
224	D86993	Human (lambda) DNA for immunoglobulin light chain.	0.1	CELM02B7_2	Caenorhabditis elegans cosmid M02B7	1.80E-09
225	AC002539	Homo sapiens chromosome 17, clone 195o20, complete sequence.	0.098	MTCY7D11_17	Mycobacterium tuberculosis cosmid Y7D11; Unknown; MTCY07D11;17c; unknown, len: 186 aa, FASTA best: Q10390 Y009_MYCTU hypothetical 31;0 KD protein MTCY190;09C (299 aa) opt: 355 z-score: 316;8	0.026
226	M88165	Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 1.	0.096	A54161	ryanodine-binding protein alpha form - bullfrog>GP:D21070_1 Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds; Ryanodine receptor alpha isoform	1
227	Z92851	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39G8; HTGS phase 1.	0.082	CYA7_BOVIN	ADENYLATE CYCLASE, TYPE VII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)	0.3

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
228	L00638	Arabidopsis thaliana ubiquitin conjugating enzyme exons 2-4.	0.072	NUCM_TRYBB	NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT HOMOLOG (EC 1.6.5.3) (NADH DEHYDROGENASE SUBUNIT 7 HOMOLOG)>PIR2:A35693 NADH dehydrogenase (EC 1.6.99.3) chain 7 - Trypanosoma brucei mitochondrion (SGC6)	0.24
229	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds.	0.071	MMU65594_1	Mus musculus Brca2 mRNA, complete cds; Similar to human breast cancer susceptibility gene BRCA2; Allele: wild type; putative tumor suppressor	1
230	AF001549	Homo sapiens chromosome 16 BAC clone CIT987SK-270G1 complete sequence.	0.07	PM22_HUMAN	PERIPHERAL MYELIN PROTEIN 22 (PMP-22)>PIR2:JN0503 peripheral myelin protein 22 - human>GP:HUMGAS3X_1 Human peripheral myelin protein 22 (GAS3) mRNA, complete cds>GP:HUMPMP22_1 Human peripheral myelin protein 22 mRNA, complete cds>GP:HUMPMP22	0.0078
231	L36829	Mus musculus alphaA-crystallin-binding protein I (AlphaA-CRYBP1) gene, complete cds.	0.066	<NONE>	<NONE>	<NONE>
232	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13;	0.058	CEZK863_1	Caenorhabditis elegans cosmid ZK863, complete sequence; ZK863;2; Similar to collagen	1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HTGS phase 1, 10 unordered pieces.				
233	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13; HTGS phase 1, 10 unordered pieces.	0.058	CAC2_HAECO	CUTICLE COLLAGEN 2C (FRAGMENT)>GP:HAECOL2C_1 H;contortus collagen 2C mRNA, 3'end	1.20E-08
234	Z23908	H. sapiens (D5S630) DNA segment containing (CA) repeat; clone AFM268zd9; single read.	0.057	VEU34999_1	Venezuelan equine encephalitis virus nonstructural and structural polyprotein genes, complete cds; Nonstructural polyprotein; Internal stop codon, readthrough occurs 5% of the time	0.0002
235	B21875	T3E8-Sp6 TAMU Arabidopsis thaliana genomic clone T3E8.	0.055	YRR2_CAEEL	HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III>GP:CELR144_7 Caenorhabditis elegans cosmid R144; Coded for by C; elegans cDNA CEESP84R; coded for by C; elegans cDNA yk23c4;5; coded for by C; elegans cDNA yk44f9;5; coded for by C; eleg	0.68
236	Z98303	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 140H19; HTGS phase 1.	0.048	AC002330_3	Arabidopsis thaliana BAC T10P11, complete sequence; Putative zinc-finger protein; C2H2 Zn-finger signature from position 80 to 100 [CEICNKGFQRDQNLQLHRRGH]	0.99

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
237	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	APP1_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)>PIR2:A46362 amyloid precursor-like protein - mouse>GP:MUSAPLP_1 Mouse amyloid precursor-like protein mRNA, complete cds	8.90E-06
238	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	MMCOL18A11_2	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exons 40-43, complete cds	1.60E-06
239	X78119	P.amygdalus, Batsch (Texas) pru1 mRNA.	0.042	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR>PIR1:CGHU1B collagen alpha 4(IV) chain precursor - human>GP:HSCOL4A4_1 H;sapiens mRNA for collagen type IV alpha 4 chain; Type IV collagen alpha 4 chain	2.00E-06
240	U72877	Rana catesbeiana L-epinephrine transporter mRNA, complete cds.	0.041	YRR6_MYCCA	HYPOTHETICAL 33.0 KD PROTEIN IN LICA 3'REGION (ORF R6)>PIR2:S42125 hypothetical protein 3 - Mycoplasma capricolum (SGC3)>GP:MYCRPMH_6 M; capricolum rpmH, rnpA and licA gene; Orf R6	0.0008
241	L39891	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds.	0.04	MUC2_HUMAN	MUCIN 2 (INTESTINAL MUCIN 2) (FRAGMENTS)	5.90E-05
242	L40390	Candida glabrata ERG3 gene, complete cds.	0.039	G01763	atrophin-1 - human>GP:HSU23851_1 Human atrophin-1 mRNA, complete cds	9.00E-07

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
243	B28113	T2L16TRB TAMU Arabidopsis thaliana genomic clone T2L16.	0.038	CELZK1248_14	Caenorhabditis elegans cosmid ZK1248	1.60E-18
244	AC000030	00175, complete sequence.	0.033	ATFCA8_40	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 8; Glycerol-3-phosphate permease homolog; Similarity to glycerol-3-phosphate permease - Haemophilus influenzae	0.63
245	B10738	F13G15-Sp6 IGF Arabidopsis thaliana genomic clone F13G15.	0.032	D87521_1	Mus musculus DNA-PKcs mRNA, complete cds	0.21
246	AF024503	Caenorhabditis elegans cosmid F31F4.	0.03	I38344	titin - human	1
247	Z49888	Caenorhabditis elegans cosmid F47A4, complete sequence.	0.027	KSU52064_1	Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds; Herpesvirus saimiri ORF73 homolog>GP:KSU75698_78 Kaposi's sarcoma-associated herpesvirus long unique region, 80 putative ORF's and kaposin gene, complete cds; OR	3.40E-10
248	Z83822	Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.	0.025	GRSB_BACBR	GRAMICIDIN S SYNTHETASE II (GRAMICIDIN S BIOSYNTHESIS GRSB PROTEIN) (EC 6.-.-.-)	1
249	Z94161	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N102C10; HTGS	0.025	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.0079

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		phase 1.				
250	AC002094	Genomic sequence from Human 17, complete sequence.	0.021	S57447	HPBRII-7 protein - human>GP:HSHPBRII 4_1 H;sapiens HPBRII-4 mRNA>GP:HSHPBRII 7_1 H;sapiens HPBRII-7 gene	8.20E-08
251	D79994	Human mRNA for KIAA0172 gene, partial cds.	0.021	CER10H10_1	Caenorhabditis elegans cosmid R10H10, complete sequence; R11A8;7; Protein predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc; No; S37771); cDNA EST CEESX25F comes from this gene;	7.00E-16
252	Z97635	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4; HTGS phase 1.	0.017	CELW05H7_4	Caenorhabditis elegans cosmid W05H7	0.24
253	X84996	X.laevis mRNA for selenocysteine tRNA acting factor (Staf).	0.017	JN0786	integrin beta-4 chain precursor - mouse	0.088
254	AC002543	Human BAC clone RG300C03 from 7q31.2, complete sequence.	0.013	MZLMTCYTBT_1	Mendozellus isis mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.044

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
255	U10401	Caenorhabditis elegans cosmid T20B12.	0.012	MMMHC29N7_2	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-	0.069
256	L14593	Saccharomyces cerevisiae protein phosphatase (PTC1) gene, complete cds.	0.011	D86995_1	Human (gene 1) DNA for phosphatase 2C motif, partial cds	2.20E-14
257	U62317	Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.	0.0093	P2Y8_XENLA	P2Y PURINOCEPTOR 8 (P2Y8)>GP:XLP2Y8_1 X;laevis mRNA for P2Y8 nucleotide receptor	0.89
258	D29655	Pig mRNA for UMP-CMP kinase, complete cds.	0.0075	AF004858_1	Mus musculus platelet activating factor receptor mRNA, partial cds; PAF-receptor	1
259	AF002992	Homo sapiens cosmid from Xq28, complete sequence.	0.0054	FBN1_BOVIN	FIBRILLIN 1 PRECURSOR>PIR2:A55567 fibrillin I - bovine>GP:BOVXAAAA_1 Bos taurus mRNA, complete cds; Putative	0.0004
260	B20752	T19M2-T7 TAMU Arabidopsis thaliana genomic clone T19M2.	0.0043	HSVT1IEP_1	Feline herpesvirus type 1 gene for immediate early protein, complete cds; Feline herpesvirus type 1 immediate early protein	3.90E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
261	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22.	0.0037	YHV5_YEAST	HYPOTHETICAL 143.6 KD PROTEIN IN SPO16-REC104 INTERGENIC REGION>PIR2:S46754 hypothetical protein YHR155w - yeast (Saccharomyces cerevisiae)>GPN:YSCH9666_15 Saccharomyces cerevisiae chromosome VIII cosmid 9666; Yhr155wp; Similar to Sip3p (Snf	0.077
262	Z99128	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 422H11; HTGS phase 1.	0.0032	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.0087
263	B21848	T2D2-Sp6 TAMU Arabidopsis thaliana genomic clone T2D2.	0.0031	B31794	mdm-1 protein (clone c103) - mouse	1.00E-05
264	L33853	Human germline immunoglobulin kappa chain variable region (Vk-IV subgroup) for anti-B-amyloid autoantibodies in Alzheimer's disease.	0.0027	B45550	cytochrome b homolog - Plasmodium yoelii	0.99
265	B36863	HS-1042-A1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=1 Row=K.	0.0027	YQK4_CAEEL	HYPOTHETICAL 64.3 KD PROTEIN C56G2.4 IN CHROMOSOME III>GP:CELC56G2_2 Caenorhabditis elegans cosmid C56G2	0.81

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
266	AC003041	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HCIT307A16; HTGS phase 1, 10 unordered pieces.	0.0024	GLB4_LAMSP	GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT)>PIR2: S01810 hemoglobin AIV - tube worm (Lamellibrachia sp.) (fragment)	0.94
267	AC002315	Mouse BAC-146N21 Chromosome X contains iduronate-2-sulfatase gene; complete sequence.	0.0022	MG42_TARMA	SRY-RELATED PROTEIN MG42 (FRAGMENT)>PIR3:I51369 Sry-related sequence - Tarentola mauritanica (fragment)>GP:TELMG42DNA_1 Gecko MG42 gene, partial cds; Sry-related sequence	0.99
268	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	SCYJL204C_1	S;cerevisiae chromosome X reading frame ORF YJL204c	1
269	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199;e; Protein predicted using Genefinder; preliminary prediction	0.97
270	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199;e; Protein predicted using Genefinder; preliminary prediction	0.97
271	Z54199	L.esculentum DNA Ailsa craig encoding 1-aminocyclopropane-1-carboxylic acid oxidase.	0.0015	CELF20A1_5	Caenorhabditis elegans cosmid F20A1; Coded for by C; elegans cDNA yk9g1;3; coded for by C; elegans cDNA yk9g1;5; coded for by C; elegans cDNA CEESU55F;	0.11

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					weak similarity to putative	
272	Z99943	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 313L4; HTGS phase 1.	0.0014	CEK08F8_5	Caenorhabditis elegans cosmid K08F8, complete sequence; K08F8;5b	0.93
273	S81083	beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].	0.0013	MTCY277_7	Mycobacterium tuberculosis cosmid Y277; Unknown; MTCY277;07c, unknown, len: 302	0.0001
274	Z82174	Human DNA sequence from cosmid B20F6 on chromosome 22q11.2-qter.	0.001	FBLA_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR>GP:HSFIBUA_1 H;sapiens mRNA for fibulin-1 A	0.00063
275	Z82215	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 68O2; HTGS phase 1.	0.00079	BFR1_SCHPO	BREFELDIN A RESISTANCE PROTEIN>PIR2:S52239 hba2 protein - fission yeast (Schizosaccharomyces pombe)>GP:SPHBA2GEN_1 S;pombe hba2 gene	0.15

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
276	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.00071	CX2_HEMHA	CYTOTOXIN 2 (TOXIN 12A)	0.32
277	Z82204	Human DNA sequence from clone J362G171.	0.00054	DMU34925_2	Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds	0.045
278	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.00053	CELT28F2_2	Caenorhabditis elegans cosmid T28F2; Weak similarity to HSP90	0.037
279	U91322	Human chromosome 16p13 BAC clone CIT987SK-276F8 complete sequence.	0.00051	CEW08D2_2	Caenorhabditis elegans cosmid W08D2, complete sequence; W08D2;3; Protein predicted using Genefinder>GP:CEW08D2_2 Caenorhabditis elegans cosmid W08D2; W08D2;3; Protein predicted using Genefinder	0.26
280	D16986	Human HepG2 partial cDNA, clone hmd2b09m5.	0.00037	POLG_PPVNA	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	0.48
281	U91318	Human chromosome 16p13 BAC clone CIT987SK-962B4 complete	0.00031	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		sequence.				
282	M93406	Human dispersed Alu repeats and dispersed L1 repeat.	0.0003	VG8_SPV4	GENE 8 PROTEIN>PIR1:G8BPSV gene 8 protein - spiroplasma virus 4 (SGC3)	0.23
283	AC002398	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence.	0.00021	HMCA_DROME	HOMEOTIC CAUDAL PROTEIN>PIR2:A26357 homeotic protein Cad - fruit fly (Drosophila melanogaster)>GP:DROCADA2_1 D;melanogaster caudal gene (cad) encoding a maternal and zygotic transcript, exon 2; Caudal protein>TFD:TFDP00159 - Polypeptides en	0.021
284	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.0002	PL0009	complement C3d/Epstein-Barr virus receptor precursor - human	0.7
285	X01871	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2).	0.00015	RVZMTCYTBT_1	Reventazonia sp; mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.73
286	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.	0.00015	ACU89984_1	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds; Similar to human transformation-	4.20E-13

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					sensitive protein: SwissProt Accession Number P31948	
287	AC002365	Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.	0.00011	S10340	DNA-directed RNA polymerase (EC 2.7.7.6) - yeast (Kluyveromyces marxianus var. lactis)	0.00062
288	AC002390	Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.	9.90E-05	D86603_1	Mouse mRNA for Bach protein 1, complete cds; Bach1	1
289	AC002980	Homo sapiens; HTGS phase 1, 34 unordered pieces.	9.20E-05	TRBKPCYB_1	Trypanosoma brucei kinetoplast apocytochrome b gene, complete cds	0.52
290	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds.	4.50E-05	S28832	microtubule-associated protein H1 (clone KS3.1) - longfin squid (fragment)	0.88
291	AC000120	Human BAC clone RG161K23 from 7q21, complete sequence.	4.00E-05	SXSCRBA_1	S;xylosus scrB and scrR genes; Sucrose repressor	0.99

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
292	AC003037	Homo sapiens; HTGS phase 1, 66 unordered pieces.	3.40E-05	S13569	hypothetical protein 5 - Lactococcus lactis subsp. lactis insertion sequence 1076>GP:LLTLE_1 Lactococcus lactis DNA for the transposon-like element on the lactose plasmid; ORF5 (AA 1 - 43)	0.018
293	Z81512	Caenorhabditis elegans cosmid F25C8, complete sequence.	2.40E-05	MUSDBPRC_1	Mus musculus DNA-binding protein Rc mRNA, complete cds; DNA binding protein Rc	1
294	B16681	343C3.TVB CIT978SKA1 Homo sapiens genomic clone A-343C03.	1.10E-05	COPP_YEAST	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)>PIR2:B55123 coatomer complex beta' chain - yeast (Saccharomyces cerevisiae)>GPN:SCYGL137W_1 S;cerevisiae chromosome VII reading frame ORF YGL137w>GP:SCU11237_1 Saccharomyces cerevisiae	0.081
295	Z16523	H. sapiens (D9S158) DNA segment containing (CA) repeat; clone AFM073yb11; single read.	1.00E-05	MMSEMF_1	M;musculus mRNA for semaphorin F; Smaphorin F	0.78
296	Z49704	S.cerevisiae chromosome XIII cosmid 8021.	5.60E-06	<NONE>	<NONE>	<NONE>
297	AC003071	Human BAC clone BK085E05 from 22q12.1-qter, complete sequence.	3.00E-06	HSRCAER_1	H;sapiens mRNA for red cell anion exchanger (EPB3, AE1, Band 3) 3' non-coding region	0.21

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
298	U20428	Human SNC19 mRNA sequence.	1.40E-06	HUMMUC2A_1	Human mucin-2 gene, partial cds	4.40E-06
299	U51903	Human RasGAP-related protein (IQGAP2) mRNA, complete cds.	6.60E-07	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)>PIR2:A54854 Ras GTPase activating-related protein - human>GP:HUMIQGA_1 Homo sapiens ras GTPase-activating-like protein (IQGAP1) mRNA, complete cds; Amino acid feature: IQ calmodulin-binding do	1.60E-14
300	AL000805	F.rubripes GSS sequence, clone 021G08aA1.	4.70E-07	MT13_MYTED	METALLOTHIONEIN 10-III (MT-10-III)>PIR2:S39418 metallothionein 10-III - blue mussel	2.20E-10
301	AC003016	Human BAC clone RG134C19 from 8q21, complete sequence.	4.30E-07	SPC57A10_5	S;pombe chromosome I cosmid c57A10; Unknown; SPAC57A10;05;c, unknown, len:606aa, similar to A; nidulans Q00659, sulfur metabolite repression control, (678aa), fasta scores, opt:1355,	0.00041
302	AC003089	Human BAC clone RG180F08A, complete sequence.	3.80E-07	HPBPRECK_1	Hepatitis B virus type 11 precore protein (pre-C region, C) gene, 5' end	0.41
303	AC002074	Human BAC clone GS056H18 from 7q31-q32, complete sequence.	2.40E-07	A47021_1	Sequence 23 from Patent WO9527787; Unnamed protein product; Author-given protein sequence is in conflict with the conceptual translation>GP:A51260_1 Sequence 23 from Patent WO9614416; Unnamed protein product; Author-given	0.0016

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					protein sequence is i	
304	U04980	Rattus norvegicus fetal troponin T 3 (fetal TnT3) mRNA, partial cds.	2.20E-07	HUMFSHD_1	Human facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4 tandem repeat unit; ORF	3.30E-08
305	U68704	Human chromosome 21q22.3 P1-clone 3804 subclone 4-52.	2.00E-07	HHV6AGNM_96	Human herpesvirus-6 (HHV-6) U1102, variant A, complete virion genome; U88; Cys repeats; this loci is open in all six reading frames, part of IE-A	2.70E-05
306	U51583	Rattus norvegicus zinc finger homeodomain enhancer-binding protein-1 (Zfhep-1) mRNA, partial cds.	8.70E-08	AF005370_67	Alcelaphine herpesvirus 1 L-DNA, complete sequence; Putative immediate early protein; ORF73; similar to H; saimiri and KSHV ORF73	6.10E-07
307	M80206	Mus domesticus poliovirus receptor homolog (MPH) mRNA, complete cds.	8.10E-08	I53960	PRR2 alpha - human	1.70E-28
308	M60854	Human ribosomal protein S16 mRNA, complete cds.	5.70E-08	OLVPOL_1	Caprine arthritis encephalitis virus (isolate OVLV-N1) pol protein gene, 3' end of cds; Nt 2497-2695 from CAEV Co	0.27
309	U82828	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds.	1.50E-08	C40201	artifact-warning sequence (translated ALU class C) - human	0.00044

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
310	Z83836	Human DNA sequence from PAC 111J24 on chromosome 22q12-qter contains ESTs.	1.40E-08	HSU64473_1	Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds>GP:HSU64498_1 Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds	0.34
311	Z50029	Caenorhabditis elegans cosmid ZC504, complete sequence.	1.40E-08	MMU88984_1	Mus musculus NIK mRNA, complete cds	1.70E-50
312	AC002351	Homo sapiens; HTGS phase 1, 17 unordered pieces.	1.20E-08	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S21932 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
313	B65763	CIT-HSP-2023A12.TR CIT-HSP Homo sapiens genomic clone 2023A12.	3.60E-09	S18106	type II site-specific deoxyribonuclease (EC 3.1.21.4) AbrI - Azospirillum brasilense	0.045
314	Z93021	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 516C23; HTGS phase 1.	2.00E-09	AB001684_134	Chlorella vulgaris C-27 chloroplast DNA, complete sequence; RNA polymerase gamma subunit	0.6
315	D88035	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds.	1.50E-09	D88035_1	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds	1.00E-33

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
316	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	1.30E-10	VGF1_IBVB	F1 PROTEIN>PIR1:VFIHB1 F1 protein - avian infectious bronchitis virus (strain Beaudette)>GP:IBACGB_1 Avian infectious bronchitis virus pol protein, spike protein, small virion-associated protein, membrane protein, and nucleocapsid protein gen	1
317	B04719	cSRL-42G12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-42G12.	7.90E-11	JC5238	galactosylceramide-like protein, GCP - human	0.31
318	M73506	Mouse Tcp-10c (t allele) gene.	2.80E-11	A39487	T-complex protein 10a (allele 129) - mouse	4.10E-16
319	U71148	Human Xq28 cosmids U225B5 and U236A12, complete sequence.	1.20E-11	A56547	sex-peptide precursor - Drosophila suzukii	0.4
320	Z95116	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57G9; HTGS phase 1.	9.90E-13	ALU2_HUMAN	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	0.0017
321	M64795	Rat MHC class I antigen gene (RT1-u haplotype), complete cds.	1.70E-14	STC_DROME	SHUTTLE CRAFT PROTEIN>GP:DMU09306_1 Drosophila melanogaster shuttle craft protein (stc) mRNA, complete cds; C-terminal 222 amino acids encode a novel single- stranded DNA binding domain	1.40E-13

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
322	Y09036	H.sapiens NTRK1 gene, exon 17.	4.20E-15	AF010403_1	Homo sapiens ALR mRNA, complete cds; Alternatively spliced; similarity to ALL-1 and Drosophila trithorax	1
323	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	2.90E-15	SPBC30D10_4	S;pombe chromosome II cosmid c30D10; Hypothetical protein; SPBC30D10;04, unknown, len:148aa	2.40E-09
324	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	2.20E-15	RPON_HALMA	DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)>PIR2:D41715 DNA-directed RNA polymerase II chain RPB10 homolog - Haloarcula marismortui>GP:HALHMAENOA_4 H;marismortui tRNA-Leu, HL29, HmaL13, HmaS9, OrfMMV, OrfMNA, 2-phosphoglycerate dehydr	0.019
325	M86917	Human oxysterol-binding protein (OSBP) mRNA, complete cds.	1.60E-15	CEF14H8_2	Caenorhabditis elegans cosmid F14H8, complete sequence; F14H8;1; Similarity to Human oxysterol-binding protein (SW:OXYB_HUMAN)	2.10E-18
326	AC001231	Genomic sequence from Human 17, complete sequence.	1.30E-15	AC002397_3	Mouse BAC284H12 Chromosome 6, complete sequence; DRPLA	0.0016
327	AL008626	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1114G22; HTGS phase 1.	5.30E-16	TAU48227_1	Triticum aestivum soluble starch synthase mRNA, partial cds	5.90E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
328	L04483	Human ribosomal protein S21 (RPS21) mRNA, complete cds.	7.60E-17	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21>PIR2:S34108 ribosomal protein S21 - human>GP:SSZ84015_1 S;scrofa mRNA; expressed sequence tag (3'; clone c11g10); 40S ribosomal protein S21; Similar to human 40S ribosomal protein S21>GP:HUMRPS21X_1 Human ribosomal	1.40E-09
329	AB001899	Homo sapiens PACE4 gene, exon 2.	6.70E-17	LRP1_HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER)>PIR2:S02392 LDL receptor-related protein precursor - human>GP:HSLDLRRL_1 Human mRNA for LDL-recept	1
330	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	4.40E-17	U97553_59	Murine herpesvirus 68 strain WUMS, complete genome; Ribonucleotide reductase large	0.06
331	AF017187	Homo sapiens LTR HERV-K repetitive element fragment ltr_19_9a sequence.	3.90E-18	D84255_1	Ovophis okinavensis mitochondrial DNA for NADH dehydrogenase subunit 1, partial cds, Ile-tRNA, Pro-tRNA, Phe-tRNA, Gln- tRNA, Met-tRNA and control region (D-loop region); This cds	0.007

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
332	B36252	HS-1038-A2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 820 Col=2 Row=M.	3.10E-18	PGBM_MOUSE	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)>PIR2:S18252 heparan sulfate proteoglycan - mouse>GP:MUSPERPA_1 Mouse perlecan mRNA, complete cds	0.00015
333	D78255	Mouse mRNA for PAP-1, complete cds.	2.70E-18	MUSPAP1_1	Mouse mRNA for PAP-1, complete cds	3.50E-18
334	AC003046	Human Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.	1.40E-18	CEC34F6_1	Caenorhabditis elegans cosmid C34F6; C34F6;1; CDNA EST yk46b12;5 comes from this gene; cDNA EST yk44c4;5 comes from this gene; cDNA EST yk46b12;3 comes from this gene	0.0015
335	AC003002	Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.	1.40E-18	MUSZFP0_1	Mouse mRNA for zinc finger protein, partial sequence	1.30E-19
336	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	3.40E-19	HS4U2IR2_1	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds; Nuclear antigen 2	2.00E-06
337	Z97876	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 295C6; HTGS	1.30E-19	AF003535_1	Homo sapiens L1 element ORF2-like protein gene, partial cds	7.00E-05

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
		phase 1.				
338	M97159	Mouse (clone pIL2) B1 dispersed repeat unit.	1.10E-19	A26882	pIL2 hypothetical protein - rat (fragment)>GP:RATTDR_1 Rat growth and transformation-dependent mRNA, 3' end; Growth and transformation dependent protein	0.2
339	U30817	Bos taurus very-long-chain acyl-CoA dehydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds.	4.70E-20	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)>PIR2:A54872 acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat>GP:RATVLCAD_1 Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, compl	8.10E-25
340	Y11535	H.sapiens mRNA for SHOXb protein.	2.80E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.00027
341	AL008730	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 487J7; HTGS phase 1.	7.10E-21	C40201	artifact-warning sequence (translated ALU class C) - human	0.001
342	U96629	Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.	5.30E-23	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	3.80E-10

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
343	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	2.10E-24	UROM_HUMAN	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)>PIR2:A30452 uromodulin precursor - human>GP:HUMUMOD_1 Human uromodulin (Tamm-Horsfall glycoprotein) mRNA, complete cds; Uromodulin precursor	1
344	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	S20790	extensin - almond>GP:PAEXTS_1 P;amygdalus mRNA for extensin	0.34
345	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	CA24_CAEEL	COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR>GP:CECOLA2IV_2 C;elegans a2(IV) collagen gene; Alternatively spliced transcript	0.1
346	Z66242	H.sapiens CpG island DNA genomic Mse1 fragment, clone 84a4, reverse read cpg84a4.rt1a.	4.80E-26	CEC35A5_8	Caenorhabditis elegans cosmid C35A5, complete sequence; C35A5;8; CDNA EST yk31f6;5 comes from this gene; cDNA EST yk38h1;3 comes from this gene; cDNA EST yk38h1;5 comes from this gene;	7.70E-19
347	L25331	Rattus norvegicus lysyl hydroxylase mRNA, complete cds.	3.90E-26	LYSH_CHICK	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE)>PIR2:A23742 procollagen-lysine 5-dioxygenase (EC 1.14.11.4) precursor - chicken>GP:CHKLYH_1 Chicken lysyl	1.10E-43

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
					hydroxylase mRNA, complete cds	
348	L81569	Drosophila melanogaster (subclone 2_d7 from P1 DS04260 (D68)) DNA sequence, complete sequence.	3.30E-26	CELC52B9_2	Caenorhabditis elegans cosmid C52B9; Coded for by C; elegans cDNA cm11d6; weakly similar to S; cervisiae PTM1 precursor (SP:P32857)	8.40E-29
349	U78082	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds.	2.30E-26	HSU78082_1	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds; H-Med6p	1.50E-16
350	U43381	Human Down Syndrome region of chromosome 21 DNA.	2.10E-28	HSMRNAEB_1	H;sapiens genomic DNA, integration site for Epstein-Barr virus; Hypothetical protein	0.18
351	D50416	Mouse mRNA for AREC3, complete cds.	2.50E-29	A29947	prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep>GP:SHPCOXA_1 Sheep prostaglandin endoperoxide synthetase (cyclooxygenase), complete cds; Cyclooxygenase precursor (EC 1;14;99;1)	0.81

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
352	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	2.20E-29	CFU30222_1	Crithidia fasciculata fully edited ATPase subunit 6 (MURF4) mRNA, partial cds; Cryptogene	0.53
353	Z92826	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone C18D11; HTGS phase 1.	1.10E-30	SPAC1B3_5	S;pombe chromosome I cosmid c1B3; Hypothetical protein; SPAC1B3;05, probable transcriptional regulator, len:630aa, similar eg; to YIL038C, NOT3_YEAST, P06102, general negative regulator,	3.20E-35
354	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	3.70E-32	PVU72769_1	Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein>GP:PVU72769_1 Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein	0.00049
355	B42455	HS-1055-B2-G03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=6 Row=N.	1.30E-32	CELT05H4_8	Caenorhabditis elegans cosmid T05H4; Similar to the beta transducin family; coded for by C; elegans cDNA yk156e11;3; coded for by C; elegans cDNA yk14c8;3; coded for by C; elegans cDNA	6.90E-14
356	AF001905	Homo sapiens cosmids E079, B0920 and A8 from Xq25 X-linked lymphoproliferative disease gene candidate region, complete sequence.	1.80E-33	I38344	titin - human	1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
357	E03743	DNA sequence including male hormone dependent gene derived from hamster frankorgan.	1.10E-34	CELC03A7_2	Caenorhabditis elegans cosmid C03A7; Weak similarity to serotonin receptors	0.59
358	U31199	Human laminin gamma2 chain gene (LAMC2), exon 22 and flanking sequences.	1.20E-35	B44018	laminin B2t chain - human>GP:HSLAMB2 TB_1 H;sapiens mRNA for laminin	1.20E-14
359	D14678	Human mRNA for kinesin-related protein, partial cds.	2.00E-36	D49544_1	Mouse mRNA for KIFC1, complete cds	1.20E-23
360	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds.	8.20E-38	POL4_DROME	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) (TRANSPOSON 412)>PIR1:GNFF42 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 412>GP:DMRT412G_4	0.65
361	U39875	Rattus norvegicus EF-hand Ca2+-binding protein p22 mRNA, complete cds.	8.80E-42	I56333	apolipoprotein B - rat (fragment)>GP:RATAPOLPB_1 Rattus norvegicus (clone rb9E) apolipoprotein B apoB mRNA, 3' end	0.23

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
362	L09647	Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds.	6.60E-42	HN3B_RAT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)>GP:RATHNF3B_1 Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds>TFD:TFDP01611 - Polypeptides entry for factor HNF-3 (beta)	8.10E-25
363	D25538	Human mRNA for KIAA0037 gene, complete cds.	4.10E-43	CELC34D4_1 2	Caenorhabditis elegans cosmid C34D4	0.018
364	Z56764	H.sapiens CpG island DNA genomic Mse1 fragment, clone 13f7, reverse read cpg13f7.rt1a.	1.40E-43	S75263	hypothetical protein - Synechocystis sp. (PCC 6803)>GP:D90904_29 Synechocystis sp; PCC6803 complete genome, 6/27, 630555-781448; Hypothetical protein; ORF_ID:sll0983	0.0028
365	AC002636	*** SEQUENCING IN PROGRESS *** Drosophila melanogaster (subclone 2_g4 from P1 DS03323 (D127)) DNA sequence; HTGS phase 2.	8.40E-44	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	3.40E-51
366	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds.	8.00E-44	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)>GP:RATGAH_1 Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	8.00E-29

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
367	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.	5.00E-45	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	4.80E-45
368	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	4.10E-45	PTPK_HUMAN	PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP-KAPPA)>GP:HSPTPKAP_1 H;sapiens mRNA for phosphotyrosine phosphatase kappa; Human phosphotyrosine phosphatase kappa	4.70E-16
369	D17218	Human HepG2 3' region MboI cDNA, clone hmd3g02m3.	9.40E-47	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein	0.00012
370	U78310	Homo sapiens pescadillo mRNA, complete cds.	8.10E-48	HSU78310_1	Homo sapiens pescadillo mRNA, complete cds	1.10E-21
371	AC000399	Genomic sequence from Mouse 9, complete sequence.	7.40E-48	KIP2_YEAST	KINESIN-LIKE PROTEIN KIP2>PIR1:C42640 kinesin-related protein KIP2 - yeast (Saccharomyces cerevisiae)>GP:SCKIP2XVI_2 S;cerevisiae PEP4 and KIP2 genes encoding PEP4 proteinase (partial) and kinesin-related protein KIP2>GP:SCLACHXVI_17 S;cerev	0.14
372	AC002327	*** SEQUENCING IN PROGRESS *** Genomic sequence from Mouse 7; HTGS phase 1, 3	1.40E-48	CHKC1A205_1	Chicken alpha-2 type-1 collagen; amino acids -16 to 3; Precollagen alpha-2	0.024

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		unordered pieces.				
373	X67016	H.sapiens mRNA for amphiglycan.	9.00E-49	CED2085_2	Caenorhabditis elegans cosmid D2085, complete sequence; D2085;1; Similar to glutamine-dependent carbamoyl-phosphate synthase, aspartate carbamoyltransferase, dihydroorotase; cDNA EST cm16f3>GP:CED2085_2 Caenorhabditis elegans cosmid D2085; D	0.14
374	L10409	Mouse fork head related protein (HNF-3beta) mRNA, complete cds.	1.50E-49	MMU04197_1	Mus musculus HNF3 beta transcription factor (HNF3b) mRNA, partial cds; Sequence of this partial cDNA begins in the first third of the conserved HNF3/forkhead DNA binding domain	1.20E-30
375	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	1.20E-49	SPBC3D5_14	S;pombe chromosome II cosmid c3D5; Unknown; SPBC3D5;14c, unknown; partial; serine rich, len:309aa, similar eg; to YNL283C, YN23_YEAST, P53832, hypothetical 52;3 kd protein, (503aa),	0.00091
376	Z82170	Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.	9.00E-50	BSU55043_3	Bacillus subtilis plasmid pPOD2000 Rep, RapAB, RapA, ParA, ParB, and ParC genes, complete cds; ORF3	0.025

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
377	Z99289	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 142L7; HTGS phase 1.	7.70E-50	A64431	hypothetical protein MJ1050 - Methanococcus jannaschii>GP:MJU67548_2 Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome; M; jannaschii predicted coding region MJ1050; Identified by GeneMark; putativ	5.60E-05
378	X98260	H.sapiens mRNA for M-phase phosphoprotein, mpp11.	6.20E-50	ZRF1_MOUSE	ZUOTIN RELATED FACTOR>GP:MMU53208_1 Mus musculus zuotin related factor (ZRF1) mRNA, complete cds; Similar to DnaJ encoded by GenBank Accession Number L16953	3.90E-30
379	M18981	Human prolactin receptor-associated protein (PRA) gene, complete cds.	9.00E-52	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH FACTOR-INDUCIBLE PROTEIN 2A9) (S100 CALCIUM-BINDING PROTEIN A6)>PIR1:BCHUY calcyclin - human>GP:HUMCACY_1 Human calcyclin gene, complete cds>GP:HUMCACYA_1 Human prolactin recept	8.80E-24
380	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds.	1.60E-53	S33015	hypothetical protein - human herpesvirus 4	0.00088

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
381	U53225	Human sorting nexin 1 (SNX1) mRNA, complete cds.	1.80E-55	G02522	sorting nexin 1 - human>GP:HSU53225_1 Human sorting nexin 1 (SNX1) mRNA, complete cds	9.20E-50
382	Z92844	Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.	6.50E-56	D14487_1	Lentinus edodes Le;MFB1 mRNA, complete cds	1
383	D87450	Human mRNA for KIAA0261 gene, partial cds.	4.30E-56	D87450_1	Human mRNA for KIAA0261 gene, partial cds; Similar to D;melanogaster parallel sister chromatids protein	4.30E-30
384	AC002301	*** SEQUENCING IN PROGRESS *** Human chromosome +16p11.2 BAC clone CIT987SK-A-328A3; HTGS phase 2, 1 ordered pieces.	9.80E-57	S62328	kinesin-like DNA binding protein KID - human>GP:HUMKID_1 Human mRNA for Kid (kinesin-like DNA binding protein), complete cds	2.60E-27
385	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	7.30E-57	HSBCTCF4_1	Homo sapiens mRNA for hTCF-4	2.30E-05
386	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.	3.30E-58	MMU58884_1	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds; similar to Human Drebrin; SH3-containing protein; similar to human drebrin	6.00E-43
387	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	9.50E-59	RNY15054_1	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial; 70 kD tumor-specific antigen	4.70E-45

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
388	AC000406	*** SEQUENCING IN PROGRESS *** Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22; HTGS phase 1, 17 unordered pieces.	7.40E-59	<NONE>	<NONE>	<NONE>
389	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds.	3.60E-59	KRHUEA	keratin, type II cytoskeletal - human (fragment)>GP:HSKERA_1 Human messenger fragment encoding cytoskeletal keratin (type II); mRNA from cultured epidermal cells from human foreskin>GP:HUMKER56K_1 Human 56k cytoskeletal type II keratin mRNA	7.60E-30
390	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	2.70E-60	EGR2_HUMAN	EARLY GROWTH RESPONSE PROTEIN 2 (EGR-2) (KROX-20 PROTEIN) (AT591)>GP:HUMEGR2A_1 Human early growth response 2 protein (EGR2) mRNA, complete cds>TFD:TFDP00485 - Polypeptides entry for factor Egr-2	7.80E-06
391	L08758	Mus musculus homeobox protein (Hox A10) gene, 5' end of cds.	1.40E-60	PAALGYGEN_1	P;aeruginosa algY gene; Alginate lyase	0.00031
392	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived	1.50E-32

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					factor-2	
393	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived factor-2	1.50E-32
394	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	1.90E-62	CHU46067_1	Capra hircus beta-mannosidase mRNA, complete cds	2.70E-39
395	U40747	Mus musculus formin binding protein 11 mRNA, partial cds.	6.90E-63	S64713	formin binding protein 11 - mouse (fragment)>GP:MMU40747_1 Mus musculus formin binding protein 11 mRNA, partial cds; FBP 11; Formin binding protein 11; tandem WWP/WW domains separated by 15 amino acid linker	3.00E-46
396	M36164	Human glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' flank.	1.10E-63	BHT1UL_12	Bovine herpesvirus type 1 UL22-35 genes; UL26;5>GP:BHU31809_2 Bovine herpesvirus 1 maturational proteinase (UL26) gene, complete cds, and scaffold protein (UL26;5) gene, complete cds	0.003
397	Y09036	H.sapiens NTRK1 gene, exon 17.	7.30E-65	MMU39060_1	Mus musculus glucocorticoid receptor interacting protein 1 (GRIP1) mRNA, complete cds; Hormone-dependent interaction with hormone binding domains of steroid receptors;	0.0054

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			**Nearest Neighbor (BlastX vs. Non-Redundant Proteins)**		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
					transactivation	
398	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	2.70E-70	JC4239	phospholipase A2-activating protein - rat	8.40E-17
399	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.	1.70E-74	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4>PIR2:A54803 microtubule-associated motor KIF4 - mouse>GP:MUSKIF4_1 Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds; ATP-binding site: base980-1037, motor domain: base732-1781, alpha-helical co	1.10E-44
400	AF007860	Xenopus laevis xl-Mago mRNA, complete cds.	4.60E-75	AF007862_1	Mus musculus mm-Mago mRNA, complete cds; Similar to Drosophila melanogaster Mago protein	6.50E-68
401	I45565	Sequence 15 from patent US 5637463.	2.30E-82	RNU57391_1	Rattus norvegicus FceRI gamma-chain interacting protein SH2- B (SH2-B) mRNA, complete cds; Putative FceRI gamma ITAM interacting protein; SH2 domain-containing protein B; Method: conceptual	9.90E-42

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	**ACCESSION**	**DESCRIPTION**	**P VALUE**	**ACCESSION**	**DESCRIPTION**	**P VALUE**
402	U29156	Mus musculus eps15R mRNA, complete cds.	1.00E-85	MMU29156_1	Mus musculus eps15R mRNA, complete cds; Involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	4.90E-62
403	U70139	Mus musculus putative CCR4 protein mRNA, partial cds.	1.00E-85	MMU70139_1	Mus musculus putative CCR4 protein mRNA, partial cds; Similar to yeast transcription factor CCR4; transcriptional readthrough occurs with transcription being initiated at the IAP and continues	7.20E-66
404	U82626	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds.	7.60E-96	RNU82626_1	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds; Chondroitin sulfate proteoglycan; CSPG	8.20E-58

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
405	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	2.00E-35	<NONE>	<NONE>	<NONE>
406	AB000516	Homo sapiens mRNA for DSIF p160, complete cds	0.41	POLG_TUMVQ	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; VPG PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI-A)	2.9
407	Z94753	Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu++-transporting P-type ATPase exons 22, 23 and STS	0.004	<NONE>	<NONE>	<NONE>
408	AB011123	Homo sapiens mRNA for KIAA0551 protein, partial cds	0	MI15_CAEEL	Q23356 caenorhabditis elegans. serine/threonine-protein kinase mig-15 (ec 2.7.1.-). 11/98	2.00E-51
409	D17218	Human HepG2 3' region MboI cDNA, clone hmd3g02m3	e-123	NARG_BACSU	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)	9.9
410	M95098	Bos taurus lysozyme gene (cow 2), complete cds	1.1	HAIR_MOUSE	HAIRLESS PROTEIN	8.00E-10

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
411	Z60048	H.sapiens CpG DNA, clone 187a9, reverse read cpg187a9.rt1a .	4.00E-54	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-21
412	Z48975	P.magnus gene for protein urPAB	0.014	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III	2.00E-12
413	AJ001296	Notophthalmus viridescens mRNA for cytokeratin 8	0.37	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	5.00E-21
414	J03831	Xenopus laevis (clone pXEC1.3) C protein mRNA, complete cds.	0.37	PDR5_YEAST	SUPPRESSOR OF TOXICITY OF SPORIDESMIN	3.3
415	AB007157	Homo sapiens gene for ribosomal protein S21, partial cds	e-142	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21	0.002
416	X86340	H.sapiens C7 gene, exon 13	3.3	STC_DROME	SHUTTLE CRAFT PROTEIN	4.3
417	U12404	Human Csa-19 mRNA, complete cds.	0	R10A_PIG	60S RIBOSOMAL PROTEIN L10A (CSA-19) (FRAGMENT)	9.00E-57
418	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-08	<NONE>	<NONE>	<NONE>
419	M80198	Human FKBP-12 pseudogene, clone lambda-512, 5' flank and complete cds.	5.00E-14	RCO1_NEUCR	TRANSCRIPTIONAL REPRESSOR RCO-1	0.008
420	AF052573	Homo sapiens DNA polymerase eta (POLH) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
421	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-131	MGN_DROME	MAGO NASHI PROTEIN	4.00E-39
422	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
423	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-05	<NONE>	<NONE>	<NONE>
424	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
425	D43952	Mouse gene for reticulocalbin, exon1 and promoter region	0.36	<NONE>	<NONE>	<NONE>
426	X68553	C.elegans repetitive DNA sequence	0.4	TCB1_RABIT	T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)	0.11
427	M83314	Tomato phenylalanine ammonia lyase (pal) gene, complete cds and promoter region.	3.3	SMB2_HUMAN	DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)	0.65
428	AF070636	Homo sapiens clone 24686 mRNA sequence	5.00E-23	<NONE>	<NONE>	<NONE>
429	<NONE>	<NONE>	<NONE>	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)	2.00E-06
430	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	5.00E-04	LOX1_LENCU	LIPOXYGENASE (EC 1.13.11.12)	9.9
431	AF020043	Homo sapiens chromosome-associated polypeptide	0	YJH4_YEAST	HYPOTHETICAL 141.3 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION	4.00E-16
432	K00046	ross river virus 26s subgenomic rna and junction region.	0.12	CUL2_HUMAN	CULLIN HOMOLOG 2 (CUL-2)	7.4

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
433	AF005664	Homo sapiens properdin (PFC) gene, complete cds	0.005	UL88_HCMVA	PROTEIN UL88	5.8
434	Z70705	H.sapiens mRNA (fetal brain cDNA com5)	2.00E-05	PH87_YEAST	INORGANIC PHOSPHATE TRANSPORTER PHO87	1.5
435	U29156	Mus musculus eps15R mRNA, complete cds.	e-125	EP15_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN)	1.00E-13
436	AE000750	Aquifex aeolicus section 82 of 109 of the complete genome	0.37	<NONE>	<NONE>	<NONE>
437	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.12	VCAP_HSV6U	MAJOR CAPSID PROTEIN (MCP)	5.6
438	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.13	WEE1_SCHPO	MITOSIS INHIBITOR PROTEIN KINASE WEE1 (EC 2.7.1.-)	3.7
439	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds	4.00E-32	<NONE>	<NONE>	<NONE>
440	U51037	Mus musculus 11-zinc-finger transcription factor	0.04	<NONE>	<NONE>	<NONE>
441	AF032456	Homo sapiens ubiquitin conjugating enzyme G2	e-110	<NONE>	<NONE>	<NONE>
442	AF009288	Homo sapiens clone HEB8 Cri-du-chat region mRNA	2.00E-14	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN)	8.1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
443	AF024578	Homo sapiens type-1 protein phosphatase skeletal muscle glycogen targeting subunit (PPP1R3) gene, exon 4, and complete cds	1.1	<NONE>	<NONE>	<NONE>
444	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	0	DACHA	<NONE>	4.00E-58
445	X96400	P.tetraurelia alpha-51D gene	0.37	<NONE>	<NONE>	<NONE>
446	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
447	X84996	X.laevis mRNA for selenocysteine tRNA acting factor (Staf)	0.12	POL_MLVRD	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))	2.00E-08
448	AF019980	Dictyostelium discoideum ZipA (zipA) gene, partial cds	3.4	HMDL_BRAFL	HOMEOBOX PROTEIN DLL HOMOLOG	0.23
449	X78424	D.carota (Queen Anne's Lace) Inv*Dc2 gene, 3432bp	0.38	<NONE>	<NONE>	<NONE>
450	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
451	X89886	P.patens mRNA for 5-aminolevulinate dehydratase	1.1	CKR6_HUMAN	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR6)	9.9
452	U67471	Methanococcus jannaschii section 13 of 150 of the complete genome	0.12	YR72_ECOLI	HYPOTHETICAL 53.2 KD PROTEIN (ORF2) (RETRON EC67)	5.8
453	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	1.00E-62	YOJ8_CAEEL	HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III	1.7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
454	U70667	Human Fas-ligand associated factor 1 mRNA, partial cds	0	YKB2_YEAST	HYPOTHETICAL 69.1 KD PROTEIN IN PUT3-CCE1 INTERGENIC REGION	3.00E-09
455	M95858	Bos taurus recoverin mRNA, complete cds.	0.35	GIDA_MYCGE	GLUCOSE INHIBITED DIVISION PROTEIN A	1.4
456	U67594	Methanococcus jannaschii section 136 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
457	X06747	Human hnRNP core protein A1	3.00E-31	<NONE>	<NONE>	<NONE>
458	Z65575	H.sapiens CpG DNA, clone 47c5, reverse read cpg47c5.rt1a .	1.3	<NONE>	<NONE>	<NONE>
459	X88893	C.jacchus intron 4 of visual pigment gene	5.00E-15	<NONE>	<NONE>	<NONE>
460	M57426	Maize stripe virus RNA 3 nonstructural protein	0.33	DSC2_MOUSE	DESMOCOLLIN 2A/2B PRECURSOR (EPITHELIAL TYPE 2 DESMOCOLLIN)	6.5
461	X01638	Yeast TEF1 gene for elongation factor EF-1 alpha	1.1	PPOL_DROME	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	3.5
462	M60064	S.typhimurium glutamate 1-semialdehyde aminotransferase (hemL) gene, complete cds.	1.1	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.5
463	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.36	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	1.5
464	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	2.00E-58	VG13_BPML5	GENE 13 PROTEIN (GP13)	2.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
465	M77235	Human cardiac tetrodotoxin-insensitive voltage-dependent sodium channel alpha subunit (HH1) mRNA, complete cds.	3.8	ZPBOC1	<NONE>	6.9
466	M58330	C.maltosa autonomously replicating sequence.	0.004	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.4
467	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.35	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	2.4
468	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	7.00E-59	VGLI_PRVRI	GLYCOPROTEIN GP63 PRECURSOR	4.3
469	U65939	Azotobacter vinelandii GTPase (ftsA) gene, partial cds, and ATP binding protein (ftsZ) gene, complete cds	1.1	TRUA_BACSP	Q45557 bacillus sp. (strain ksm-64). trna pseudouridine synthase a (ec 4.2.1.70) (pseudouridylate synthase i) (pseudouridine synthase i) (uracil hydrolyase). 11/98	0.001
470	U51037	Mus musculus 11-zinc-finger transcription factor	0.041	<NONE>	<NONE>	<NONE>
471	M32685	Human platelet glycoprotein IIIa, exon 14.	3.6	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
472	U82691	Phrynocephalus raddei CAS 179770 NADH dehydrogenase subunit 1 (ND1), partial cds, tRNA-Gln, tRNA-Ile and tRNA-Met, NADH dehydrogenase subunit 2 tRNA-Cys and tRNA-Tyr and c...	1.1	<NONE>	<NONE>	<NONE>
473	D85430	Mouse Murr1 mRNA, exon	0.12	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.5
474	U20661	Dictyostelium discoideum unknown internal repeat protein gene, complete cds, and unknown orf1, orf2 and orf3 genes, partial cds	0.36	YHL1_EBV	HYPOTHETICAL BHLF1 PROTEIN	4.00E-04
475	X56537	Human novel homeobox mRNA for a DNA binding protein	0.04	FA5_HUMAN	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)	9.5
476	U32843	Haemophilus influenzae Rd section 158 of 163 of the complete genome	5	<NONE>	<NONE>	<NONE>
477	U67554	Methanococcus jannaschii section 96 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
478	AB004244	Narke japonica mRNA for Nj-synaphin 1b, complete cds	1.1	NIA1_ORYSA	NITRATE REDUCTASE 1 (EC 1.6.6.1) (NR1)	1.00E-07
479	AF075079	Homo sapiens full length insert cDNA YQ80A08	1.00E-12	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
480	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1	YKK0_YEAST	HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION	9.1
481	X73902	H.sapiens mRNA for nicein B2 chain	0	LMG2_HUMAN	LAMININ GAMMA-2 CHAIN PRECURSOR	3.00E-93
482	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	P53_CRIGR	CELLULAR TUMOR ANTIGEN P53	5.7
483	AL010240	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-64, complete sequence	1.2	<NONE>	<NONE>	<NONE>
484	U49919	Arabidopsis thaliana lupeol synthase mRNA, complete cds	0.54	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	6.00E-10
485	AF077618	Homo sapiens p73 gene, exon 3	0.39	MYOD_MOUSE	MYOBLAST DETERMINATION PROTEIN 1	2.1
486	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
487	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
488	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	5.00E-04	ACE2_YEAST	METALLOTHIONEIN EXPRESSION ACTIVATOR	1.5
489	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-07	RINI_PIG	RIBONUCLEASE INHIBITOR	0.19

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
490	L77886	Human protein tyrosine phosphatase mRNA, complete cds	1.00E-21	VS48_TBRVS	SATELLITE RNA 48 KD PROTEIN	1.6
491	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-04	CRP3_LIMPO	C-REACTIVE PROTEIN 3.3 PRECURSOR	3.5
492	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.7
493	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	<NONE>	<NONE>	<NONE>
494	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.37	<NONE>	<NONE>	<NONE>
495	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.37	NCPR_YEAST	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	7.00E-05
496	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.013	YMB3_CAEEL	PROBABLE INTEGRIN ALPHA CHAIN F54G8.3 PRECURSOR	3.3
497	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
498	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	<NONE>	<NONE>	<NONE>
499	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	VGLY_LYCVW	GLYCOPROTEIN POLYPROTEIN PRECURSOR (CONTAINS: GLYCOPROTEINS G1 AND G2)	3.2

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
500	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-06	HR78_DROME	NUCLEAR HORMONE RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F)	2.5
501	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	4.00E-04
502	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	BAL_HUMAN	BILE-SALT-ACTIVATED LIPASE PRECURSOR (EC 3.1.1.3) (EC 3.1.1.13) (BAL) (BILE-SALT-STIMULATED LIPASE) (BSSL) ESTERASE) (PANCREATIC LYSOPHOSPHOLIPASE)	2.6
503	AF080399	Drosophila melanogaster mitotic checkpoint control protein kinase BUB1 (Bub1) mRNA, complete cds	1.1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88)	2.00E-23
504	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	<NONE>	<NONE>	<NONE>
505	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
506	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
507	AF100661	Caenorhabditis elegans cosmid H20E11	0.38	<NONE>	<NONE>	<NONE>
508	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	0.024
509	U47322	Cloning vector DNA, complete sequence.	2.00E-38	COA1_SV40	COAT PROTEIN VP1	6.2
510	AF031924	Homo sapiens homeobox transcription factor barx2	e-156	CCMA_HAEIN	HEME EXPORTER PROTEIN A (CYTOCHROME C-TYPE BIOGENESIS ATP-BINDING PROTEIN CCMA)	3.5
511	AF010484	Homo sapiens ICI YAC 9IA12, right end sequence	3.00E-10	<NONE>	<NONE>	<NONE>
512	Z63829	H.sapiens CpG DNA, clone 90h2, forward read cpg90h2.ft1a .	5.00E-22	NFIR_MESAU	NUCLEAR FACTOR 1 CLONE PNF1/RED1 (NF-I) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN)	2.4
513	Z35094	H.sapiens mRNA for SURF-2	5.00E-97	SUR2_HUMAN	SURFEIT LOCUS PROTEIN 2	1.00E-46
514	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>
515	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-154	TEGU_EBV	LARGE TEGUMENT PROTEIN	3.4
516	L10911	Homo sapiens splicing factor (CC1.4) mRNA, complete cds.	e-117	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	X17093	Human HLA-F gene for human leukocyte antigen F	0.009	YEN1_SCHPO	O13695 schizosaccharomyces pombe (fission yeast). hypothetical 52.9 kd serine-rich protein c11g7.01 in chromosome i. 11/98	5.4
518	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	1.00E-40
519	X55038	Mouse mCENP-B gene for centromere autoantigen B	0.001	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	3.00E-04
520	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	2.3
521	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.002
522	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	e-110
523	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	8.00E-07
524	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	0	NOT2_YEAST	GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 2	8.00E-05
525	AB019488	Homo sapiens DNA for TRKA, exon 17 and complete cds	0	TRKA_HUMAN	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR PROTEIN) (P140-TRKA)	2.00E-27

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-15	CNG4_BOVIN	240K PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) MODULATORY SUBUNIT))	0.018
527	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	HMZ1_DROME	ZERKNUELLT PROTEIN 1 (ZEN-1)	0.88
528	J03750	Mouse single stranded DNA binding protein p9 mRNA, complete cds.	e-135	P15_HUMAN	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14)	3.00E-21
529	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-12	RS5_DROME	40S RIBOSOMAL PROTEIN S5	0.42
530	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	8.00E-61	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-15
531	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-60	<NONE>	<NONE>	<NONE>
532	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-11	<NONE>	<NONE>	<NONE>
533	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.1
534	X92841	H.sapiens MICA gene	1.00E-55	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-09

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
535	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	NODC_BRAEL	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)	1.4
536	M21731	Human lipocortin-V mRNA, complete cds.	e-169	ANX5_HUMAN	ANNEXIN V (LIPOCORTIN V) (ENDONEXIN II) (CALPHOBINDIN I) (CBP-I) (PLACENTAL ANTICOAGULANT PROTEIN I) (PAP-I) ANTICOAGULANT-ALPHA) (VAC-ALPHA) (ANCHORIN CII)	1.00E-05
537	Y08013	S.salar DNA segment containing GT repeat	0.006	<NONE>	<NONE>	<NONE>
538	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
539	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	2.00E-17	DYNA_CHICK	DYNACTIN, 117 KD ISOFORM	7.4
540	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.6
541	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-13	AMO_KLEAE	AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (MONAMINE OXIDASE) (TYRAMINE OXIDASE)	1.5
542	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	e-133	CA34_HUMAN	PROCOLLAGEN ALPHA 3(IV) CHAIN PRECURSOR	1.5
543	J03746	Human glutathione S-transferase mRNA, complete cds.	e-170	GTMI_HUMAN	GLUTATHIONE S-TRANSFERASE, MICROSOMAL (EC 2.5.1.18)	5.00E-39

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
544	U67522	Methanococcus jannaschii section 64 of 150 of the complete genome	0.37	A1AA_HUMAN	ALPHA-1A ADRENERGIC RECEPTOR	4.3
545	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
546	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
547	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
548	D87001	Human (lambda) DNA for immunoglobulin light chain	0.35	VAL3_TYLCU	AL3 PROTEIN (C3 PROTEIN)	3.2
549	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-08	TEGU_HSV11	LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36)	0.004
550	D16991	Human HepG2 partial cDNA, clone hmd2d01m5	8.00E-09	PTM1_YEAST	PROTEIN PTM1 PRECURSOR	0.033
551	M34025	Human fetal Ig heavy chain variable region	3.2	<NONE>	<NONE>	<NONE>
552	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	5.00E-14	<NONE>	<NONE>	<NONE>
553	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
554	Z78730	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15C3	3.00E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	5.00E-06
555	U74496	Human chromosome 4q35 subtelomeric sequence	8.00E-08	ICP4_VZVD	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP4	0.39

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	U39875	Rattus norvegicus EF-hand Ca2+-binding protein p22 mRNA, complete cds.	2.00E-56	YHFK_ECOLI	HYPOTHETICAL 79.5 KD PROTEIN IN CRP-ARGD INTERGENIC REGION (O696)	9.8
557	U65416	Human MHC class I molecule (MICB) gene, complete cds	0.12	<NONE>	<NONE>	<NONE>
558	AG000037	Homo sapiens genomic DNA, 21q region, clone: 9H11A22	5.00E-25	<NONE>	<NONE>	<NONE>
559	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-05	<NONE>	<NONE>	<NONE>
560	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.015	VGLE_HSV11	GLYCOPROTEIN E PRECURSOR	2.2
561	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin	1.00E-73	YCV2_YEAST	HYPOTHETICAL 13.8 KD PROTEIN IN PWP2-SUP61 INTERGENIC REGION	2.6
562	AB007878	Homo sapiens KIAA0418 mRNA, complete cds	e-110	GLU2_MAIZE	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)	0.72
563	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	YJD6_YEAST	HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION	1.4
564	U27873	Stealth virus 1 clone 3B11 T7	0.002	SYN1_HUMAN	SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1)	1.6
565	L38951	Homo sapiens importin beta subunit mRNA, complete cds	2.00E-68	VP2_BRD	STRUCTURAL CORE PROTEIN VP2	1.1
566	AF007155	Homo sapiens clone 23763 unknown mRNA, partial cds	e-165	YOHI_AZOVI	HYPOTHETICAL 33.2 KD PROTEIN IN IBPB 5'REGION	7.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	Z56295	H.sapiens CpG DNA, clone 10c2, forward read cpg10c2.ft1a .	0.12	A1AB_CANFA	ALPHA-1B ADRENERGIC RECEPTOR (FRAGMENT)	0.85
568	Z83792	G.gallus microsatellite DNA (LEI0222	0.12	<NONE>	<NONE>	<NONE>
569	U11820	Feline immunodeficiency virus USIL2489_7B gag polyprotein (gag) gene, complete cds, polymerase polyprotein (pol) gene, partial cds, vif protein (vif), complete cds, and envelope glycoprotein (env), complete cds, complete g...	1.1	<NONE>	<NONE>	<NONE>
570	M18065	Mouse 18S and 28S ribosomal DNA, 5' hypervariable (Vr) region, clone M1.	6.00E-04	CC40_YEAST	CELL DIVISION CONTROL PROTEIN 40	3.7
571	AF053645	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 3 through 10	2.00E-07	YMQ4_CAEEL	HYPOTHETICAL 25.8 KD PROTEIN K02D10.4 IN CHROMOSOME III	4.3
572	X04588	Human 2.5 kb mRNA for cytoskeletal tropomyosin TM30(nm)	0	<NONE>	<NONE>	<NONE>
573	AC001159	Homo sapiens (subclone 1_h9 from PAC H92) DNA sequence	5.00E-04	XYND_CELFI	ENDO-1,4-BETA-XYLANASE D PRECURSOR (EC 3.2.1.8)	7.3
574	Z60625	H.sapiens CpG DNA, clone 2c10, forward read cpg2c10.ft1aa .	4.00E-13	<NONE>	<NONE>	<NONE>
575	AF070640	Homo sapiens clone 24781	e-164	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA sequence				
576	Y11306	Homo sapiens mRNA for hTCF-4	2.00E-48	TCF1_HUMAN	T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)	2.00E-15
577	X65279	pWE15 cosmid vector DNA	7.00E-69	OCLN_POTTR	Q28793 potorous tridactylus (potoroo). occludin. 11/98	0.71
578	M10296	Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.	0.001	LMB1_HYDAT	LAMININ BETA-1 CHAIN PRECURSOR (FRAGMENTS)	1.9
579	X53744	Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)	e-162	SR68_CANFA	SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)	5.00E-16
580	AF086438	Homo sapiens full length insert cDNA clone ZD80G11	2.00E-04	<NONE>	<NONE>	<NONE>
581	U15140	Mycobacterium bovis ribosomal proteins IF-1 complete cds, and S4 (rpsD) gene, partial cds	1.3	<NONE>	<NONE>	<NONE>
582	D13292	Human mRNA for ryudocan core protein	e-166	RSP4_ARATH	40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)	1.4
583	S71022	neoplasm-related C140 product [human, thyroid carcinoma cells, mRNA, 670 nt]	9.00E-30	RL6_HUMAN	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107)	5.6
584	L20934	Anopheles gambiae complete mitochondrial genome	0.014	<NONE>	<NONE>	<NONE>
585	Z49269	H.sapiens gene for chemokine HCC-1.	1.1	AMY1_DICTH	ALPHA-AMYLASE 1 (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	2.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
586	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>
587	AF029893	Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase mRNA, complete cds	0.13	HEMO_PIG	HEMOPEXIN PRECURSOR (HYALURONIDASE) (EC 3.2.1.35)	3.5
588	J05109	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds.	0.014	<NONE>	<NONE>	<NONE>
589	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	<NONE>	<NONE>	<NONE>
590	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	1.00E-83	SCRB_PEDPE	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE)	10
591	Y11966	B.aphidicola (host T.suberi) plasmid pBTs1 genes leuA, hspA, repA2, repA1, leuB, leuC, leuD, leuA	0.37	<NONE>	<NONE>	<NONE>
592	U20428	Human SNC19 mRNA sequence	1.00E-64	YY22_MYCTU	HYPOTHETICAL 30.8 KD PROTEIN CY49.22	0.29
593	AF043084	Lycopersicon esculentum ethylene receptor homolog (ETR1) mRNA, complete cds	0.37	KNIR_DROME	ZYGOTIC GAP PROTEIN KNIRPS	9.9
594	X65279	pWE15 cosmid vector DNA	5.00E-66	COA1_SV40	COAT PROTEIN VP1	0.001
595	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial	0.041	UL88_HSV7J	PROTEIN U59	5.8

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
596	M91452	Sus scrofa ryanodine receptor (RYR1) gene, complete cds.	3.2	<NONE>	<NONE>	<NONE>
597	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	e-158	GAT1_CHICK	ERYTHROID TRANSCRIPTION FACTOR (GATA-1) (ERYF1)	1.2
598	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	0	RPB7_ARATH	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 5)	6.2
599	Y16964	Saccharomyces sp. mitochondrial DNA for OLI1 gene, strain CID1	0.37	NMD5_YEAST	NONSENSE-MEDIATED MRNA DECAY PROTEIN 5	1.9
600	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	<NONE>	<NONE>	<NONE>
601	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	<NONE>	<NONE>	<NONE>
602	AF091046	Brugia pahangi nuclear hormone receptor (bhr-1) gene, partial cds	1.1	INVO_PONPY	INVOLUCRIN	0.23
603	M87339	Human replication factor C, 37-kDa subunit mRNA, complete cds	0	AC12_HUMAN	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37)	1.00E-38
604	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon	0.39	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		1'				
605	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
606	AE001149	Borrelia burgdorferi (section 35 of 70) of the complete genome	0.13	<NONE>	<NONE>	<NONE>
607	X14168	Human pLC46 with DNA replication origin	6.00E-16	Z136_HUMAN	ZINC FINGER PROTEIN 136	0.31
608	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	7.00E-90	HN3B_RAT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
609	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.043	PGCV_MOUSE	VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M)	3.5
610	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	CA11_CHICK	PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR	0.4
611	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	e-106	RRPB_CVMA5	RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B)	9.7
612	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
613	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	UL52_EBV	HELICASE/PRIMASE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN BSLF1)	5.9
614	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-71	POLG_PVYHU	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	4.3
615	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	VP3_ROTPC	INNER CORE PROTEIN VP3	7.7
616	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	e-143	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)	7.00E-67
617	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.37	Y642_METJA	HYPOTHETICAL PROTEIN MJ0642	5.8
618	M21191	Human aldolase pseudogene mRNA, complete cds.	1.00E-32	LIN1_NYCCO	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-17
619	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	NUCM_BOVIN	NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-49KD) (CI-49KD)	0.044

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
620	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	HEMZ_RHOCA	FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE)	4.4
621	AF041428	Homo sapiens ribosomal protein s4 X isoform gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
622	X07158	Chironomus thummi DNA for Cla repetitive element	0.13	<NONE>	<NONE>	<NONE>
623	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-04	<NONE>	<NONE>	<NONE>
624	AF100470	Rattus norvegicus ribosome attached membrane protein 4 (RAMP4) mRNA, complete cds	1.00E-53	<NONE>	<NONE>	<NONE>
625	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	2.00E-38	<NONE>	<NONE>	<NONE>
626	M13452	Human lamin A mRNA, 3'end.	6.00E-16	<NONE>	<NONE>	<NONE>
627	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.014	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)	4.00E-20
628	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
629	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
630	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
631	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
632	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	YS83_CAEEL	HYPOTHETICAL 86.9 KD PROTEIN ZK945.3 IN CHROMOSOME II	0.65
633	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	NRP_MOUSE	NEUROPILIN PRECURSOR (A5 PROTEIN)	2.7
634	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-05	Y4JN_RHISN	HYPOTHETICAL 16.3 KD PROTEIN Y4JN	5.9
635	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
636	X64707	H.sapiens BBC1 mRNA	e-179	RL13_HUMAN	60S RIBOSOMAL PROTEIN L13 (BREAST BASIC CONSERVED PROTEIN 1)	5.00E-40
637	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-08	<NONE>	<NONE>	<NONE>
638	X14168	Human pLC46 with DNA replication origin	5.00E-14	SP3_HUMAN	TRANSCRIPTION FACTOR SP3 (SPR-2) (FRAGMENT)	0.19
639	X90999	H.sapiens mRNA for Glyoxalase II	9.00E-20	GLO2_HUMAN	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)	0.007
640	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	9.00E-51	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	0.005

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
641	Z12002	M.musculus Pvt-1 mRNA.	0.36	CP5F_CANTR	CYTOCHROME P450 LIIA6 (ALKANE-INDUCIBLE) (EC 1.14.14.1) (P450-ALK3)	5.6
642	M10206	R.sphaeroides reaction center L subunit (complete cds) and M subunit (5' end) genes.	1.1	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	0.006
643	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	3.3	ANKB_HUMAN	ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)	7.00E-07
644	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
645	X53616	C.domesticus calnexin (pp90) mRNA	1.1	<NONE>	<NONE>	<NONE>
646	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15	3.3	PRIO_PIG	MAJOR PRION PROTEIN PRECURSOR (PRP)	1.9
647	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	1.1	UL07_HSV2H	PROTEIN UL7	7.3
648	X52956	Human CAMII-psi3 calmodulin retropseudogene	0.37	PRTP_EBV	PROBABLE PROCESSING AND TRANSPORT PROTEIN	7.5
649	M93425	Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds.	0	PTNC_HUMAN	PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1)	e-107
650	L47615	Mus musculus DNA-binding protein (Fli-1) gene, 5' end of cds.	0.13	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	2.00E-07
651	U60337	Homo sapiens beta-mannosidase mRNA, complete	0	GIL1_ENTHI	GALACTOSE-INHIBITABLE LECTIN 170 KD	0.22

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds			SUBUNIT	
652	U08813	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds.	1.00E-22	NAG1_HUMAN	SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER)	0.1
653	Y00282	Human mRNA for ribophorin II	2.00E-78	RIB2_HUMAN	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (RIBOPHORIN II)	5.00E-19
654	D10051	Human gene for 92-kDa type IV collagenase, 5'-flanking region	0.014	TAGB_DICDI	PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR (EC 3.4.21.-)	7.6
655	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	8.00E-08	<NONE>	<NONE>	<NONE>
656	U78310	Homo sapiens pescadillo mRNA, complete cds	0	YG2S_YEAST	HYPOTHETICAL 69.9 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION	0.002
657	X68792	S.coelicolor A3(2) promoter sequence pth270	3.2	YBS0_YEAST	HYPOTHETICAL 27.0 KD PROTEIN IN VAL1-HSP26 INTERGENIC REGION	0.073
658	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.2

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
659	U15522	Sus scrofa clone pvg1a Ig heavy chain variable VDJ region mRNA, partial cds.	3.2	Z165_HUMAN	ZINC FINGER PROTEIN 165	3.2
660	M20918	C.thummi piger haemoglobin (Hb) gene DNA, complete cds.	0.12	YT25_CAEEL	HYPOTHETICAL 59.9 KD PROTEIN B0304.5 IN CHROMOSOME II	0.033
661	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
662	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.001	ENV_MLVFP	ENV POLYPROTEIN PRECURSOR (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN)	3.3
663	M97287	Human MAR/SAR DNA binding protein (SATB1) mRNA, complete cds. > :: gb|I58691|I58691 Sequence 1 from patent US 5652340	0	SAT1_HUMAN	DNA-BINDING PROTEIN SATB1 (SPECIAL AT-RICH SEQUENCE BINDING PROTEIN 1)	2.00E-20
664	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds	e-168	K2C4_BOVIN	KERATIN, TYPE II CYTOSKELETAL 59 KD, COMPONENT IV	4.00E-10
665	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	e-152	PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)	4.00E-13
666	M73047	Homo sapiens tripeptidyl peptidase II mRNA, complete cds.	0	MERT_STRLI	MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)	4.4

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	0	RL9_HUMAN	60S RIBOSOMAL PROTEIN L9	2.00E-11
668	X98330	H.sapiens mRNA for ryanodine receptor 2	1.1	HS74_MOUSE	HEAT SHOCK 70 KD PROTEIN AGP-2	0.034
669	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	RPC2_DROME	DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE	1.1
670	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	7.00E-80	LEGB_PEA	LEGUMIN B (FRAGMENT)	0.011
671	Z71419	S.cerevisiae chromosome XIV reading frame ORF YNL143c	1.1	FOCD_ECOLI	OUTER MEMBRANE USHER PROTEIN FOCD PRECURSOR	9.7
672	AF044965	Homo sapiens polio virus related protein 2 gene, alpha isoform, exon 6 and partial cds	e-167	PVR_MOUSE	POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR	1.00E-12
673	X65319	Cloning vector pCAT-Enhancer	2.00E-80	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) CALCIUM-BINDING PROTEIN A6)	3.00E-15
674	D29655	Pig mRNA for UMP-CMP kinase, complete cds	e-103	V319_ASFB7	J319 PROTEIN	4.3
675	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	VEGR_RAT	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR RECEPTOR FLT) (FLT-1)	3.3

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
676	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	2.00E-07	MALY_ECOLI	MALY PROTEIN (EC 2.6.1.-)	5.6
677	AF038952	Homo sapiens cofactor A protein mRNA, complete cds	e-160	T1CA_MOUSE	TCP1-CHAPERONIN COFACTOR A	4.00E-19
678	Z96950	Gorilla gorilla DNA sequence orthologous to the human Xp:Yp telomere-junction region	5.00E-14	YHBZ_ECOLI	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION (F390)	3.3
679	D50418	Mouse mRNA for AREC3, partial cds	2.00E-79	CYGX_RAT	OLFACTORY GUANYLYL CYCLASE GC-D PRECURSOR (EC 4.6.1.2)	1.1
680	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	P2C2_SCHPO	PROTEIN PHOSPHATASE 2C HOMOLOG 2 (EC 3.1.3.16)	1.00E-04
681	AL010280	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-106, complete sequence	0.12	<NONE>	<NONE>	<NONE>
682	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-04	VSM2_TRYBB	VARIANT SURFACE GLYCOPROTEIN MITAT 1.2 PRECURSOR (VSG 221)	4.3
683	U00238	Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
684	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	PRPR_SALTY	PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN	1.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
685	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	YAND_SCHPO	HYPOTHETICAL 30.4 KD PROTEIN C3H1.13 IN CHROMOSOME I	0.38
686	D25538	Human mRNA for KIAA0037 gene, complete cds	0	<NONE>	<NONE>	<NONE>
687	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	A1AA_RAT	ALPHA-1A ADRENERGIC RECEPTOR (RA42)	4.4
688	L26956	Mesocricetus auratus stearyl-CoA desaturase sequence including male hormone dependent gene derived from hamster frankorgan	4.00E-33	<NONE>	<NONE>	<NONE>
689	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
690	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	2.00E-08
691	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-09	<NONE>	<NONE>	<NONE>
692	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_RABIT	OXYSTEROL-BINDING PROTEIN	1.00E-34
693	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	UFO2_MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91)	3.1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
694	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-04	<NONE>	<NONE>	<NONE>
695	U34954	Caenorhabditis elegans cyclophilin isoform 10	5.00E-24	CYPA_CAEEL	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8)	2.00E-29
696	AB011167	Homo sapiens mRNA for KIAA0595 protein, partial cds	0	RFX5_HUMAN	BINDING REGULATORY FACTOR	2.1
697	U03886	Human GS2 mRNA, complete cds.	2.00E-28	SKD1_MOUSE	SKD1 PROTEIN	4.00E-17
698	AF086275	Homo sapiens full length insert cDNA clone ZD45C02	3.00E-41	SPT7_YEAST	TRANSCRIPTIONAL ACTIVATOR SPT7	0.82
699	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	CA1E_HUMAN	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR	1.1
700	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-11	E434_ADECC	Q65962 canine adenovirus type 1 (strain cll). early e4 31 kd protein. 11/98	4.4
701	L17340	Drosophila melanogaster germline transcription factor gene, complete cds.	3.3	CISY_TETTH	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM FILAMENT-FORMING PROTEIN)	9.7
702	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	2.00E-45	PME2_LYCES	PECTINESTERASE 2 PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE) (PE 2)	7.4
703	Z96207	H.sapiens telomeric DNA sequence, clone 12PTEL049, read 12PTELOO049.se	8.00E-08	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		q				
704	X58430	Human Hox1.8 gene	e-146	HXAA_HUMAN	HOMEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)	4.00E-05
705	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-06	YN39_SYNP7	HYPOTHETICAL 9.2 KD PROTEIN IN CYST-CYSR INTERGENIC REGION (ORF 81)	0.89
706	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	0.001
707	M19961	Human cytochrome c oxidase subunit Vb (coxVb) mRNA, complete cds.	e-123	OTHU5B	<NONE>	3.00E-30
708	X68380	M.musculus gene for cathepsin D, exon 3	5.00E-04	42_MOUSE	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN)	9.9
709	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.00E-11	TCPA_DROME	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)	4.3
710	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
711	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
712	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
713	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	3.4
714	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	YM8L_YEAST	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION	3.00E-08
715	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	PSC_DROME	POSTERIOR SEX COMBS PROTEIN	0.6
716	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	7.00E-07	IRKX_RAT	INWARD RECTIFIER POTASSIUM CHANNEL BIR9 (KIR5.1)	5.4
717	AC001038	Homo sapiens (subclone 2_h2 from P1 H49) DNA sequence	8.00E-09	MGMT_YEAST	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFE RASE	0.48
718	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	YWDE_BACSU	HYPOTHETICAL 19.9 KD PROTEIN IN SACA-UNG INTERGENIC REGION PRECURSOR	1.8
719	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	e-110	GSC_DROME	HOMEOBOX PROTEIN GOOSECOID	7.2
720	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.17
721	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.001	CPCF_SYNP2	PHYCOCYANOBIL IN LYASE BETA SUBUNIT (EC 4.-.-.-)	2.4
722	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
723	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.04	YKK7_CAEEL	HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III	0.057
724	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	H5_CAIMO	HISTONE H5	0.39
725	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	DED1_YEAST	PUTATIVE ATP-DEPENDENT RNA HELICASE DED1	0.5
726	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj|E02629|E02629 DNA of human polypeptide chain elongation factor-1 alpha	5.00E-36	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	0.84
727	X54859	Porcine TNF-alpha and TNF-beta genes for tumour necrosis factors alpha and beta, respectively.	3.3	Z165_HUMAN	ZINC FINGER PROTEIN 165	5.6
728	D49911	Thermus thermophilus UvrA gene, complete cds	0.014	CC48_CAPAN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG	9.9
729	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-06	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.011
730	D15057	Human mRNA for DAD-1, complete cds	0	DAD1_HUMAN	DEFENDER AGAINST CELL DEATH 1 (DAD-1)	8.00E-16
731	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-06	ANFD_RHOCA	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1) (NITROGENASE COMPONENT I) (DINITROGENASE	9.6

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					)	
732	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	7.00E-07	EFTU_CHLVI	ELONGATION FACTOR TU (EF-TU)	2.5
733	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	0	TRYM_RAT	MAST CELL TRYPTASE PRECURSOR (EC 3.4.21.59)	5.6
734	X98743	H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)	0.04	<NONE>	<NONE>	<NONE>
735	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-07	<NONE>	<NONE>	<NONE>
736	Z49314	S.cerevisiae chromosome X reading frame ORF YJL039c	3.2	<NONE>	<NONE>	<NONE>
737	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	2.00E-76
738	J04038	Human glyceraldehyde-3-phosphate dehydrogenase	2.00E-47	SDC1_HUMAN	SYNDECAN-1 PRECURSOR (SYND1) (CD138)	3.5
739	AF010238	Homo sapiens von Hippel-Lindau tumor suppressor	1.00E-09	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.001
740	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	YQJX_BACSU	HYPOTHETICAL 13.2 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION	9.9

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
741	L21186	Human lysyl oxidase-like protein mRNA, complete cds.	e-145	OXRTL	<NONE>	1.00E-34
742	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	CC48_SOYBN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP)	7.6
743	AF009203	Homo sapiens YAC clone 377A1 unknown mRNA, 3'untranslated region	3.3	<NONE>	<NONE>	<NONE>
744	Z74894	S.cerevisiae chromosome XV reading frame ORF YOL152w	0.12	CD14_RABIT	Q28680 oryctolagus cuniculus (rabbit). monocyte differentiation antigen cd14 precursor. 11/98	1.9
745	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9.00E-10	KIN3_YEAST	SERINE/THREONINE-PROTEIN KINASE KIN3 (EC 2.7.1.-)	2.5
746	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	7.00E-17
747	S61044	ALDH3=aldehyde dehydrogenase isozyme 3 [human, stomach, mRNA Partial, 1362 nt]	0	DHAP_HUMAN	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (CLASS 3)	2.00E-71
748	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-08	CA1E_CHICK	COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)	0.36
749	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
750	L14815	Entamoeba histolytica HM-1:IMSS galactose-specific adhesin 170kD subunit (hgl3) gene, complete cds.	0.12	<NONE>	<NONE>	<NONE>
751	X63785	T.thermophila gene for snRNA U2-2	1.1	<NONE>	<NONE>	<NONE>
752	M83756	Mytilus edulis mitochondrial NADH dehydrogenase subunit 5 (ND5) gene, 3' end; NADH dehydrogenase subunit 6 (ND6) gene, complete cds; and cytochrome b (cyt b), 5' end.	0.042	DSC1_HUMAN	DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3)	2.6
753	AB001066	Brown trout microsatellite DNA sequence	0.38	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	1.2
754	AF064787	Lotus japonicus rac GTPase activating protein 1 mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
755	U20608	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds	0.043	<NONE>	<NONE>	<NONE>
756	M77812	Rabbit myosin heavy chain mRNA, complete cds.	1.2	RBL1_HUMAN	RETINOBLASTOMA-LIKE PROTEIN 1 (107 KD RETINOBLASTOMA-ASSOCIATED PROTEIN) (PRB1) (P107)	4.9

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	X63789	T.thermophila genes for snRNA U5-1, snRNA U5-2	0.058	<NONE>	<NONE>	<NONE>
758	D50646	Mouse mRNA for SDF2, complete cds	2.00E-27	PMT3_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 3 (EC 2.4.1.109)	0.002
759	L81583	Homo sapiens (subclone 3_g2 from P1 H11) DNA sequence	3.00E-19	ALU5_HUMAN	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	0.86
760	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	SYFA_YEAST	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC	5.7
761	AF000370	Homo sapiens polymorphic CA dinucleotide repeat flanking region	6.00E-89	APP1_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)	5.7
762	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
763	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	PSF_HUMAN	PTB-ASSOCIATED SPLICING FACTOR (PSF)	0.72
764	AB018288	Homo sapiens mRNA for KIAA0745 protein, partial cds	0	TC2A_CAEBR	TRANSPOSABLE ELEMENT TCB2 TRANSPOSASE	1.5
765	AF020282	Dictyostelium discoideum DG2033 gene, partial cds	0.38	PMT2_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109)	0.18

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
766	AF017357	Oryza sativa low molecular early light-inducible protein mRNA, complete cds	0.38	RGS3_HUMAN	REGULATOR OF G-PROTEIN SIGNALLING 3 (RGS3) (RGP3)	0.23
767	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
768	X74178	B.taurus microsatellite DNA INRA153	0.13	FAG1_SYNY3	P73574 synechocystis sp. (strain pcc 6803). 3-oxoacyl-[acyl-carrier protein] reductase 1 (ec 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase 1). 11/98	5.00E-16
769	AF041858	Mus musculus synaptojanin 2 isoform delta mRNA, partial cds	0.043	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR	0.24
770	J01404	Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A6l, 2 and 3.	0.021	NU1M_CITLA	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3)	7.2
771	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	3.00E-41	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	4.00E-08
772	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-09	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
773	AF095927	Rattus norvegicus protein phosphatase 2C mRNA, complete cds	0	P2C_PARTE	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)	1.00E-16
774	X87212	H.sapiens mRNA for cathepsin C	0	CATC_HUMAN	DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1)	2.00E-46
775	X05283	Drosophila melanogaster PKCG7 gene exons 7-14 for protein kinase C	4.5	<NONE>	<NONE>	<NONE>
776	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	1.00E-83
777	X06960	Aspergillus nidulans mitochondrial DNA for cytochrome oxidase subunit 3, tRNA-Tyr	0.23	<NONE>	<NONE>	<NONE>
778	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	5.00E-07
779	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	NAT1_YEAST	N-TERMINAL ACETYLTRANSFE RASE 1 (EC 2.3.1.88)	5.00E-23
780	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	PPOL_SARPE	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	0.021
781	U57391	Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds	1.00E-84	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
782	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	7.00E-57	SSGP_VOLCA	SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	5.3
783	AJ008065	Chrysolina bankii 16S rRNA gene, mitotype B2	0.043	<NONE>	<NONE>	<NONE>
784	AF067212	Caenorhabditis elegans cosmid F37F2	0.005	MEK1_RAT	MAPK/ERK KINASE KINASE 1 (EC 2.7.1.-) (MEK KINASE 1)	4.5
785	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.042	<NONE>	<NONE>	<NONE>
786	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	<NONE>	<NONE>	<NONE>
787	Y13401	Homo sapiens CD3 delta gene, enhancer sequence	8.00E-08	<NONE>	<NONE>	<NONE>
788	AE001038	Archaeoglobus fulgidus section 69 of 172 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
789	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
790	AF041463	Manihot esculenta elongation factor 1-alpha	1.4	<NONE>	<NONE>	<NONE>
791	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.7
792	Z12112	pWE15A cosmid vector DNA	3.00E-29	PKWA_THECU	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)	2.00E-04

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
793	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	4.00E-44	<NONE>	<NONE>	<NONE>
794	U89331	Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds	7.00E-06	NRL_HUMAN	NEURAL RETINA-SPECIFIC LEUCINE ZIPPER PROTEIN (NRL)	6.3
795	AF055666	Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds	0.52	PSPD_BOVIN	PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR	0.33
796	L13321	Homo sapiens iduronate-2-sulfatase (IDS) gene, exon 1, incomplete 5' end.	0.14	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	0.27
797	AL010270	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-96, complete sequence	0.37	YTH3_CAEEL	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II	2
798	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.015	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	0.063
799	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	0	CCR4_YEAST	GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (CARBON CATABOLITE REPRESSOR PROTEIN 4)	5.00E-11
800	L26507	Mouse myocyte nuclear factor (MNF) mRNA, complete cds.	3.00E-41	MNF_MOUSE	MYOCYTE NUCLEAR FACTOR (MNF)	4.00E-18

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
801	U20527	Mus musculus chemokine KC gene, 5' region.	0	GRO_MOUSE	GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51)	1.00E-28
802	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	MYSA_DROME	MYOSIN HEAVY CHAIN, MUSCLE	0.089
803	U05823	Mus musculus pericentrin mRNA, complete cds.	1.00E-94	M84D_DROME	MALE SPECIFIC SPERM PROTEIN MST84DD	0.099
804	U67468	Methanococcus jannaschii section 10 of 150 of the complete genome	0.4	<NONE>	<NONE>	<NONE>
805	U14178	Human type II IL-1 receptor gene, exon 1B	1.00E-19	AMPH_HUMAN	AMPHIPHYSIN	2.9
806	L40411	Homo sapiens thyroid receptor interactor	0	TRI8_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
807	D17218	Human HepG2 3' region MboI cDNA, clone hmd3g02m3	e-136	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	3.00E-04
808	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-24
809	D14678	Human mRNA for kinesin-related protein, partial cds	0	NCD_DROME	CLARET SEGREGATIONAL PROTEIN	1.00E-70

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
810	X56317	Xiphophorus maculatus Xmrk(proto-oncogene) gene for receptor tyrosine kinase.	0.49	WN1B_MOUSE	WNT-10B PROTEIN PRECURSOR (WNT-12)	7.2
811	M36200	Human synaptobrevin 1 (SYB1) gene, exon 5.	0.2	VE2_HPV14	REGULATORY PROTEIN E2	3.1
812	M18157	Human glandular kallikrein gene, complete cds.	1.5	EKLF_MOUSE	ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR (EKLF)	1.1
813	D25215	Human mRNA for KIAA0032 gene, complete cds	1.9	YXIS_SACER	HYPOTHETICAL 28.9 KD PROTEIN IN XIS 5'REGION (ORF1)	1.3
814	M96628	Human gene sequence, 5' end.	2.00E-06	AGRI_DISOM	AGRIN (FRAGMENT)	9.5
815	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a .	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
816	X14168	Human pLC46 with DNA replication origin	5.00E-16	ZN44_HUMAN	ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7)	1.6
817	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.28	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.7
818	AF058055	Mus musculus monocarboxylate transporter 1	0.2	<NONE>	<NONE>	<NONE>
819	AB014570	Homo sapiens mRNA for KIAA0670 protein, partial cds	0.16	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	4.00E-06
820	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.27	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
821	Z54367	H.sapiens gene for plectin	0.29	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	1.00E-14
822	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	2.00E-49
823	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	1.00E-20	UL52_HSV11	DNA HELICASE/PRIMASE COMPLEX PROTEIN (DNA REPLICATION PROTEIN UL52)	5.3
824	X58430	Human Hox1.8 gene	0	HXAA_HUMAN	HOMEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)	1.00E-44
825	X53754	Porcine sarcoplasmic/endoplasmic-reticulum Ca(2+) pump gene 2 3'-end region	1.3	<NONE>	<NONE>	<NONE>
826	AB005786	Arabidopsis thaliana tRNA-Glu gene	0.46	<NONE>	<NONE>	<NONE>
827	AB012130	Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds	1.9	<NONE>	<NONE>	<NONE>
828	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.063
829	AB007886	Homo sapiens KIAA0426 mRNA, complete cds	0.042	YDF3_SCHPO	PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03	0.52
830	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	e-172	UROT_BOVIN	TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68)	0.86

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
831	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	9.00E-96
832	U38376	Rattus norvegicus cytosolic phospholipase A2 mRNA, complete cds	0.048	<NONE>	<NONE>	<NONE>
833	L40411	Homo sapiens thyroid receptor interactor	0	TRI8_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
834	U08110	Mus musculus RNA1 homolog (Fug1) mRNA, complete cds.	8.00E-04	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	0.02
835	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
836	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
837	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	5.00E-05	GCS1_HUMAN	MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106)	9.2
838	U18657	Haemophilus influenzae LeuA (leuA) gene, partial cds, DprA (dprA+), orf272 and orf193 genes, complete cds, and PfkA (pfkA) gene, partial cds.	0.01	STE6_YEAST	MATING FACTOR A SECRETION PROTEIN STE6 (MULTIPLE DRUG RESISTANCE PROTEIN HOMOLOG) (P-GLYCOPROTEIN)	7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
839	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	1.00E-10	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	2.00E-06
840	D78255	Mouse mRNA for PAP-1, complete cds	e-175	<NONE>	<NONE>	<NONE>
841	D17263	Human HepG2 3' region MboI cDNA, clone hmd5f07m3	1.00E-58	<NONE>	<NONE>	<NONE>
842	AF006751	Homo sapiens ES/130 mRNA, complete cds	0.061	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	2.00E-07
843	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	6.00E-05	YC14_METJA	HYPOTHETICAL PROTEIN MJ1214	8.1
844	D88689	Mus musculus mRNA for flt-1, complete cds	0.084	ICP0_HSV2H	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN)	0.014

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001340B:A06	17062	3	0	0	0	0	0
M00001340D:F10	11589	2	2	1	3	3	8
M00001341A:E12	4443	10	6	2	6	3	11
M00001342B:E06	39805	2	0	0	0	1	0
M00001343C:F10	2790	7	15	13	14	6	0
M00001343D:H07	23255	3	0	1	1	0	0
M00001345A:E01	6420	8	0	2	0	1	0
M00001346A:F09	5007	4	8	3	6	2	6
M00001346D:E03	6806	5	2	1	2	0	3
M00001346D:G06	5779	5	4	3	4	0	0
M00001346D:G06	5779	5	4	3	4	0	0
M00001347A:B10	13576	5	0	0	0	12	11
M00001348B:B04	16927	4	0	0	2	0	0
M00001348B:G06	16985	4	0	0	0	0	0
M00001349B:B08	3584	5	11	5	0	0	2
M00001350A:H01	7187	5	3	1	0	1	0
M00001351B:A08	3162	10	14	1	6	6	5
M00001351B:A08	3162	10	14	1	6	6	5
M00001352A:E02	16245	4	0	0	0	0	0
M00001353A:G12	8078	4	3	1	0	1	0
M00001353D:D10	14929	4	0	0	1	23	16
M00001355B:G10	14391	3	1	0	0	0	0
M00001357D:D11	4059	8	6	8	16	0	1
M00001361A:A05	4141	5	2	10	16	4	27
M00001361D:F08	2379	26	13	4	2	2	3
M00001362B:D10	5622	7	4	2	13	1	2
M00001362C:H11	945	9	21	2	1	0	0
M00001365C:C10	40132	2	0	0	0	3	0
M00001370A:C09	6867	7	3	0	0	0	0
M00001371C:E09	7172	3	5	1	2	0	1
M00001376B:G06	17732	1	3	5	0	1	4
M00001378B:B02	39833	2	0	0	0	0	0
M00001379A:A05	1334	27	38	35	28	3	0
M00001380D:B09	39886	2	0	0	0	0	0
M00001382C:A02	22979	2	1	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001386C:B12	5178	5	5	4	2	5	2
M00001387A:C05	2464	5	19	25	16	1	0
M00001387B:G03	7587	6	2	1	0	0	0
M00001388D:G05	5832	10	3	0	1	5	0
M00001389A:C08	16269	3	0	0	0	1	1
M00001394A:F01	6583	2	7	3	2	0	0
M00001395A:C03	4016	5	14	0	6	0	0
M00001396A:C03	4009	6	4	13	5	4	10
M00001402A:E08	39563	2	0	0	0	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001407B:D11	5556	8	1	5	0	2	0
M00001409C:D12	9577	5	2	0	1	11	12
M00001410A:D07	7005	8	2	0	0	0	0
M00001412B:B10	8551	4	4	0	3	0	0
M00001415A:H06	13538	5	0	0	0	9	1
M00001416A:H01	7674	5	2	0	5	0	0
M00001416B:H11	8847	4	1	3	0	6	1
M00001417A:E02	36393	2	0	0	1	0	0
M00001418B:F03	9952	4	2	1	1	0	0
M00001418D:B06	8526	3	2	1	5	1	0
M00001421C:F01	9577	5	2	0	1	11	12
M00001423B:E07	15066	4	0	0	0	0	0
M00001424B:G09	10470	5	1	0	2	0	1
M00001425B:H08	22195	3	0	0	0	0	0
M00001426D:C08	4261	4	9	7	9	12	15
M00001428A:H10	84182	1	0	0	0	0	0
M00001429A:H04	2797	15	11	18	16	1	14
M00001429B:A11	4635	7	9	2	0	0	0
M00001429D:D07	40392	2	0	1	8	12	16
M00001439C:F08	40054	1	0	0	0	0	0
M00001442C:D07	16731	3	1	0	0	0	0
M00001445A:F05	13532	3	2	1	0	1	2
M00001446A:F05	7801	5	2	4	6	1	0
M00001447A:G03	10717	7	2	0	5	8	0
M00001448D:C09	8	1850	2127	1703	3133	1355	122
M00001448D:H01	36313	2	0	0	0	1	30
M00001449A:A12	5857	6	2	3	4	0	0
M00001449A:B12	41633	1	1	0	0	0	0
M00001449A:D12	3681	12	5	10	1	2	5
M00001449A:G10	36535	2	0	0	0	0	0
M00001449C:D06	86110	1	0	0	0	0	0
M00001450A:A02	39304	2	0	0	0	0	0
M00001450A:A11	32663	1	1	0	0	0	0
M00001450A:B12	82498	1	0	0	0	0	0
M00001450A:D08	27250	2	0	0	0	0	0
M00001452A:B04	84328	1	0	0	0	0	0
M00001452A:B12	86859	1	0	0	0	0	0
M00001452A:D08	1120	44	41	5	11	5	0
M00001452A:F05	85064	1	0	0	0	0	0
M00001452C:B06	16970	4	0	0	0	3	4
M00001453A:E11	16130	3	1	0	0	0	1
M00001453C:F06	16653	3	1	0	0	0	0
M00001454A:A09	83103	1	0	0	0	0	0
M00001454B:C12	7005	8	2	0	0	0	0
M00001454D:G03	689	58	95	17	36	66	95
M00001455A:E09	13238	4	1	0	0	0	0
M00001455B:E12	13072	4	1	0	0	0	0
M00001455D:F09	9283	4	1	0	1	0	1

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001455D:F09	9283	4	1	0	1	0	1
M00001460A:F06	2448	23	22	2	3	3	1
M00001460A:F12	39498	2	0	0	0	0	0
M00001461A:D06	1531	20	23	32	17	14	14
M00001463C:B11	19	1415	1203	1364	525	479	774
M00001465A:B11	10145	2	0	2	0	0	0
M00001466A:E07	4275	11	2	5	0	4	2
M00001467A:B07	38759	2	0	0	0	1	1
M00001467A:D04	39508	2	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:E10	39442	2	0	0	0	0	0
M00001468A:F05	7589	6	2	1	1	1	0
M00001469A:C10	12081	4	0	0	0	0	0
M00001469A:H12	19105	2	0	2	0	1	0
M00001470A:B10	1037	53	48	4	22	0	0
M00001470A:C04	39425	2	0	0	0	0	0
M00001471A:B01	39478	2	0	0	0	0	0
M00001481D:A05	7985	3	1	4	0	1	0
M00001490B:C04	18699	2	1	0	0	0	3
M00001494D:F06	7206	4	3	3	1	2	0
M00001497A:G02	2623	12	4	31	4	6	1
M00001499B:A11	10539	2	1	1	0	1	0
M00001500A:C05	5336	9	2	4	8	3	15
M00001500A:E11	2623	12	4	31	4	6	1
M00001500C:E04	9443	4	2	1	1	0	0
M00001501D:C02	9685	3	2	0	7	2	3
M00001504C:A07	10185	5	1	0	0	2	4
M00001504C:H06	6974	7	3	0	1	0	0
M00001504D:G06	6420	8	0	2	0	1	0
M00001507A:H05	39168	2	0	0	0	0	0
M00001511A:H06	39412	2	0	0	0	0	0
M00001512A:A09	39186	2	0	0	0	0	0
M00001512D:G09	3956	9	9	5	2	0	0
M00001513A:B06	4568	10	4	0	9	2	0
M00001513C:E08	14364	1	0	0	0	0	0
M00001514C:D11	40044	2	0	0	0	0	0
M00001517A:B07	4313	13	6	1	0	1	0
M00001518C:B11	8952	3	4	0	4	2	0
M00001528A:C04	7337	4	4	3	16	12	21
M00001528A:F09	18957	3	0	0	0	0	0
M00001528B:H04	8358	3	3	2	0	0	0
M00001531A:D01	38085	2	0	0	0	0	0
M00001532B:A06	3990	6	12	4	1	3	1
M00001533A:C11	2428	14	14	13	9	2	19
M00001534A:C04	16921	4	0	0	1	2	1
M00001534A:D09	5097	6	5	1	1	3	2
M00001534A:F09	5321	11	7	1	5	10	26

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001534C:A01	4119	9	4	2	2	5	3
M00001535A:B01	7665	3	1	5	0	0	0
M00001535A:C06	20212	2	0	1	1	0	0
M00001535A:F10	39423	2	0	0	0	0	0
M00001536A:B07	2696	23	11	9	18	10	21
M00001536A:C08	39392	2	0	0	0	0	0
M00001537A:F12	39420	2	0	0	0	0	0
M00001537B:G07	3389	4	11	13	2	0	0
M00001540A:D06	8286	6	1	0	3	4	0
M00001541A:D02	3765	19	6	0	0	0	0
M00001541A:F07	22085	3	0	0	0	0	1
M00001541A:H03	39174	2	0	0	0	0	0
M00001542A:A09	22113	3	0	0	0	0	0
M00001542A:E06	39453	2	0	0	0	0	0
M00001544A:E03	12170	2	1	2	0	0	0
M00001544A:G02	19829	2	0	1	0	0	0
M00001544B:B07	6974	7	3	0	1	0	0
M00001545A:C03	19255	2	0	0	0	0	0
M00001545A:D08	13864	3	0	2	1	2	4
M00001546A:G11	1267	43	55	5	0	0	0
M00001548A:E10	5892	5	1	4	4	1	3
M00001548A:H09	1058	40	44	37	47	39	59
M00001549A:B02	4015	10	5	8	15	2	0
M00001549A:D08	10944	3	0	3	1	0	7
M00001549B:F06	4193	12	7	2	2	0	1
M00001549C:E06	16347	4	0	0	0	0	0
M00001550A:A03	7239	5	2	1	0	2	0
M00001550A:G01	5175	8	1	3	2	0	0
M00001551A:B10	6268	6	4	3	18	5	0
M00001551A:F05	39180	2	0	0	0	0	0
M00001551A:G06	22390	2	1	0	0	0	1
M00001551C:G09	3266	12	14	0	1	0	6
M00001552A:B12	307	73	60	196	75	79	27
M00001552A:D11	39458	2	0	0	0	0	0
M00001552B:D04	5708	5	4	4	3	1	4
M00001553A:H06	8298	4	3	1	3	0	0
M00001553B:F12	4573	5	7	2	5	0	1
M00001553D:D10	22814	3	0	0	0	0	0
M00001555A:B02	39539	2	0	0	0	1	0
M00001555A:C01	39195	2	0	0	0	0	0
M00001555D:G10	4561	8	4	4	8	0	0
M00001556A:C09	9244	2	0	3	2	10	17
M00001556A:F11	1577	12	40	25	3	4	0
M00001556A:H01	15855	2	1	1	2	12	213
M00001556B:C08	4386	7	8	3	1	3	21
M00001556B:G02	11294	4	0	2	0	0	1
M00001557A:D02	7065	5	3	2	1	0	0
M00001557A:D02	7065	5	3	2	1	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001557A:F01	9635	3	0	2	1	0	0
M00001557A:F03	39490	2	0	0	0	1	0
M00001557B:H10	5192	8	5	0	5	0	0
M00001557D:D09	8761	3	4	0	1	0	1
M00001558B:H11	7514	5	3	0	0	0	0
M00001560D:F10	6558	4	3	4	0	0	5
M00001561A:C05	39486	2	0	0	0	0	0
M00001563B:F06	102	289	233	278	116	123	184
M00001564A:B12	5053	11	4	2	2	1	1
M00001571C:H06	5749	4	1	9	0	0	0
M00001578B:E04	23001	2	1	0	2	0	0
M00001579D:C03	6539	8	3	0	0	0	1
M00001583D:A10	6293	3	5	2	6	0	0
M00001586C:C05	4623	3	4	12	2	1	1
M00001587A:B11	39380	2	0	0	0	0	0
M00001594B:H04	260	189	188	27	2	15	0
M00001597C:H02	4837	6	2	10	0	3	1
M00001597D:C05	10470	5	1	0	2	0	1
M00001598A:G03	16999	4	0	0	0	0	0
M00001601A:D08	22794	2	0	0	0	0	0
M00001604A:B10	1399	49	27	19	7	10	23
M00001604A:F05	39391	2	0	0	0	0	0
M00001607A:E11	11465	5	0	0	0	0	0
M00001608A:B03	7802	5	4	0	1	0	0
M00001608B:E03	22155	3	0	0	0	0	0
M00001614C:F10	13157	4	1	0	3	1	0
M00001617C:E02	17004	4	0	1	0	1	0
M00001619C:F12	40314	2	0	0	0	1	0
M00001621C:C08	40044	2	0	0	0	0	0
M00001623D:F10	13913	2	1	2	0	0	1
M00001624A:B06	3277	10	11	8	3	5	1
M00001624C:F01	4309	4	13	3	10	0	0
M00001630B:H09	5214	10	2	2	2	4	3
M00001644C:B07	39171	2	0	0	0	0	0
M00001645A:C12	19267	2	0	0	0	0	1
M00001648C:A01	4665	5	9	0	0	0	0
M00001657D:C03	23201	3	0	0	0	3	0
M00001657D:F08	76760	1	0	2	2	0	5
M00001662C:A09	23218	3	0	0	0	0	0
M00001663A:E04	35702	2	0	0	0	0	0
M00001669B:F02	6468	4	3	3	8	1	0
M00001670C:H02	14367	3	0	0	0	0	0
M00001673C:H02	7015	6	3	1	2	1	1
M00001675A:C09	8773	4	1	4	4	4	6
M00001676B:F05	11460	4	2	0	0	0	0
M00001677C:E10	14627	1	2	1	0	1	0
M00001677D:A07	7570	5	3	0	0	0	0
M00001678D:F12	4416	9	5	2	6	1	3

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001679A:A06	6660	7	0	4	2	1	0
M00001679A:F10	26875	1	0	0	0	1	0
M00001679B:F01	6298	2	4	5	3	1	0
M00001679C:F01	78091	1	0	0	0	0	0
M00001679D:D03	10751	3	2	0	1	0	1
M00001679D:D03	10751	3	2	0	1	0	1
M00001680D:F08	10539	2	1	1	0	1	0
M00001682C:B12	17055	4	0	0	0	0	0
M00001686A:E06	4622	7	6	4	2	3	0
M00001688C:F09	5382	6	2	6	2	0	3
M00001693C:G01	4393	10	6	2	4	1	1
M00001716D:H05	67252	1	0	0	1	0	0
M00003741D:C09	40108	2	0	0	0	0	0
M00003747D:C05	11476	6	0	0	0	0	0
M00003759B:B09	697	76	52	30	72	21	30
M00003762C:B08	17076	4	0	0	0	0	0
M00003763A:F06	3108	14	11	7	5	0	1
M00003774C:A03	67907	1	0	0	0	0	0
M00003796C:D05	5619	3	5	3	3	0	4
M00003826B:A06	11350	3	3	0	0	1	0
M00003833A:E05	21877	2	1	0	0	0	1
M00003837D:A01	7899	5	4	0	2	1	0
M00003839A:D08	7798	5	2	2	0	0	1
M00003844C:B11	6539	8	3	0	0	0	1
M00003846B:D06	6874	6	3	0	0	0	0
M00003851B:D10	13595	4	0	1	0	0	1
M00003853A:D04	5619	3	5	3	3	0	4
M00003853A:F12	10515	5	1	0	1	1	2
M00003856B:C02	4622	7	6	4	2	3	0
M00003857A:G10	3389	4	11	13	2	0	0
M00003857A:H03	4718	4	5	5	2	4	6
M00003871C:E02	4573	5	7	2	5	0	1
M00003875B:F04	12977	5	0	0	0	0	0
M00003875B:F04	12977	5	0	0	0	0	0
M00003875C:G07	8479	4	3	1	1	2	4
M00003876D:E12	7798	5	2	2	0	0	1
M00003879B:C11	5345	7	1	7	4	6	27
M00003879B:D10	31587	1	1	0	0	1	0
M00003879D:A02	14507	3	1	0	0	3	1
M00003885C:A02	13576	5	0	0	0	12	11
M00003885C:A02	13576	5	0	0	0	12	11
M00003906C:E10	9285	4	3	0	0	1	2
M00003907D:A09	39809	1	0	0	0	2	1
M00003907D:H04	16317	3	0	0	0	0	0
M00003909D:C03	8672	4	4	0	0	0	0
M00003912B:D01	12532	4	1	0	1	0	1
M00003914C:F05	3900	9	6	8	1	7	13
M00003922A:E06	23255	3	0	1	1	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00003958A:H02	18957	3	0	0	0	0	0
M00003958A:H02	18957	3	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003968B:F06	24488	2	0	1	4	0	0
M00003970C:B09	40122	2	0	0	0	0	0
M00003974D:E07	23210	3	0	0	0	0	0
M00003974D:H02	23358	3	0	0	0	1	0
M00003975A:G11	12439	4	0	0	0	0	0
M00003978B:G05	5693	7	4	1	3	1	1
M00003981A:E10	3430	9	10	7	3	0	0
M00003982C:C02	2433	10	13	21	18	8	8
M00003983A:A05	9105	5	1	1	1	0	0
M00004028D:A06	6124	4	8	1	9	1	0
M00004028D:C05	40073	2	0	1	0	0	1
M00004031A:A12	9061	5	2	0	0	0	0
M00004031A:A12	9061	5	2	0	0	0	0
M00004035C:A07	37285	2	0	0	1	0	1
M00004035D:B06	17036	4	0	0	0	0	0
M00004059A:D06	5417	10	4	0	9	2	0
M00004068B:A01	3706	7	14	4	22	1	0
M00004072B:B05	17036	4	0	0	0	0	0
M00004081C:D10	15069	3	0	0	1	0	0
M00004081C:D12	14391	3	1	0	0	0	0
M00004086D:G06	9285	4	3	0	0	1	2
M00004087D:A01	6880	2	6	1	1	0	0
M00004093D:B12	5325	5	5	2	0	2	1
M00004093D:B12	5325	5	5	2	0	2	1
M00004105C:A04	7221	5	2	2	2	0	0
M00004108A:E06	4937	4	9	3	1	3	1
M00004111D:A08	6874	6	3	0	0	0	0
M00004114C:F11	13183	2	3	0	7	0	1
M00004138B:H02	13272	3	2	0	3	0	0
M00004146C:C11	5257	2	8	5	5	5	25
M00004151D:B08	16977	4	0	0	0	0	0
M00004157C:A09	6455	3	1	6	0	0	0
M00004169C:C12	5319	6	2	8	2	2	3
M00004171D:B03	4908	6	7	2	2	2	0
M00004172C:D08	11494	4	0	0	0	0	0
M00004183C:D07	16392	3	0	0	0	0	0
M00004185C:C03	11443	5	1	0	0	0	0
M00004197D:H01	8210	2	6	0	0	0	0
M00004203B:C12	14311	4	0	0	0	1	2
M00004212B:C07	2379	26	13	4	2	2	3
M00004214C:H05	11451	3	2	1	2	1	1
M00004223A:G10	16918	4	0	0	0	0	0
M00004223B:D09	7899	5	4	0	2	1	0
M00004223D:E04	12971	4	0	0	0	1	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00004229B:F08	6455	3	1	6	0	0	0
M00004230B:C07	7212	3	5	2	1	3	0
M00004269D:D06	4905	7	6	3	1	3	1
M00004275C:C11	16914	3	0	0	1	0	0
M00004283B:A04	14286	3	1	0	1	1	1
M00004285B:E08	56020	1	0	0	0	0	0
M00004295D:F12	16921	4	0	0	1	2	1
M00004296C:H07	13046	4	1	0	1	0	0
M00004307C:A06	9457	2	0	5	0	3	0
M00004312A:G03	26295	2	0	0	0	0	0
M00004318C:D10	21847	2	1	0	0	0	0
M00004372A:A03	2030	13	10	32	4	0	0
M00004377C:F05	2102	12	20	23	21	6	5

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001340B:A06	17062	0	0	0	0	0	0
M00001340D:F10	11589	0	0	0	0	0	0
M00001341A:E12	4443	0	0	0	1	0	0
M00001342B:E06	39805	0	0	0	0	0	0
M00001343C:F10	2790	0	0	0	0	0	0
M00001343D:H07	23255	0	0	0	0	0	0
M00001345A:E01	6420	0	0	0	0	0	0
M00001346A:F09	5007	0	0	0	0	0	0
M00001346D:E03	6806	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001347A:B10	13576	0	0	0	0	0	0
M00001348B:B04	16927	0	0	0	0	0	0
M00001348B:G06	16985	0	0	0	0	0	0
M00001349B:B08	3584	0	0	0	0	0	0
M00001350A:H01	7187	0	0	0	0	0	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001352A:E02	16245	0	0	0	0	0	0
M00001353A:G12	8078	0	0	0	0	0	0
M00001353D:D10	14929	0	3	1	0	5	0
M00001355B:G10	14391	0	0	0	0	0	0
M00001357D:D11	4059	0	0	0	0	0	0
M00001361A:A05	4141	0	0	0	0	0	0
M00001361D:F08	2379	0	0	0	0	0	0
M00001362B:D10	5622	0	0	0	0	0	0
M00001362C:H11	945	0	0	0	0	0	1
M00001365C:C10	40132	0	0	0	0	0	0
M00001370A:C09	6867	0	0	0	0	0	0
M00001371C:E09	7172	0	0	0	0	0	0
M00001376B:G06	17732	0	0	0	0	0	1
M00001378B:B02	39833	0	0	0	0	0	0
M00001379A:A05	1334	0	0	0	0	0	1
M00001380D:B09	39886	0	0	0	0	0	0
M00001382C:A02	22979	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001386C:B12	5178	0	0	0	0	0	0
M00001387A:C05	2464	0	0	0	0	0	0
M00001387B:G03	7587	0	0	0	0	0	0
M00001388D:G05	5832	0	0	0	0	0	0
M00001389A:C08	16269	0	1	0	0	0	0
M00001394A:F01	6583	1	4	1	0	0	0
M00001395A:C03	4016	0	0	0	0	0	0
M00001396A:C03	4009	0	0	0	0	0	0
M00001402A:E08	39563	0	0	0	0	0	0
M00001407B:D11	5556	0	0	0	0	0	0
M00001409C:D12	9577	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001410A:D07	7005	0	0	0	0	0	0
M00001412B:B10	8551	0	0	0	0	0	0
M00001415A:H06	13538	0	0	0	0	0	0
M00001416A:H01	7674	0	0	0	0	0	0
M00001416B:H11	8847	0	0	0	0	0	0
M00001417A:E02	36393	0	0	0	0	0	0
M00001418B:F03	9952	0	0	0	0	0	0
M00001418D:B06	8526	0	0	0	0	0	0
M00001421C:F01	9577	0	0	0	0	0	0
M00001423B:E07	15066	0	0	0	0	0	0
M00001424B:G09	10470	0	0	0	0	0	0
M00001425B:H08	22195	0	0	0	0	0	0
M00001426D:C08	4261	0	0	1	0	0	1
M00001428A:H10	84182	0	0	0	0	0	0
M00001429A:H04	2797	0	0	0	0	0	0
M00001429B:A11	4635	0	0	0	0	0	0
M00001429D:D07	40392	0	0	0	0	0	0
M00001439C:F08	40054	0	0	0	0	0	0
M00001442C:D07	16731	0	0	0	0	0	0
M00001445A:F05	13532	0	0	0	0	0	0
M00001446A:F05	7801	0	0	0	0	0	0
M00001447A:G03	10717	0	0	0	0	0	0
M00001448D:C09	8	1	6	6	1	14	1
M00001448D:H01	36313	0	3	0	0	3	0
M00001449A:A12	5857	0	0	0	0	0	0
M00001449A:B12	41633	0	0	0	0	0	0
M00001449A:D12	3681	0	0	0	0	0	0
M00001449A:G10	36535	0	0	0	0	0	0
M00001449C:D06	86110	0	0	0	0	0	0
M00001450A:A02	39304	0	0	0	0	0	0
M00001450A:A11	32663	0	0	0	0	0	0
M00001450A:B12	82498	0	0	0	0	0	0
M00001450A:D08	27250	0	0	0	0	0	0
M00001452A:B04	84328	0	0	0	0	0	0
M00001452A:B12	86859	0	0	0	0	0	0
M00001452A:D08	1120	0	0	0	0	0	0
M00001452A:F05	85064	0	0	0	0	0	0
M00001452C:B06	16970	0	0	2	0	1	0
M00001453A:E11	16130	0	0	0	0	0	0
M00001453C:F06	16653	0	0	0	0	0	0
M00001454A:A09	83103	0	0	0	0	0	0
M00001454B:C12	7005	0	0	0	0	0	0
M00001454D:G03	689	0	2	2	0	4	2
M00001455A:E09	13238	0	0	0	0	0	0
M00001455B:E12	13072	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001460A:F06	2448	0	0	0	0	0	0
M00001460A:F12	39498	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001461A:D06	1531	0	0	0	0	0	0
M00001463C:B11	19	2	13	13	0	69	10
M00001465A:B11	10145	0	0	0	0	0	0
M00001466A:E07	4275	0	0	0	0	0	0
M00001467A:B07	38759	0	0	0	0	0	0
M00001467A:D04	39508	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:E10	39442	0	0	0	0	0	0
M00001468A:F05	7589	0	0	0	0	0	0
M00001469A:C10	12081	0	0	0	0	0	0
M00001469A:H12	19105	0	0	0	0	0	0
M00001470A:B10	1037	0	0	0	0	0	0
M00001470A:C04	39425	0	0	0	0	0	0
M00001471A:B01	39478	0	0	0	0	0	0
M00001481D:A05	7985	0	0	0	0	0	0
M00001490B:C04	18699	0	0	0	0	0	0
M00001494D:F06	7206	0	0	0	0	0	0
M00001497A:G02	2623	0	0	0	0	0	0
M00001499B:A11	10539	0	0	0	0	0	0
M00001500A:C05	5336	0	0	0	0	0	0
M00001500A:E11	2623	0	0	0	0	0	0
M00001500C:E04	9443	0	0	0	0	0	0
M00001501D:C02	9685	0	0	0	0	0	0
M00001504C:A07	10185	0	0	0	0	0	0
M00001504C:H06	6974	0	0	0	0	0	0
M00001504D:G06	6420	0	0	0	0	0	0
M00001507A:H05	39168	0	0	0	0	0	0
M00001511A:H06	39412	0	0	0	0	0	0
M00001512A:A09	39186	0	0	0	0	0	0
M00001512D:G09	3956	0	0	1	0	0	0
M00001513A:B06	4568	0	0	0	0	0	0
M00001513C:E08	14364	0	0	0	0	0	0
M00001514C:D11	40044	0	1	0	0	0	0
M00001517A:B07	4313	0	0	0	0	0	0
M00001518C:B11	8952	0	0	0	0	0	0
M00001528A:C04	7337	0	0	0	0	0	0
M00001528A:F09	18957	0	0	0	0	0	0
M00001528B:H04	8358	0	0	0	0	0	0
M00001531A:D01	38085	0	0	0	0	0	0
M00001532B:A06	3990	1	1	0	0	0	0
M00001533A:C11	2428	0	0	1	0	0	0
M00001534A:C04	16921	0	0	0	0	0	0
M00001534A:D09	5097	0	0	0	0	0	0
M00001534A:F09	5321	0	1	0	0	2	0
M00001534C:A01	4119	0	0	0	0	0	0
M00001535A:B01	7665	0	0	0	0	0	0
M00001535A:C06	20212	0	0	0	0	0	0
M00001535A:F10	39423	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001536A:B07	2696	0	0	0	0	3	0
M00001536A:C08	39392	0	0	0	0	0	0
M00001537A:F12	39420	0	0	0	0	0	0
M00001537B:G07	3389	0	0	0	0	0	0
M00001540A:D06	8286	0	0	0	0	0	0
M00001541A:D02	3765	0	0	0	0	0	0
M00001541A:F07	22085	0	0	0	0	0	0
M00001541A:H03	39174	0	0	0	0	0	0
M00001542A:A09	22113	0	0	0	0	0	0
M00001542A:E06	39453	0	0	0	0	0	0
M00001544A:E03	12170	0	0	0	0	0	0
M00001544A:G02	19829	0	0	0	0	0	0
M00001544B:B07	6974	0	0	0	0	0	0
M00001545A:C03	19255	0	0	0	0	0	0
M00001545A:D08	13864	0	0	0	0	0	0
M00001546A:G11	1267	1	0	0	0	7	0
M00001548A:E10	5892	0	0	0	0	0	0
M00001548A:H09	1058	0	0	1	0	0	0
M00001549A:B02	4015	0	0	0	0	0	0
M00001549A:D08	10944	0	0	0	0	0	0
M00001549B:F06	4193	0	0	0	0	0	0
M00001549C:E06	16347	0	0	0	0	0	0
M00001550A:A03	7239	0	0	0	0	0	0
M00001550A:G01	5175	0	0	0	0	0	0
M00001551A:B10	6268	0	0	0	0	0	0
M00001551A:F05	39180	0	0	0	0	0	0
M00001551A:G06	22390	0	0	0	0	0	0
M00001551C:G09	3266	0	0	1	0	0	0
M00001552A:B12	307	0	0	0	0	3	0
M00001552A:D11	39458	0	0	0	0	0	0
M00001552B:D04	5708	0	1	0	0	0	0
M00001553A:H06	8298	0	0	0	0	0	0
M00001553B:F12	4573	0	0	0	0	0	0
M00001553D:D10	22814	0	0	0	0	0	0
M00001555A:B02	39539	0	0	0	0	0	0
M00001555A:C01	39195	0	0	0	0	0	0
M00001555D:G10	4561	0	0	0	0	0	0
M00001556A:C09	9244	0	0	0	0	0	0
M00001556A:F11	1577	0	0	0	0	0	0
M00001556A:H01	15855	3	5	5	0	3	1
M00001556B:C08	4386	1	2	0	0	0	0
M00001556B:G02	11294	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:F01	9635	0	0	0	0	0	0
M00001557A:F03	39490	0	0	0	0	0	0
M00001557B:H10	5192	0	0	0	0	0	0
M00001557D:D09	8761	0	0	0	0	0	0
M00001558B:H11	7514	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001560D:F10	6558	0	0	0	0	0	0
M00001561A:C05	39486	0	0	0	0	0	0
M00001563B:F06	102	22	38	65	7	43	10
M00001564A:B12	5053	0	0	1	0	0	0
M00001571C:H06	5749	0	0	0	0	0	0
M00001578B:E04	23001	0	0	0	0	0	0
M00001579D:C03	6539	0	0	0	0	0	0
M00001583D:A10	6293	0	0	0	0	0	0
M00001586C:C05	4623	0	0	0	0	1	0
M00001587A:B11	39380	0	0	0	0	0	0
M00001594B:H04	260	0	0	0	0	1	0
M00001597C:H02	4837	0	0	0	0	0	0
M00001597D:C05	10470	0	0	0	0	0	0
M00001598A:G03	16999	1	1	1	0	0	0
M00001601A:D08	22794	0	0	0	0	0	0
M00001604A:B10	1399	0	0	0	0	0	0
M00001604A:F05	39391	0	0	0	0	0	0
M00001607A:E11	11465	0	0	0	0	0	0
M00001608A:B03	7802	0	0	0	0	0	0
M00001608B:E03	22155	0	0	0	0	0	0
M00001614C:F10	13157	0	0	0	0	0	0
M00001617C:E02	17004	0	0	0	0	1	0
M00001619C:F12	40314	0	0	0	0	0	0
M00001621C:C08	40044	0	1	0	0	0	0
M00001623D:F10	13913	0	0	0	0	0	0
M00001624A:B06	3277	0	0	0	0	0	0
M00001624C:F01	4309	0	0	0	0	0	0
M00001630B:H09	5214	1	0	0	1	1	0
M00001644C:B07	39171	0	0	0	0	0	0
M00001645A:C12	19267	0	0	0	0	1	0
M00001648C:A01	4665	0	0	0	0	0	0
M00001657D:C03	23201	0	0	0	0	0	0
M00001657D:F08	76760	0	0	0	0	0	0
M00001662C:A09	23218	0	0	0	0	0	0
M00001663A:E04	35702	0	0	0	0	0	0
M00001669B:F02	6468	0	0	0	0	0	0
M00001670C:H02	14367	0	0	0	0	0	0
M00001673C:H02	7015	0	0	0	0	0	0
M00001675A:C09	8773	0	0	0	0	0	0
M00001676B:F05	11460	0	0	0	0	0	0
M00001677C:E10	14627	0	1	0	0	0	0
M00001677D:A07	7570	0	0	0	0	0	0
M00001678D:F12	4416	0	0	0	0	0	0
M00001679A:A06	6660	0	0	0	0	0	0
M00001679A:F10	26875	0	0	0	0	0	0
M00001679B:F01	6298	0	0	0	0	0	0
M00001679C:F01	78091	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001680D:F08	10539	0	0	0	0	0	0
M00001682C:B12	17055	0	0	0	0	0	0
M00001686A:E06	4622	0	0	0	0	0	0
M00001688C:F09	5382	0	0	0	0	0	0
M00001693C:G01	4393	0	0	0	0	0	0
M00001716D:H05	67252	0	0	0	0	0	0
M00003741D:C09	40108	0	0	0	0	0	0
M00003747D:C05	11476	0	0	0	0	0	0
M00003759B:B09	697	0	0	0	0	1	0
M00003762C:B08	17076	0	0	0	0	0	0
M00003763A:F06	3108	0	0	0	0	0	0
M00003774C:A03	67907	0	0	0	0	0	0
M00003796C:D05	5619	0	0	0	0	0	0
M00003826B:A06	11350	0	0	0	0	0	0
M00003833A:E05	21877	0	0	0	0	0	0
M00003837D:A01	7899	0	0	0	0	0	0
M00003839A:D08	7798	0	0	0	0	0	0
M00003844C:B11	6539	0	0	0	0	0	0
M00003846B:D06	6874	0	0	1	0	0	0
M00003851B:D10	13595	0	0	0	0	0	0
M00003853A:D04	5619	0	0	0	0	0	0
M00003853A:F12	10515	0	0	0	0	0	0
M00003856B:C02	4622	0	0	0	0	0	0
M00003857A:G10	3389	0	0	0	0	0	0
M00003857A:H03	4718	0	0	0	0	0	0
M00003871C:E02	4573	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875C:G07	8479	0	0	0	0	0	1
M00003876D:E12	7798	0	0	0	0	0	0
M00003879B:C11	5345	0	0	0	2	0	1
M00003879B:D10	31587	0	0	0	0	0	0
M00003879D:A02	14507	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003906C:E10	9285	0	0	0	0	0	0
M00003907D:A09	39809	0	0	0	0	0	0
M00003907D:H04	16317	0	0	0	0	0	0
M00003909D:C03	8672	0	0	0	0	0	0
M00003912B:D01	12532	0	0	0	0	0	0
M00003914C:F05	3900	0	0	0	0	1	0
M00003922A:E06	23255	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003968B:F06	24488	0	0	0	0	0	0
M00003970C:B09	40122	0	0	0	0	0	0
M00003974D:E07	23210	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00003974D:H02	23358	0	0	0	0	0	0
M00003975A:G11	12439	0	0	0	0	0	0
M00003978B:G05	5693	0	0	0	0	0	0
M00003981A:E10	3430	0	0	0	0	1	0
M00003982C:C02	2433	0	0	0	0	0	0
M00003983A:A05	9105	0	0	0	0	0	0
M00004028D:A06	6124	0	0	0	0	0	0
M00004028D:C05	40073	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004035C:A07	37285	0	0	0	0	0	0
M00004035D:B06	17036	0	0	0	0	0	0
M00004059A:D06	5417	0	0	0	0	0	0
M00004068B:A01	3706	0	0	0	0	0	0
M00004072B:B05	17036	0	0	0	0	0	0
M00004081C:D10	15069	0	0	0	0	0	0
M00004081C:D12	14391	0	0	0	0	0	0
M00004086D:G06	9285	0	0	0	0	0	0
M00004087D:A01	6880	0	0	0	0	0	0
M00004093D:B12	5325	1	1	0	1	0	1
M00004093D:B12	5325	1	1	0	1	0	1
M00004105C:A04	7221	0	0	0	0	0	0
M00004108A:E06	4937	0	0	0	0	0	0
M00004111D:A08	6874	0	0	1	0	0	0
M00004114C:F11	13183	0	0	0	0	0	0
M00004138B:H02	13272	0	0	0	0	0	0
M00004146C:C11	5257	0	1	0	0	0	0
M00004151D:B08	16977	0	0	0	0	0	0
M00004157C:A09	6455	0	0	0	0	0	0
M00004169C:C12	5319	0	0	0	0	0	0
M00004171D:B03	4908	0	0	0	0	0	0
M00004172C:D08	11494	0	0	0	0	0	0
M00004183C:D07	16392	0	0	0	0	0	0
M00004185C:C03	11443	0	0	0	0	0	0
M00004197D:H01	8210	0	0	0	0	0	0
M00004203B:C12	14311	0	0	0	0	0	0
M00004212B:C07	2379	0	0	0	0	0	0
M00004214C:H05	11451	0	0	0	0	0	0
M00004223A:G10	16918	0	0	0	0	0	0
M00004223B:D09	7899	0	0	0	0	0	0
M00004223D:E04	12971	0	0	0	0	0	0
M00004229B:F08	6455	0	0	0	0	0	0
M00004230B:C07	7212	0	0	0	0	0	0
M00004269D:D06	4905	0	0	0	0	0	0
M00004275C:C11	16914	0	0	0	0	0	0
M00004283B:A04	14286	0	0	0	0	0	0
M00004285B:E08	56020	0	0	0	0	0	0
M00004295D:F12	16921	0	0	0	0	0	0
M00004296C:H07	13046	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00004307C:A06	9457	0	0	0	0	0	0
M00004312A:G03	26295	0	0	0	0	0	0
M00004318C:D10	21847	0	0	0	0	0	0
M00004372A:A03	2030	0	0	0	0	0	0
M00004377C:F05	2102	0	0	0	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001340B:A06	17062	0	0	0
M00001340D:F10	11589	0	0	0
M00001341A:E12	4443	4	2	0
M00001342B:E06	39805	0	0	0
M00001343C:F10	2790	0	0	0
M00001343D:H07	23255	0	0	0
M00001345A:E01	6420	0	0	0
M00001346A:F09	5007	0	0	0
M00001346D:E03	6806	0	1	1
M00001346D:G06	5779	0	0	0
M00001346D:G06	5779	0	0	0
M00001347A:B10	13576	0	0	0
M00001348B:B04	16927	0	0	0
M00001348B:G06	16985	0	0	0
M00001349B:B08	3584	0	0	0
M00001350A:H01	7187	0	0	0
M00001351B:A08	3162	0	0	1
M00001351B:A08	3162	0	0	1
M00001352A:E02	16245	0	0	0
M00001353A:G12	8078	0	0	0
M00001353D:D10	14929	0	1	0
M00001355B:G10	14391	0	0	0
M00001357D:D11	4059	0	0	0
M00001361A:A05	4141	1	2	1
M00001361D:F08	2379	0	0	0
M00001362B:D10	5622	0	2	1
M00001362C:H11	945	0	0	0
M00001365C:C10	40132	0	0	0
M00001370A:C09	6867	0	0	0
M00001371C:E09	7172	0	0	1
M00001376B:G06	17732	2	0	0
M00001378B:B02	39833	0	0	0
M00001379A:A05	1334	0	0	0
M00001380D:B09	39886	0	0	0
M00001382C:A02	22979	1	0	0
M00001383A:C03	39648	0	0	0
M00001383A:C03	39648	0	0	0
M00001386C:B12	5178	0	0	0
M00001387A:C05	2464	0	0	0
M00001387B:G03	7587	0	0	0
M00001388D:G05	5832	0	0	0
M00001389A:C08	16269	2	0	0
M00001394A:F01	6583	0	0	0
M00001395A:C03	4016	0	0	0
M00001396A:C03	4009	2	0	0
M00001402A:E08	39563	0	0	0
M00001407B:D11	5556	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001409C:D12	9577	0	0	0
M00001410A:D07	7005	0	0	0
M00001412B:B10	8551	0	0	0
M00001415A:H06	13538	0	0	0
M00001416A:H01	7674	0	0	0
M00001416B:H11	8847	1	0	0
M00001417A:E02	36393	0	0	0
M00001418B:F03	9952	0	0	0
M00001418D:B06	8526	0	0	0
M00001421C:F01	9577	0	0	0
M00001423B:E07	15066	0	0	0
M00001424B:G09	10470	0	0	0
M00001425B:H08	22195	0	0	0
M00001426D:C08	4261	0	0	0
M00001428A:H10	84182	0	0	0
M00001429A:H04	2797	0	0	0
M00001429B:A11	4635	0	0	0
M00001429D:D07	40392	0	0	0
M00001439C:F08	40054	0	0	0
M00001442C:D07	16731	0	0	0
M00001445A:F05	13532	0	0	0
M00001446A:F05	7801	0	1	0
M00001447A:G03	10717	0	0	0
M00001448D:C09	8	7	6	9
M00001448D:H01	36313	1	0	0
M00001449A:A12	5857	0	0	0
M00001449A:B12	41633	0	0	0
M00001449A:D12	3681	1	0	0
M00001449A:G10	36535	0	0	0
M00001449C:D06	86110	0	0	0
M00001450A:A02	39304	0	1	0
M00001450A:A11	32663	0	0	0
M00001450A:B12	82498	0	0	0
M00001450A:D08	27250	0	0	0
M00001452A:B04	84328	0	0	0
M00001452A:B12	86859	0	0	0
M00001452A:D08	1120	0	0	0
M00001452A:F05	85064	0	0	0
M00001452C:B06	16970	1	0	0
M00001453A:E11	16130	0	0	0
M00001453C:F06	16653	0	0	0
M00001454A:A09	83103	0	0	0
M00001454B:C12	7005	0	0	0
M00001454D:G03	689	0	0	1
M00001455A:E09	13238	0	0	0
M00001455B:E12	13072	0	0	0
M00001455D:F09	9283	0	0	0
M00001455D:F09	9283	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001460A:F06	2448	0	0	0
M00001460A:F12	39498	0	0	0
M00001461A:D06	1531	0	0	1
M00001463C:B11	19	17	32	31
M00001465A:B11	10145	0	0	0
M00001466A:E07	4275	0	0	0
M00001467A:B07	38759	0	0	0
M00001467A:D04	39508	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:E10	39442	0	0	0
M00001468A:F05	7589	0	0	0
M00001469A:C10	12081	0	0	0
M00001469A:H12	19105	0	0	0
M00001470A:B10	1037	0	0	0
M00001470A:C04	39425	0	0	0
M00001471A:B01	39478	0	0	0
M00001481D:A05	7985	0	0	0
M00001490B:C04	18699	0	0	0
M00001494D:F06	7206	0	0	0
M00001497A:G02	2623	1	0	0
M00001499B:A11	10539	0	1	0
M00001500A:C05	5336	0	0	0
M00001500A:E11	2623	1	0	0
M00001500C:E04	9443	0	0	0
M00001501D:C02	9685	0	0	0
M00001504C:A07	10185	0	0	0
M00001504C:H06	6974	0	0	0
M00001504D:G06	6420	0	0	0
M00001507A:H05	39168	0	0	0
M00001511A:H06	39412	0	0	0
M00001512A:A09	39186	0	0	0
M00001512D:G09	3956	0	0	0
M00001513A:B06	4568	0	0	0
M00001513C:E08	14364	0	0	0
M00001514C:D11	40044	0	0	0
M00001517A:B07	4313	0	0	0
M00001518C:B11	8952	0	0	0
M00001528A:C04	7337	1	2	2
M00001528A:F09	18957	0	0	0
M00001528B:H04	8358	0	0	0
M00001531A:D01	38085	0	0	0
M00001532B:A06	3990	0	0	0
M00001533A:C11	2428	0	0	0
M00001534A:C04	16921	0	0	0
M00001534A:D09	5097	0	0	0
M00001534A:F09	5321	4	7	6
M00001534C:A01	4119	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001535A:B01	7665	0	2	4
M00001535A:C06	20212	0	0	0
M00001535A:F10	39423	0	0	0
M00001536A:B07	2696	0	0	0
M00001536A:C08	39392	0	0	0
M00001537A:F12	39420	0	0	0
M00001537B:G07	3389	0	0	0
M00001540A:D06	8286	0	0	0
M00001541A:D02	3765	0	0	0
M00001541A:F07	22085	0	0	0
M00001541A:H03	39174	0	0	0
M00001542A:A09	22113	0	0	0
M00001542A:E06	39453	0	0	0
M00001544A:E03	12170	0	0	0
M00001544A:G02	19829	0	0	0
M00001544B:B07	6974	0	0	0
M00001545A:C03	19255	0	0	0
M00001545A:D08	13864	0	0	0
M00001546A:G11	1267	0	0	0
M00001548A:E10	5892	0	1	0
M00001548A:H09	1058	1	3	0
M00001549A:B02	4015	0	1	0
M00001549A:D08	10944	1	0	0
M00001549B:F06	4193	0	0	0
M00001549C:E06	16347	0	0	0
M00001550A:A03	7239	0	1	0
M00001550A:G01	5175	1	0	0
M00001551A:B10	6268	0	0	1
M00001551A:F05	39180	0	0	0
M00001551A:G06	22390	0	0	1
M00001551C:G09	3266	0	0	0
M00001552A:B12	307	6	11	4
M00001552A:D11	39458	0	0	0
M00001552B:D04	5708	0	0	0
M00001553A:H06	8298	0	0	0
M00001553B:F12	4573	0	0	0
M00001553D:D10	22814	0	0	0
M00001555A:B02	39539	0	0	0
M00001555A:C01	39195	0	0	0
M00001555D:G10	4561	0	0	0
M00001556A:C09	9244	0	1	0
M00001556A:F11	1577	0	0	2
M00001556A:H01	15855	1	1	0
M00001556B:C08	4386	3	0	1
M00001556B:G02	11294	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:F01	9635	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001557A:F03	39490	0	0	0
M00001557B:H10	5192	0	0	0
M00001557D:D09	8761	0	0	0
M00001558B:H11	7514	0	0	0
M00001560D:F10	6558	0	0	0
M00001561A:C05	39486	0	0	0
M00001563B:F06	102	2	1	2
M00001564A:B12	5053	0	0	0
M00001571C:H06	5749	0	0	0
M00001578B:E04	23001	0	0	0
M00001579D:C03	6539	0	0	0
M00001583D:A10	6293	0	0	0
M00001586C:C05	4623	0	0	0
M00001587A:B11	39380	0	0	0
M00001594B:H04	260	1	0	0
M00001597C:H02	4837	1	0	0
M00001597D:C05	10470	0	0	0
M00001598A:G03	16999	4	2	6
M00001601A:D08	22794	0	0	0
M00001604A:B10	1399	6	3	3
M00001604A:F05	39391	0	0	0
M00001607A:E11	11465	0	0	0
M00001608A:B03	7802	0	0	0
M00001608B:E03	22155	0	0	0
M00001614C:F10	13157	0	0	0
M00001617C:E02	17004	0	0	0
M00001619C:F12	40314	0	0	0
M00001621C:C08	40044	0	0	0
M00001623D:F10	13913	0	0	0
M00001624A:B06	3277	0	0	0
M00001624C:F01	4309	0	0	0
M00001630B:H09	5214	0	1	2
M00001644C:B07	39171	0	0	0
M00001645A:C12	19267	0	0	0
M00001648C:A01	4665	0	0	0
M00001657D:C03	23201	0	0	0
M00001657D:F08	76760	0	0	0
M00001662C:A09	23218	0	0	0
M00001663A:E04	35702	0	0	0
M00001669B:F02	6468	0	0	0
M00001670C:H02	14367	0	0	0
M00001673C:H02	7015	0	0	0
M00001675A:C09	8773	0	0	0
M00001676B:F05	11460	2	0	0
M00001677C:E10	14627	0	0	0
M00001677D:A07	7570	0	0	0
M00001678D:F12	4416	1	2	0
M00001679A:A06	6660	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001679A:F10	26875	0	0	0
M00001679B:F01	6298	0	0	0
M00001679C:F01	78091	0	0	0
M00001679D:D03	10751	0	0	0
M00001679D:D03	10751	0	0	0
M00001680D:F08	10539	0	1	0
M00001682C:B12	17055	0	0	0
M00001686A:E06	4622	0	0	0
M00001688C:F09	5382	0	0	0
M00001693C:G01	4393	0	0	0
M00001716D:H05	67252	0	0	0
M00003741D:C09	40108	0	0	0
M00003747D:C05	11476	0	0	0
M00003759B:B09	697	0	0	0
M00003762C:B08	17076	0	0	0
M00003763A:F06	3108	0	0	0
M00003774C:A03	67907	0	0	0
M00003796C:D05	5619	0	1	0
M00003826B:A06	11350	0	0	0
M00003833A:E05	21877	0	0	0
M00003837D:A01	7899	0	0	0
M00003839A:D08	7798	0	0	0
M00003844C:B11	6539	0	0	0
M00003846B:D06	6874	0	0	0
M00003851B:D10	13595	0	0	0
M00003853A:D04	5619	0	1	0
M00003853A:F12	10515	0	0	1
M00003856B:C02	4622	0	0	0
M00003857A:G10	3389	0	0	0
M00003857A:H03	4718	0	0	0
M00003871C:E02	4573	0	0	0
M00003875B:F04	12977	0	0	0
M00003875B:F04	12977	0	0	0
M00003875C:G07	8479	1	0	0
M00003876D:E12	7798	0	0	0
M00003879B:C11	5345	4	8	3
M00003879B:D10	31587	0	0	0
M00003879D:A02	14507	0	0	0
M00003885C:A02	13576	0	0	0
M00003885C:A02	13576	0	0	0
M00003906C:E10	9285	0	0	0
M00003907D:A09	39809	0	0	0
M00003907D:H04	16317	0	0	0
M00003909D:C03	8672	0	0	0
M00003912B:D01	12532	0	0	0
M00003914C:F05	3900	0	1	0
M00003922A:E06	23255	0	0	0
M00003958A:H02	18957	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00003958A:H02	18957	0	0	0
M00003958C:G10	40455	0	0	0
M00003958C:G10	40455	0	0	0
M00003968B:F06	24488	0	0	0
M00003970C:B09	40122	0	0	0
M00003974D:E07	23210	0	0	0
M00003974D:H02	23358	0	0	0
M00003975A:G11	12439	0	0	0
M00003978B:G05	5693	0	0	0
M00003981A:E10	3430	0	0	0
M00003982C:C02	2433	2	4	0
M00003983A:A05	9105	0	0	0
M00004028D:A06	6124	0	0	0
M00004028D:C05	40073	0	1	0
M00004031A:A12	9061	0	0	0
M00004031A:A12	9061	0	0	0
M00004035C:A07	37285	0	0	0
M00004035D:B06	17036	0	0	0
M00004059A:D06	5417	0	0	0
M00004068B:A01	3706	0	0	0
M00004072B:B05	17036	0	0	0
M00004081C:D10	15069	0	0	0
M00004081C:D12	14391	0	0	0
M00004086D:G06	9285	0	0	0
M00004087D:A01	6880	0	0	0
M00004093D:B12	5325	0	0	0
M00004093D:B12	5325	0	0	0
M00004105C:A04	7221	0	0	0
M00004108A:E06	4937	0	0	0
M00004111D:A08	6874	0	0	0
M00004114C:F11	13183	0	0	0
M00004138B:H02	13272	0	0	0
M00004146C:C11	5257	0	0	1
M00004151D:B08	16977	0	0	0
M00004157C:A09	6455	0	0	0
M00004169C:C12	5319	0	0	0
M00004171D:B03	4908	0	0	0
M00004172C:D08	11494	0	0	0
M00004183C:D07	16392	0	0	0
M00004185C:C03	11443	2	0	0
M00004197D:H01	8210	0	0	0
M00004203B:C12	14311	0	0	0
M00004212B:C07	2379	0	0	0
M00004214C:H05	11451	0	0	0
M00004223A:G10	16918	0	0	0
M00004223B:D09	7899	0	0	0
M00004223D:E04	12971	0	0	0
M00004229B:F08	6455	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00004230B:C07	7212	0	0	1
M00004269D:D06	4905	0	0	0
M00004275C:C11	16914	0	0	0
M00004283B:A04	14286	0	0	0
M00004285B:E08	56020	0	0	0
M00004295D:F12	16921	0	0	0
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We Claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844.

2. The library of claim 1, wherein the library is provided on a nucleic acid array.

3. The library of claim 1, wherein the library is provided in a computer-readable format.

4. The library of claim 1, wherein the library comprises a differentially expressed polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379.

5. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

6. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

7. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

8. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof.

9. An isolated polynucleotide according to claim 8, wherein the polynucleotide comprises a seqeuence encoding a polypeptide of a protein family selected from the group consisting of: 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins.

10. The polynucleotide of claim 9, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379 , and 395.

11. The polynucleotide of claim 8, wherein the polynucleotide comprises a seqeuence encoding a polypeptide having a functional domain selected from the group consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease domain.

12. The polynucleotide of claim 11, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and 395.

13. A recombinant host cell containing the polynucleotide of claim 8.

14. An isolated polypeptide encoded by the polynucleotide of claim 8.

15. An antibody that specifically binds a polypeptide of claim 14.

16. A vector comprising the polynucleotide of claim 8.

17. A polynucleotide comprising the nucleotide sequence of an insert contained in a clone deposited as ATCC accession number xx, xx, xx, xx, xx, xx, xx, xx, or xx.

18. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

19. The method of claim 18, wherein said detecting step is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS:1-844.

20. The method of claim 18, wherein the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

21. The method of claim 18, wherein the cell is a colon tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

22. The method of claim 18, wherein the cell is a lung tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

SEQUENCE LISTING

<110> Lewis T. Williams
Jaime Escobedo
Michael A. Innis
Pablo Dominiguez Garcia
Julie Sudduth-Klinger
Christoph Reinhard
Klause Giese
Filippo Randazzo
Giulia C. Kennedy
David Pot
Altaf Kassan
George Lamson
Radoje Drmanac
Radomir Crkvenjakov
Mark Dickson
Snezana Drmanac
Ivan Labat
Dena Leshkowitz
David Kita
Veronica Garcia
William Lee Jones
Birjit Stache-Crain

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<213> Homo sapiens

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<212> DNA
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<212> DNA
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<213> Homo sapiens

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<210> 45
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 47
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<212> DNA
<213> Homo sapiens

<400> 47
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<210> 48
<211> 300
<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA
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<212> DNA
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<400> 53
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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

<400> 56
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<212> DNA
<213> Homo sapiens

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<210> 59
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<212> DNA
<213> Homo sapiens

<400> 64
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<210> 65
<211> 300

<212> DNA
<213> Homo sapiens

<400> 65
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<212> DNA
<213> Homo sapiens

<400> 66
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 68
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<211> 300
<212> DNA
<213> Homo sapiens

<400> 69
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<211> 300
<212> DNA
<213> Homo sapiens

<400> 70
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<210> 71
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<213> Homo sapiens

<400> 71
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<210> 72
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<212> DNA
<213> Homo sapiens

<400> 72
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<210> 73
<211> 300
<212> DNA
<213> Homo sapiens

<400> 73
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<210> 74
<211> 300
<212> DNA
<213> Homo sapiens

<400> 74
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<210> 75
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<212> DNA
<213> Homo sapiens

<400> 75
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<210> 76
<211> 300
<212> DNA
<213> Homo sapiens

<400> 76
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<210> 77
<211> 300
<212> DNA
<213> Homo sapiens

<400> 77
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<212> DNA
<213> Homo sapiens

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<210> 79
<211> 278
<212> DNA
<213> Homo sapiens

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<210> 80
<211> 300
<212> DNA
<213> Homo sapiens

<400> 80
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<210> 81
<211> 300
<212> DNA
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<400> 81
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<210> 82

<211> 300
<212> DNA
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<400> 82
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<210> 83
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<212> DNA
<213> Homo sapiens

<400> 83
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<210> 84
<211> 300
<212> DNA
<213> Homo sapiens

<400> 84
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<210> 85
<211> 300
<212> DNA
<213> Homo sapiens

<400> 85
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<210> 86
<211> 300
<212> DNA
<213> Homo sapiens

<400> 86
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<210> 87
<211> 300
<212> DNA
<213> Homo sapiens

<400> 87
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<210> 88
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<212> DNA
<213> Homo sapiens

<400> 88
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<212> DNA
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<400> 89
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<210> 90
<211> 300
<212> DNA
<213> Homo sapiens

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<212> DNA
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<400> 91
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<210> 92
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<212> DNA
<213> Homo sapiens

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<210> 93
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<212> DNA
<213> Homo sapiens

<400> 93
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<210> 94
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<212> DNA
<213> Homo sapiens

<400> 94
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<213> Homo sapiens

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<210> 98
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<212> DNA
<213> Homo sapiens

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<211> 300
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<212> DNA
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<213> Homo sapiens

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<212> DNA
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<212> DNA
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<213> Homo sapiens

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<213> Homo sapiens

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<210> 110
<211> 300
<212> DNA
<213> Homo sapiens

<400> 110
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gacaaggccg cgctcctgca ggagcagcag cagcagcagc agccgggatt ctggaccttc 180
agctactatc agagcttctt tgacgtggac acctcacagg tcctggaccg gatcaaaggc 240
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<210> 111
<211> 271
<212> DNA
<213> Homo sapiens

<400> 111
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tggggggggt ggggnnttcc ttctannccn ntacnctatg tgtttaatnn ncntantnct 180
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<210> 112
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<212> DNA
<213> Homo sapiens

<400> 112
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aattacattt gttcatgatg tcaagtgtct ggtatgtagc taatgcttat tgaacacata 180
gtaatttatt gaataattgt catgatcact ggatgagata tagccactgt ggaggtaggc 240
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<210> 113
<211> 300
<212> DNA
<213> Homo sapiens

<400> 113
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acatgcgatt tgaagacacg ttttatggag cagacattat ccaaggggag agaaagagac 180
aaagagtgct gagctccagg tttaagaatg aatatgtggc cgaccctgta taccgcactt 240
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<210> 114
<211> 300
<212> DNA
<213> Homo sapiens

<400> 114
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gttgaaaaat taaccaaagg tgcagctatc ttctttgaat tcaaacacta caagcctaaa 180
aaaaggttta ccagcaccaa gtgttttgct ttcatggaga tggatgaaat taaacctggg 240
ccaattgtaa tagaactata cacgaaaccc actgacttta aaagaaagaa attgcaatta 300

<210> 115
<211> 288
<212> DNA
<213> Homo sapiens

<400> 115
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gacatggcag cgggtagctc ctggggctga gccagaagca tcactgcagt gaaagtctct 180
gcttacctgt ctggctcagc ttgggcaagg gctgggccat atgtgctcag ggacgtgctt 240
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<210> 116
<211> 300

<212> DNA
<213> Homo sapiens

<400> 116
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taacattcac tgggtctgcc aaaaatgtgg atttgtggtc tgcttagatt gttacaaggc 180
aaaggaaagg aagagttcta gagataaaga actatatgct tggatgaagt gtgtgaaggg 240
acagcctcat gatcacaaac atttaatgcc aacccaaatt atacctggtt ctgttttgac 300

<210> 117
<211> 300
<212> DNA
<213> Homo sapiens

<400> 117
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tgaggaactg cctcagaagc tgcgatcaca actttggctg aagcccctgc ctcactctag 180
ggcacctgac ctggcctctt gcctaaacca caaggctaag ggctatagac aatggtttcc 240
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<210> 118
<211> 300
<212> DNA
<213> Homo sapiens

<400> 118
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tgtggaagtt cagaggctac ttatgctcaa gcagcagata actatggaga tgagtgcact 180
gaggacccat agaatacaga ttctacaggg attacaagaa acatatgaac cttctgagca 240
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<210> 119
<211> 300
<212> DNA
<213> Homo sapiens

<400> 119
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gatgtacagt gctggggctg gtattctagg gcctgcattg agactcacat tttgccatca 180
aaagcctttt aagaggtgga ggttgcggtg agctgacatg gtgccactgc actccggcct 240
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<210> 120
<211> 273
<212> DNA
<213> Homo sapiens

<400> 120
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aagcccaaca gagagtgtgc accccagatt ccttgtagta ctcctattgc tactgaaagg 180
acagttgcac atttgaacac tctgaaggac cgtcacccag gtgatttgtg ggcccgcatg 240
cacatctcat cccttggaat atgctgcagg aga 273

<210> 121
<211> 300
<212> DNA
<213> Homo sapiens

<400> 121
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tgtggaagtt cagaggctac ttatgctcaa gcagcagata actatggaga tgagtgcact 180
gaggacccat agaatacaga ttctacaggg attacaagaa acatatgaac cttctgagca 240
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<210> 122
<211> 300
<212> DNA
<213> Homo sapiens

<400> 122
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gagaaggctt cagcagcaga actgatggtg aaggctcgtg ttctccatcc tcaactttct 180
ttgcttcgat catacacaag aatacatttg gaagggcaaa aaaatgaaca ctgtcgttca 240
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<210> 123
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<212> DNA
<213> Homo sapiens

<400> 123
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cctttaaata gcaaagcagc ctacctggag gctaagtctg ggcagtgggc tggcccctgg 180
tgtgagcatt agaccagcca cagtgcctga ttggtatagc cttatgtgct ttcctacaaa 240
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<210> 124
<211> 300
<212> DNA
<213> Homo sapiens

<400> 124
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gatgactgac agggccactg gggcatttcc acgttaacag cagctgccac tggcaaaaga 180
agtgactcgc caatggaggc atctcagatg tgggcccagg agtctgggga gctactttga 240
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<210> 125
<211> 300
<212> DNA
<213> Homo sapiens

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ttgatttagg ttttcaaaag ctagaaataa aatttacatg ccttagattt cataaaattc 180
tgctctaatt gggtggaagg tgctgtatct aacttgtgtt cctcctaagg ttatgtccta 240
ataactattc ttttaggagt atacttctac tttatagaag gttgcttttc tttttaattt 300

<210> 126
<211> 300
<212> DNA
<213> Homo sapiens

<400> 126
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aactccaaat caacagtatt ttcaacaaga aatgtgcaat tgaaatcaag tgctgtttaa 120
gtgcagctag gatttccaca ggaagacact tgcagtgaac agagttatgg agcagcaaaa 180
acacagatct atttggaaaa agagaaaaca tatgcgttgt attttgcttc aattataaaa 240
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<210> 127
<211> 300
<212> DNA
<213> Homo sapiens

<400> 127
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ggacccactg caccaggaca agaaatccac cccaggcctc tccccagacc cactgcacca 180
ggacaagaaa tccacccccca ggccacgccc cagacccact gccctaggat gtgggggtgg 240
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<210> 128
<211> 300
<212> DNA
<213> Homo sapiens

<400> 128
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gcgttgtatt ttgcttcaat tataaaatac catcctctca aaggtggttc taaattacaa 300

<210> 129
<211> 285
<212> DNA
<213> Homo sapiens

<400> 129
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<210> 130
<211> 300
<212> DNA
<213> Homo sapiens

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tgctgcggcc tggggagcag gcgctgggtg gtggttctgc ctgcttgctg ctcgttcccc 240
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<210> 131
<211> 300
<212> DNA
<213> Homo sapiens

<400> 131
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ataaggagat catattccaa aaggttgtca gttggttgtt tgcaacctgg aatgtatttt 240
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<210> 132
<211> 300
<212> DNA
<213> Homo sapiens

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<210> 133
<211> 269
<212> DNA

<213> Homo sapiens

<400> 133
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gacctacagc tcccagacga cagccatcct gggcgcactg ctgggcagct gctgccccca 180
gctccaggtc ctggaggtga gcaccggcat caaccgtaat agcattcccc ttcagctgcc 240
tgtccaggct ntgcaaaaag gctgccctc 269

<210> 134
<211> 300
<212> DNA
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<400> 134
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tgcaagtatc agtgatgctg ccctgttaga catcatttat atgcaatttc atcagcacca 240
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<210> 135
<211> 300
<212> DNA
<213> Homo sapiens

<400> 135
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ctgacaacaa tcctgaaggc ctgggatttt ttgtctgaaa atcaactgca gactgtaaat 180
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<212> DNA
<213> Homo sapiens

<400> 136
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ccaaaaatgt ggatttgtgg tctgcttaga ttgttacaag gcaaaggaaa ggaagagttc 240
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<210> 137
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<212> DNA
<213> Homo sapiens

<400> 137

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tatttcttta attttaatac aaaaaataca tcatttaatt tttgttacat atgaacattc 240
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<211> 300
<212> DNA
<213> Homo sapiens

<400> 138
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<213> Homo sapiens

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cggcactctt cttacctttg gggaagcta tctggagtta tgactgatgt gtaaagtggt 240
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<213> Homo sapiens

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gaggtgggat ccagcccact tccgtctgac cccaagcccc tgctgttaac ccctgcccca 240
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<212> DNA
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<211> 300
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<213> Homo sapiens

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tcatttgagg ccaggagttc gagaccagct tggccaacat gatgagaccc cgtctctatt 240
aaaaatacaa aaattagcca ggcgtggtgg cgcctgtagt cccagctact caggaggttg 300

<210> 147
<211> 295
<212> DNA
<213> Homo sapiens

<400> 147
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caaannaagg anganngnta ggngngaaaa anaanaacaa anggggaaaa ngggaaaaaa 180
ggcganaaag gnaanannag nanaaggngg aananannnn annagaaagg ncaanaaaag 240
aagnacaaag aaaaangana anaagnaann annanannga cagagacaag aagga 295

<210> 148
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<212> DNA
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<400> 148
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<213> Homo sapiens

<400> 149
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aatatctttt cttttgagag tacccccagt ttatttctac tgtgctttat tgctactgtt 180
ctttattgtg aatgttgtaa cattttaaaa atgttttgcc atagcttttt aggacttggt 240
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<210> 150
<211> 300
<212> DNA

<213> Homo sapiens

<400> 150
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ctattctgac aactttttaa ttcctttgat cttataagtt aaagctgtaa caactgaaat 120
tgcatggatc aagtaagcat agttttatcc agggagaaaa ataaaaggaa gccatagaat 180
tgctctggtc aaaaccaagc acaccatagc cttaactgaa tatttaggaa atctgcctaa 240
tctgcttata tttggtgttt gtttttgac tgttgggctt tgggaagatg ttatttatga 300

<210> 151
<211> 300
<212> DNA
<213> Homo sapiens

<400> 151
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gcagaagaaa agagaactcg catgatggaa atattttctg aaacaaaaga tgtatttcaa 120
ttaaaagact tggagaagat tgctcccaaa gagaaaggca ttactgctat gtcagtaaaa 180
gaagtccttc aaagcttagt tgatgatggt atggttgact gtgagaggat cggaacttct 240
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<210> 152
<211> 300
<212> DNA
<213> Homo sapiens

<400> 152
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tttaaagtaa aaactttggg ctgggcacag tggctcacac ctgtaatccc agcacttggg 180
gaagctgagg tgggcagatc agttgaggtc aggagttcta gaccagcctg gtcaacatgg 240
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<210> 153
<211> 300
<212> DNA
<213> Homo sapiens

<400> 153
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cagagggagg cacagtccac ccagatccac ctttccagca agacccccag tggctgccca 180
gcctgggagc acctctttgc ttttcacacc aaaccaaaac tggcgagagc ccctcctagc 240
caccagtgat ccccaagcat ccagtacaga accaggcatc gagctagctc cctgcacggc 300

<210> 154
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<212> DNA
<213> Homo sapiens

<400> 154
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ttaaaaactc atttacagta gaaaccattc ttctttctcc caacagtatc ctttgccaag 180
accatgagaa cagtatggga gcatgttgtt ggtcagggtt tcagaatacg cgtgatgtca 240
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<210> 155
<211> 81
<212> DNA
<213> Homo sapiens

<400> 155
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ggggaggtgt gggaggtttt a 81

<210> 156
<211> 300
<212> DNA
<213> Homo sapiens

<400> 156
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aataaaagac tctgcaaaag tacaatagaa ctttcagaaa attctttact tccagcttct 120
tctatgttga ctggcacaca aagcttgctg caacctcatt tagagagggt tgccatcgat 180
gctctacagt tatgttgttt gttacttccc ccaccaaatc gtagaaagct tcaactttta 240
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<210> 157
<211> 300
<212> DNA
<213> Homo sapiens

<400> 157
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gaggagcggg cccaccagag catcctgaca cagcgggtgc actgggccga ggcgctgcag 120
aaacttgaca ccatccgcac tggcctggtg ggcatgctta ctcacctgga tgacctccag 180
ctgattcaga aggagcaaga gattttcgag aggaccgaag aagcagaggg cattttggat 240
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<210> 158
<211> 300
<212> DNA
<213> Homo sapiens

<400> 158
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gtttaatttt tgaaaactgg ctactgctct gtgtttacag acgtgtgcag ttgtaggcat 120
gtagctacag gacattttta agggcccagg atcgtttttt cccagggcaa gcagaagaga 180
aaatgttgta tatgtctttt acccggcaca ttccccttgc ctaaatacaa gggctggagt 240
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<210> 159
<211> 300
<212> DNA
<213> Homo sapiens

<400> 159
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gccagtgaga agaatgagta taaaggatgg gttttaacta cagacccagt ctctgccaat 180
attgtccttg tgaacttcct tgaagatggc agcatgtctg tgaccggaat tatgggacat 240
gctgtgcaga ctgttgaaac tatgaatgaa ggggaccata gagtgaggga gaagctgatg 300

<210> 160
<211> 294
<212> DNA
<213> Homo sapiens

<400> 160
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aaaatgagaa ctctggagtg agctaaattg atcccaatta agtttttctg cttagcagac 180
agaaggtata attttttgac accctttccc acctggtgcc tatgctaggc ttgtnctgat 240
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<210> 161
<211> 300
<212> DNA
<213> Homo sapiens

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ccaggtggca atcatgagtg aatggatgaa gaaaggcccc ttagaatggc aagattacat 120
ttacaaagag gtccgagtga cagccagtga gaagaatgag tataaaggat gggttttaac 180
tacagaccca gtctctgcca atattgtcct tgtgaacttc cttgaagatg gcagcatgtc 240
tgtgaccgga attatgggac atgctgtgca gactgttgaa actatgaatg aaggggacca 300

<210> 162
<211> 300
<212> DNA
<213> Homo sapiens

<400> 162
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cgcctcccct ctcccctcag agggcacagc tgcaggcctg accaaggcca cgcccggctc 120
tcgtgctcta ggacctgcac gggacttgtg gatgggcctg gactctccag aaactacttg 180
ggccagagca aaggaaaacc tcttgtttta aaaaaatttt tttcagagtg ttttggggag 240
gagttttagg gcttggggag agggaggaca catctggagg aaatggcctt ctttttaaaa 300

<210> 163
<211> 300
<212> DNA

<213> Homo sapiens

<400> 163
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cagccttaag gtctgcagtt ccaccctgcc catcaagccc tttctctcct gcttccctga 180
ggtacgagtg tatgacctga cacaatatga gcactgccca gatgatgtgc tagtcctggg 240
aacagatggc ctgtgggatg tcactactga ctgtgaggta tctgccactg tggacagggt 300

<210> 164
<211> 300
<212> DNA
<213> Homo sapiens

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gtttattaat tctatttaat caaggaaaat aacttcagat tccataaagt ttcagtttat 180
ttttagttta ctactaggtg agatagcaca ttacatactt ttactatcaa atattatttt 240
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<210> 165
<211> 300
<212> DNA
<213> Homo sapiens

<400> 165
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gctggttgaa gaccagaggt aaactgcaga ggtcaccacc cccaccatgt cccaggtgat 180
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<210> 166
<211> 300
<212> DNA
<213> Homo sapiens

<400> 166
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gaattgcata aaatagtggt agcagcttat ttcttaagta ctttattatt tgtgctttac 180
catttcaggt tcttatcttt aacccttatt tactcagttt tccatctgaa tgatcctatc 240
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<210> 167
<211> 300
<212> DNA
<213> Homo sapiens

<400> 167

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ttaggaaccg gggcaagggc gtccgagccg tgttgagcct ctgtcagcag acttccagga 120
gtcagccgcc ggtccgagcc ttcctgctca tctccaccct gaaggacaag cgcgggaccc 180
gctatgagct aagggagaac attgagcaat tcttcaccaa atttgtagat gaggggaaag 240
ccactgttcg gttaaaggag cctcctgtgg atatctgtct aagtaaggat tccatatggc 300

<210> 168
<211> 300
<212> DNA
<213> Homo sapiens

<400> 168
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aagacaaata caagtgaaaa aaatatacta atggattaac gtccctgtcg agtgacattt 180
tctgactatg gaaatgatat tagacaaaaa gcaacttcaa gtgggtttct tatttgagtt 240
caaaatgggt cataacgcag catagataac ttgaaacatg aacagcgcat ttggcccagg 300

<210> 169
<211> 296
<212> DNA
<213> Homo sapiens

<400> 169
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ttggcgcctt gtgatgagcc caggaggacc ctgcacccag cacccagccc cagcctgcca 180
ccccagtgtt cttactacac cacggaaggc tggggagccc aagccctgat ggccccgtgc 240
cctncattgg gncccctggc tanttcancn agncccncag gtngagncca aagcca 296

<210> 170
<211> 300
<212> DNA
<213> Homo sapiens

<400> 170
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aggaactaga tccaccactt cctctgctgg gcatgctcca aaaatggttg tggcttccag 120
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agtttctgaa aaaatattga aagtttctat ggtgaaatag gaagttaatg tgcttaggaa 240
gaaaaaagtg gtaatgattc aaggaaacat aatcacacac ggttttagtt ttaatggaca 300

<210> 171
<211> 300
<212> DNA
<213> Homo sapiens

<400> 171
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ctgggaaaag ccggggggca aggctggcat gggaatgaac acctgctggt gacacctctc 180

tgagcttcag ttcccttaac tagaaaaata gaacaggccc ggtgcggtgg ctcatacctg 240
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<210> 172
<211> 300
<212> DNA
<213> Homo sapiens

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gagagaatat cagcgacagg actacatgga tgccatggct gagaagcaaa aattggatgc 240
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<210> 173
<211> 300
<212> DNA
<213> Homo sapiens

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<211> 300
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<213> Homo sapiens

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aggcctatgc atagttaata aggttataat ctactcaaca tggaaaatgg agcctatttg 240
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<212> DNA
<213> Homo sapiens

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cggagagaat atcagcgaca ggactacatg gatgccatgg ctgagaagca aaaattggat 240
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<212> DNA
<213> Homo sapiens

<400> 176
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cacttacaat accagcatgc ttctatcact gtaattctat tcaattctca ggcccatgag 240
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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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tggcatgagt aggtgatttc agaaacagaa ctcacttttg ttgtttggtc ttaaaattag     180
gaacttttct tcatctgggc ttcatttccc tgcaccttcc cagctttcta gtcatgcaag     240
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      <212> DNA
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catgacataa aagccaaagg tcacaaggga aaaaactgat agatttgtct gtgatattga     180
gagatgtatg cacatataca tacaacagtc atagtaagac accgttagac aaaaggtgat     240
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      <210> 187
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      <212> DNA
      <213> Homo sapiens

      <400> 187
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gcccaggctg gagtgcaatg gcatgatctt ggctcactgc aacccctgcc ttgcgagttc     180
aagtgattct tctgcctcag cctcctgagt agctgggatt acaggcgctc accaccacac     240
ccagctaatt tctgtatttt tagtagacac agggttttac catgttggcc angctggtct     300

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      <213> Homo sapiens

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tttaaatccc tgggcagcac cgcagggaca gatattaccg tcaacagtgt gattctactt     180
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<210> 189
<211> 300
<212> DNA
<213> Homo sapiens

<400> 189
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<212> DNA
<213> Homo sapiens

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cgaacctggg gatcgggtaa agataccagt gatgtggagc caactgcacc gatggaggaa 240
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<213> Homo sapiens

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ttctaaaata ggactttcat attattaaaa cctcaaaaga tgatccaccc aggatgaaca 240
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<213> Homo sapiens

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ggctgaagga gaagggagcc gcccatccat ggacttattc agggccatct ttgccagttc 240
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ggtttttcttg tagcattttt ctagttctga gattgctact acccaaagta ttcatttctt 240
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ctttgactac atagactaaa atattccatg gtggtgaagg atgtacaagc ttgtgaatat 240
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<210> 201
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<212> DNA
<213> Homo sapiens

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ttcaggcttg ccctcaccag cggccgtcag ccgacactca gggatgtagc taacaccact     180
ccgccagtgc tttcagtagg aagagctgag gctgcctggg aggcccgggg cgaccggaaa     240
agggctctct caagttctga aaagagaatc tgccaccaga tcgaatttcg acccctgagc     300

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ctccagccct tgctccactc atgcctgggg gcctggggct gagtggtatc cctacctggc     240
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      <212> DNA
      <213> Homo sapiens

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gagccagaga gttgggatgg gggcaggctg ggggcattgg gaagagcgag gagcagggaa     180
gaggagaatg agcatcatgg gccttcaatg cccgctctga tagcccctga ggactctcct     240
cactgtgacc tgtttcagga gcctcatat                                       269

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      <212> DNA
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<212> DNA
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actgtgaact cttcgaatgt aggactccta gagctagata ctcaattatt ttttattaaa 180
ttgaatgact tgaaactaca gatcctttat ttaaacttcc caaatttctg ctttatctag 240
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tacacctcct gccaggcctg tgggaacagg gctggtgcga gatcacggcc cacctcctgg 240
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<210> 209
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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<211> 300
<212> DNA
<213> Homo sapiens

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<210> 212
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<212> DNA
<213> Homo sapiens

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<210> 213
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<212> DNA
<213> Homo sapiens

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<211> 300
<212> DNA

<213> Homo sapiens

<400> 214
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 218
<211> 300
<212> DNA
<213> Homo sapiens

<400> 218

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<212> DNA
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<212> DNA
<213> Homo sapiens

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<210> 221
<211> 300
<212> DNA
<213> Homo sapiens

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<210> 222
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<212> DNA
<213> Homo sapiens

<400> 222
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<210> 223
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 225
<211> 300
<212> DNA
<213> Homo sapiens

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<210> 226
<211> 300
<212> DNA
<213> Homo sapiens

<400> 226
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<210> 227
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<212> DNA
<213> Homo sapiens

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<210> 228
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<212> DNA
<213> Homo sapiens

<400> 228
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<212> DNA
<213> Homo sapiens

<400> 229
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<210> 230
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<213> Homo sapiens

<400> 230
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ttgagatatt aaaaaaaaaa agaaaaggaa aaaagtaaat gannnnnnnn nnnnnaaccc 240
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<212> DNA

<213> Homo sapiens

<400> 231
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ctgaaggaat ctctttcttc gggacctttt gttaaactcg gttnaagctg taaaccttat 240
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<213> Homo sapiens

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<212> DNA
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<213> Homo sapiens

<400> 234
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gctcttggtt ttttgctcac ttttatatgt aaggtattag tacaaaccta aaggagagaa 240
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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 236
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<212> DNA
<213> Homo sapiens

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gacatatcgg accaggaggc cctggacgtc ttcctgaact ctggaggaga agagaacact 180
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<212> DNA
<213> Homo sapiens

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<210> 239
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<212> DNA
<213> Homo sapiens

<400> 239
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gcggccaagg cctgcccctg gaggcactag aggagggcat ctgtctgtgg gagcccagag 180

gctgcaggga ggaggaggag ggaggtatct ggtgtgagcg ttgcccctgc gacatttggg 240
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<210> 240
<211> 274
<212> DNA
<213> Homo sapiens

<400> 240
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aaatgttttt aatatacatt cttattttgt cccacccctc cagaaataag ctggaaatct 120
taactttttg gggggtcttt tttggtgttt taatgggccc agaactgtgg tttaaatttt 180
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tactcctcag gttgatgtat tcatgaaagt ttta 274

<210> 241
<211> 300
<212> DNA
<213> Homo sapiens

<400> 241
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<211> 300
<212> DNA
<213> Homo sapiens

<400> 242
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<211> 300
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<213> Homo sapiens

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gcctttaaaa ccccagaggt catcagattg tttgcaaaga aacaaccagg tcagcttcgg 240
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<210> 244
<211> 300
<212> DNA
<213> Homo sapiens

<400> 244
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gattttggat gcatctatgc cttgagaaat gaatggtttg atgtaaatgc atggtagcaa 120
gaataaataa ttatgttaat tcatataata tgttatatat agttttaaag aaaattctat 180
cactgtcttc ctatgggtag ggctataatg tccagttctt tcagggatta agagggtagg 240
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<210> 245
<211> 300
<212> DNA
<213> Homo sapiens

<400> 245
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agcatttaca ttccttgcca gggagtttga aatttatact atagaaataa ctttaggttt 180
taggtagagt taaagaggta aagcacatgt tgccacaacc caggaaagta tttttaagaa 240
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<210> 246
<211> 300
<212> DNA
<213> Homo sapiens

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tatatttact gctccaatat ccgttatttt ccaaaggatt ttgtatcttt ttgaaaatgt 240
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<210> 247
<211> 300
<212> DNA
<213> Homo sapiens

<400> 247
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attgaagaaa acaagctcaa actagtccaa caagaaatga tgtttcagag actccagaaa 180
gagagagaaa gtgaagaaag caaattagaa accagtaaag tgacactgaa ggagcaacag 240
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<210> 248
<211> 300
<212> DNA

<213> Homo sapiens

<400> 248
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<210> 249
<211> 300
<212> DNA
<213> Homo sapiens

<400> 249
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<212> DNA
<213> Homo sapiens

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<210> 251
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<212> DNA
<213> Homo sapiens

<400> 251
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<213> Homo sapiens

<400> 252

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<212> DNA
<213> Homo sapiens

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tcaacacttg acagaaagat acatattttt tttatacaaa ctacatatat ttgagcaatc 180
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<212> DNA
<213> Homo sapiens

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<211> 300
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<213> Homo sapiens

<400> 256
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gttccttaaa caagcttcca gccagaagcc tgcctggaaa gatgggtcca ctgccacgtg 240
tgttctggct gtagacaaca ttctttatat tgccaacctc ggagatagtc gggcaatctt 300

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<212> DNA
<213> Homo sapiens

<400> 257
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<211> 285
<212> DNA
<213> Homo sapiens

<400> 258
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<210> 259
<211> 300
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 261
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<210> 262
<211> 300
<212> DNA
<213> Homo sapiens

<400> 262
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<210> 263
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<213> Homo sapiens

<400> 263
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<210> 264
<211> 300
<212> DNA
<213> Homo sapiens

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tactcagtaa cttgaatatt gtttaatgtg ttgtaagacg tagagtttat ctcaagctgt 240
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<210> 265
<211> 300
<212> DNA

<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 266
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<212> DNA
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<400> 267
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<210> 268
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<212> DNA
<213> Homo sapiens

<400> 268
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tttcattttc tacaaacttg aaattagcct gctaattgta aagttgtttt aataatgctg 240
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<210> 269
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<212> DNA
<213> Homo sapiens

<400> 269

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attaaaaaaa agaagtaacc tatgtagatc caaacttaaa atgtgagaaa ttattgaaat 180
ttcattttct acaaacttga aattagcctg ctaattgtaa agttgtttta ataatgctga 240
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<210> 270
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<212> DNA
<213> Homo sapiens

<400> 270
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attaaaaaaa agaagtaacc tatgtagatc caaacttaaa atgtgagaaa ttattgaaat 180
ttcattttct acaaacttga aattagcctg ctaattgtaa agttgtttta ataatgctga 240
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<210> 271
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<212> DNA
<213> Homo sapiens

<400> 271
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gaattgtatt tggaagaaga actggggagc ccacctctgg tatttttttt atgtccctca 180
tatggacaaa taaacctctg gtattaaatg aattttcttt tgggggattc tatatattcg 240
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<210> 272
<211> 300
<212> DNA
<213> Homo sapiens

<400> 272
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tatcaagggt ccaccatgtg ccagccactg aagtagatat aaatacaagg atgtgtaagg 120
tatggatgat ggtatacgaa ctgtcatctt actggatttg tccgctctgt taaagatacg 180
gttccgaaaa ctttttaaag ccctagagag ggctttaagg caatgtagca tcatatatag 240
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<210> 273
<211> 300
<212> DNA
<213> Homo sapiens

<400> 273
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cgtctccgac tgaggagcaa agccctcggc tcaagatcct cacctacttc acagggattt 180

gaaatagtgc agtcaacagg aaaagaaaag cgctatagaa atgctcgacg ctatcacttg 240
gggcccacgt ggaagtatca acgtataaat tggcccaggc agacagaagg atgcagggga 300

<210> 274
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<212> DNA
<213> Homo sapiens

<400> 274
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<210> 275
<211> 300
<212> DNA
<213> Homo sapiens

<400> 275
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<210> 276
<211> 300
<212> DNA
<213> Homo sapiens

<400> 276
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tgcccagcca aagatcattt ttttatatag acttcagccc tttgtaaata ttgtaactgg 180
ggagtataga gtagaaaaaa agtatagtta aaacatttgt tctacaaatt aacctttaaa 240
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<210> 277
<211> 300
<212> DNA
<213> Homo sapiens

<400> 277
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tgaatttttc acaagtttcc cagtggtgct gatacttctg gtccaggaac ttagtgggag 180
agaacgacta atctagacca tttcacttca cattctgagc ttcttgtaca ctgtcacact 240
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<210> 278
<211> 300
<212> DNA
<213> Homo sapiens

<400> 278
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actggtatca agaatcagtc agcaaggagg ccctcaccag acgccagtgc catgttcttg 180
gacttctcag cctccatatt catgaactaa gtttttggaa tccttaggct tccacgtgtg 240
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<210> 279
<211> 300
<212> DNA
<213> Homo sapiens

<400> 279
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gatattatat attaaatggg cagataatag aaatctgtcc aagcaaaact ctggataatt 120
tttatgttgc cttatttttt gttttctgtg aactccaaga aaaatgagat accagtttgg 180
aacagatgta atattgctga tttaacagtt tagggatact ccccaagttc aataattttg 240
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<210> 280
<211> 300
<212> DNA
<213> Homo sapiens

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tcaggcactg gaactatctg taatactgga acctctgcga agtgccaggt ataaagtttt 120
tcccactgcc aagcatccag agctttggga aatttggaaa tcagagagat cagggcattg 180
ttttgttcct ctgatgatga aagtgaaaag caagtactac tgaagtctgg aaatataaaa 240
gctgtgcttg gcctgacaaa gaggaggcta gttagtagca gtgggaccct ttctgatcaa 300

<210> 281
<211> 300
<212> DNA
<213> Homo sapiens

<400> 281
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gcatgagcca ctacccttgg ctgtgatcaa gtatttagtc tgttgttaaa tgtttactaa 180
atagtctgaa gtagagaaaa tagcacccaa tctaaaataa ggtgaggtct agtcacttat 240
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<210> 282
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<212> DNA

<213> Homo sapiens

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atcatgttgg ccaggctggt ctcaaactcc tgatctcaag taatctgccc actttggcct 180
cccaaagtgc tggcattaca ggaatggagc caccgcgccc agcctgattt cttttttag 240
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<210> 283
<211> 300
<212> DNA
<213> Homo sapiens

<400> 283
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gcaacagagt gagaccctgt cttaaaaaaa gaagggagaa agtgtcagat ggtgatgagg 180
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<212> DNA
<213> Homo sapiens

<400> 284
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aaaggagaca gttgatagcc aaacaacagt tttggattca ctgactgatt atgaaagaag 180
cagtagactg gtatcaagaa tcagtcaggt ttttggaatc cttaggcttc cacgtgtgga 240
aagcctgagc taacctactg gaggatgagc catcacctgg agcagattca ggccatccta 300

<210> 285
<211> 300
<212> DNA
<213> Homo sapiens

<400> 285
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tttatattta tgtcttttat gtacaacagg attataagta gcttgagtcc agtgaatata 180
ccatttcatt ttgctatcct tcactgcact tagcttagag gaaataatca cagcttatta 240
ttgattaatt aattaattaa tagatgaatg gtgaacacat gactatcatc ccaagaaatg 300

<210> 286
<211> 300
<212> DNA
<213> Homo sapiens

<400> 286

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gcgcaagtgg gatggtgacc actatgatgc cctgagggac tgcctcaagg ccatctccct 180
aaacccatgc cacctgaagg cacactttcg cctggcccgc tgcctctttg agctcaagta 240
tgtggctgaa gccctggagt gcctggacga cttcaaaggg aaatttccgg agcaggccca 300

<210> 287
<211> 300
<212> DNA
<213> Homo sapiens

<400> 287
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gaacaaaaat tttgtgatgg aaggattcta gttaatgagt attgcatcaa gatttacatc 120
tttcttacta aggaaaagag ttaataaaaa ttgttcttta ttttacaggc agttactgag 180
gctcttccca gatctcagta aacagccact cagccttgaa aatggagtgt tgttgtttct 240
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<210> 288
<211> 300
<212> DNA
<213> Homo sapiens

<400> 288
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gattgcaaca tgactatcaa ttcttccctt cccatcaaag gagagagtcc gtttatccag 180
cctttgaatc ttgattattc aagtgacttg cttcacccaa tgtaacatta ataagcacaa 240
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<210> 289
<211> 300
<212> DNA
<213> Homo sapiens

<400> 289
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cctttaattt tatttctaga gtgacaaatt tttggttttg acagtttttt tctagcttta 120
tagtttcttc ttggggagag aatatgtcaa cctcactcca tcatgctgaa gtaaatcttc 180
atctcttaat tttatctctc aaaaatatcc taaggattcc ctctggagcc tgataagtaa 240
ttgcagtatc tggtttctat ggttggatga ttcaggattc caggaataat agttactttt 300

<210> 290
<211> 300
<212> DNA
<213> Homo sapiens

<400> 290
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caaataatgt gatttcctgg ctattttgtt gggggcttaa gatttttttt tttcaaatgc 180

atttttagtc actaaaaatt aactgtcgta ccatctagaa ctatactgtc cagtaccata 240
gcctctagcc gtatgtagct atttgtatta agattaatgg aaattttaaa tccagttcct 300

<210> 291
<211> 300
<212> DNA
<213> Homo sapiens

<400> 291
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gaaatttata cttgaaatta aaagtctaca agggggagga ccttaaagct aagctaccag 120
taagacaatg aataattcag aagagaacac tattctttta ctgactgagt gcccaagatg 180
ccaatttcca tgaagtcttg atttatatat atgtacacat gttatgcaca tacatgtttg 240
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<210> 292
<211> 278
<212> DNA
<213> Homo sapiens

<400> 292
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atccaggtgt ttctgatgca cagtgaaatt ggggtaccac tggtattagg tttggtatgg 120
caactttttc atcacttgtt ttatgtagtt gtctgatcaa ttgtgaaaac ataatgaatg 180
ttggaaatgg aacagtaaaa taacgaaagc caactttttt ttttttttn nnnnnnnnnn 240
nntgntttnn cccccaggnt gnanngcagg gncccaat 278

<210> 293
<211> 297
<212> DNA
<213> Homo sapiens

<400> 293
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cagctcctct gccaagcccc ctcagcgcga agtcctcgtc cagagaaggc aacggcgaga 120
aacaaatcca acatcctggg ctgcttttc cttcccccac tttttaaaag tttggtgtcc 180
aagtcacttg acaaacccag accctaacaa tgatattttg tgtagaattc tgggatcaaa 240
atataatttc aaaaataata tattttctga catcccccaa aaaaaaaaaa aaaaaaa 297

<210> 294
<211> 300
<212> DNA
<213> Homo sapiens

<400> 294
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tagaactaat aggatttctt attggaacgt agggtgtaag agaaaagagg agtcaaaaag 120
agccacaaga tttttggtct cagcaattag aaggatagaa ttgacattta ctgagatttt 180
tgtttttgtt tttgagacgg agtttcgcta ttgttgccca agctggcgtg caatggcgtg 240
atctcggctc agtgcaacct ccacctccca gattcaagcg attctcctgc ctcagcctcc 300

<210> 295
<211> 299
<212> DNA
<213> Homo sapiens

<400> 295
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actgtcacag aatggctggg ctgagaacgc tgcccagggc cctgcagctg gcgggagnnn 120
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gctacnnctt nnatcccctt gtnaatatgt tgagntnnct tngcnttcnn gntnntccng 240
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<210> 296
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<212> DNA
<213> Homo sapiens

<400> 296
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tggtcatact cataaatagc actaaagtgt tataacattt tcatttacct atttttagtt 240
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<210> 297
<211> 300
<212> DNA
<213> Homo sapiens

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<210> 298
<211> 300
<212> DNA
<213> Homo sapiens

<400> 298
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<210> 299
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<213> Homo sapiens

<400> 299

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tcaaagccag caagacttct ctgctgctgt gatctgcaca ccctccaacc tgggcaggga     180
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<210> 301
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aagcaatggg atgtgtgtgc atgtgtttgt gcagagacag aaagagagat tttaaggaac     240
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<210> 302
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acgagatctg atgggtttat caggggtttc cacttttgtt tcttcatttt ctcttgccac     240
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<400> 303

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<213> Homo sapiens

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<210> 305
<211> 300
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<400> 305
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<210> 306
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<212> DNA
<213> Homo sapiens

<400> 306
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ggaggaggac ccggaagaag ataggaaatc cacaaaagaa gaagggagtg aggtgccgaa 240
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<210> 307
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<212> DNA
<213> Homo sapiens

<400> 307
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tcaggtgttg ggaaatgggg accccgtctt ctggacacca gtagtccctg gtcccatgga 180

accagatggc aaggatgagg aggaggagga ggaggannnn nnnnnnnnna ntggccttnt 240
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<210> 308
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<212> DNA
<213> Homo sapiens

<400> 308
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acatgtaaag tgcttagaat agattggtac tgttaaatat gagctaacgt cacatttgat 180
attttttaa aaagaaaaaa tcattatgga gtctcagtcc tagagattct gattcattaa 240
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<210> 309
<211> 300
<212> DNA
<213> Homo sapiens

<400> 309
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tacagctcaa caacgcccct ctgaaagtag gactcttgga aatgaacctt gttgggagta 180
aagctgaacc ttcacctctc ctttccagga ttctactcca ttcatacggc ctcacactga 240
attaatggtt ctagcagcca catcactttg ttacccaatt gatctagtag taaagtcttc 300

<210> 310
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<212> DNA
<213> Homo sapiens

<400> 310
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tatcatgaga gcagctcagg aaacacccac tcccgtgatt cagttacatc ccactgggtc 180
tgtcccacaa attgtgggag ctacaattca agatgaggtt tgggtgggga cacagccaaa 240
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<210> 311
<211> 300
<212> DNA
<213> Homo sapiens

<400> 311
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ctcttatgat atctacatac catctcatat tcagggcaat atcactcctc atgctattgt 180
catcttgcct aaaacagatg gaatggaaat gcntgtttgc tatgaggatg angggtgna 240
tgtaaacacc tatggccgga taacnaagga tgtggtgctc caatggggag aaatgcccac 300

<210> 312
<211> 275
<212> DNA
<213> Homo sapiens

<400> 312
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tntnnatttn ttcctntttt ttttnnnttn aaatatnntg nnntttttn ntantantta 180
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natntttttt ttgttcttct nttntattnn atctt 275

<210> 313
<211> 300
<212> DNA
<213> Homo sapiens

<400> 313
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aagaggaaca cactggcaga agaacacatc gaaagacgct ggcaggccat tgatggtgga 180
acgattcgga cgccaaggga aattcggcca aggacagtag gagatcccgg ctgctgagca 240
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<210> 314
<211> 300
<212> DNA
<213> Homo sapiens

<400> 314
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agcccttatc aggaacagac ttggctagca ccttcatcgt ggacctccag cctccagaat 180
tgcaagaaaa tacatttccg tcgttgaaac cacccagtct gtggtatttt gttatggcag 240
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<210> 315
<211> 300
<212> DNA
<213> Homo sapiens

<400> 315
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gacggccggg tagtgggctt ccacacagca tgggagccca gcaggccctt ccctgtggat 120
atggctggat ttgccgtggc cctgcccttg ctgttagata agcccaatgc ccaatttgat 180
tccaccgctc cccgggggcca cctggagagc agtcttctga gccaccttgt ggatcccaag 240
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<210> 316
<211> 300
<212> DNA

<213> Homo sapiens

<400> 316
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aggggaatca tgattataag tccttcagcc cttggactct aaattgaggg gattaaaaag 180
aatttaaaat aattttgaac gaatttattt tcccctcagt ttttgagggc attaaaaagg 240
cattaaatca agacaaatca tgtgcttgag aaaaataaaa ttaatgaaaa cacagcactt 300

<210> 317
<211> 295
<212> DNA
<213> Homo sapiens

<400> 317
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caggtgtgtg ccatcacacc tggctttaca tttttctgtg gggacttact atgttgccca 180
ggccggcctc aaactcctga gctcaagtga tcctctgcct cagcctccag agtatctggg 240
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<210> 318
<211> 261
<212> DNA
<213> Homo sapiens

<400> 318
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ggaaaggtgg aaaaggttta taagaatggg tgccgtgtta tactgtttcc caatggaact 120
cgaaaggaag tgagtgcaga tgggaagacc atcactgtca ctttctttaa tggtgacgtg 180
aagcaggtca tgccgaccca agaannnnnn nnnnnnnnnn nnntngccnn aacnnttcac 240
caaatncccc ggggggggctt g 261

<210> 319
<211> 300
<212> DNA
<213> Homo sapiens

<400> 319
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tgagatatgg cctcatggga agggaaagac ctgactgtcc cccagcccga cacctgtaaa 120
gggtcggtgc tgaggaggaa tagtgaagga gggaggcctc tttgcagttg agataagagg 180
aaggcttctg tctcctgctt gtccctggta atggaatgtc tcggtgtaaa gctgaccatt 240
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<210> 320
<211> 289
<212> DNA
<213> Homo sapiens

<400> 320

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tcaggacaca ttttgagtgg tattttcttt tcttttttc ttcttttttt ttttnnnnnn 180
nnnnnntngt tntgtnnccc aggctgnann gcaggggcct gatntnggnt aantgnaacc 240
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<210> 321
<211> 300
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<213> Homo sapiens

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aagagaacgc accagagaga gagagaggga gcgtgatcac agtcctacac caagtgtttt 120
caacagcgat gaagaacgat acagatacag ggaatatgca gaaagaggtt atgagcgtca 180
cagagcaagt cgagaaaaag aagaacgaca tagagaaaga cgacacaggg agaaagagga 240
aaccagacat aagtcttctc gaagtaatag tagacgtcgc catgaaagtg aagaaggaga 300

<210> 322
<211> 300
<212> DNA
<213> Homo sapiens

<400> 322
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gcccctcgcc ttcctcaacc cacctggcaa gtcttcttag gatctgatcc cagttttctg 180
gaagcaatcc taccccagcc caagcttccc aagagtcgag ccttaatcct tctcacttct 240
cagtgtcaga gcagaaatga atcctggggt tgactgtgtc cattcgggtt attagcagct 300

<210> 323
<211> 300
<212> DNA
<213> Homo sapiens

<400> 323
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tgtacctcca aagagaacag ttaaaagaaa tatacccaag ctggatgctc agagattaat 180
ttcagagaga ggacttccag ccttaaggca tgtatttgat aaggcaaaat tcaaaggtaa 240
aggtcatgag gctgaagact tgaagatgct aatcagacac atggagcact gggcacatag 300

<210> 324
<211> 300
<212> DNA
<213> Homo sapiens

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ataagaactc cagaccccaa actcagctca tacacacacg gaagagagaa gcatctgaac 180

atcaagaaga gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggctga 240
gctccagggg aagactgcct gcacattcta tccccttttc agttccccat cctgctgtca 300

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<211> 283
<212> DNA
<213> Homo sapiens

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aaaatgtatt ggaatggaac tatccaagat cacgatgcca gttatattta atgagcctct 180
gagcttccta cagcgcctaa ctgaatacat ggagcatact tacctcgtcc acaaggccag 240
ttcactctct gatcctgtgg aaaggatgcn ngtgtgtagc tgc 283

<210> 326
<211> 300
<212> DNA
<213> Homo sapiens

<400> 326
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tactcacatg cctggcatct tgacagggac agctggaagg caaggttcag ctgggactgt 240
ccacagagct cctccctgtg gcctttccag catggtggtc tcagggtagc tggacttcct 300

<210> 327
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<212> DNA
<213> Homo sapiens

<400> 327
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ttctgtggat ttccaactca agattgcagc atcaactcac acctgaagtt ctggcttccc 240
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<210> 328
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<212> DNA
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<400> 328
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gactgggctg gccgcctgcc gcttcttgag ggtggaagag gggtgctctg agaagacact 240
caggcagcag actctgcctc tcacttaagg tgcccccccg accccgctcc accatagtca 300

<210> 329
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<212> DNA
<213> Homo sapiens

<400> 329
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ggtattttta aaatttcaat ttctaattgt tcattataga aacacaattg ggttttatat 120
attggcattg tattttgcaa ctttcctaaa ctcactagta attctagtag cttttttttgg 180
tagattctta aggattttct gtgtaaatag tcatgtcatt tgtgaataaa gccatttttt 240
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<210> 330
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<212> DNA
<213> Homo sapiens

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cagaccccaa actcagctca tacacacacg gaagagagaa gcatctgaac atcaagaaga 180
gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggctga gctccagggg 240
aagactgcct gcacattcta tccccttttc agttccccat cctgctgtca gccacattta 300

<210> 331
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<212> DNA
<213> Homo sapiens

<400> 331
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gtacctttcc ttgaacttat tcgtgataca gattcctttg ctcacatgtt tccctgctga 180
ccttcttccc acctgttgcc ctgctacact cccctcgcta agacagtaaa aataatgatc 240
aataaatact gagggaactc agaggccagc gccggtgcgg gtcccccccca tgctgagcgc 300

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<213> Homo sapiens

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ggttgtcaag gttgtcccca gaccttgctt gcagtggttg gagaacccag gggcctgcct 180
tgggccctct ggccagaggg aagcgggcag ctctagccct ggagattgtg gtcacattgg 240
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<213> Homo sapiens

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gatcaagtag cggaggccag gattttggcc acctcccggg caagttgcag ggcagtggcg 180
ccgggagcaa aagcagcatg atgcagctca tgcacctgga gtccttttat gaaaaaacct 240
cctcctgggc ttatcaagga agatgacact aagccagaag actgcatacc agatgtacca 300

<210> 334
<211> 262
<212> DNA
<213> Homo sapiens

<400> 334
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cagaaaaaaa ccttgttgac ccctgcttta gagaatgaga agccatgcag ggatcagtga 180
tgccagagga agggaaggaa ctgcttccag ctattgtgac aataataata ataataatat 240
tgggtctttg actagaacgt gt 262

<210> 335
<211> 300
<212> DNA
<213> Homo sapiens

<400> 335
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<210> 336
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<212> DNA
<213> Homo sapiens

<400> 336
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atcctcaagc tggaagatac ctctctggcc ccggcacatg tcacccctgc actcctgcct 180
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<213> Homo sapiens

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<210> 338
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<212> DNA
<213> Homo sapiens

<400> 338
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<210> 340
<211> 300
<212> DNA
<213> Homo sapiens

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ttattttgta gagatggggt ctcactatgt tgcccaggct agtcttgaac tcctggcctc 180
aagcaatcct cccacctcgg cctcccaaag tgctgggatt aaaggcgtga gccaccgtac 240
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<210> 341
<211> 296
<212> DNA
<213> Homo sapiens

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ttggaaatgg aacagtaaaa taacgaaagc caactttttt tttttttttt ttnnnnnnnn 180

nnnnnnnnnt tnncccccng ncngnanngc aggggcccaa nntnggntnn ntgnanccnc 240
cnccnccggg ntnnncccct ttntcnngcc taacccnccc nagnacnngg aactac 296

<210> 342
<211> 300
<212> DNA
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agatagtaca taaacgtccc aaaattagaa gataaaaaga catgagggat ccattctaat 180
ttgtgtttgg agtgtaatgg tccagctcca ttcttctgca catggatatc cagttttaca 240
caacactgtg aatgtaatga atgccactga atcatacact caaaaatagc taaaatggca 300

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<213> Homo sapiens

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gccctgctct ggcgcgtcca aaatactacc tagcacaggc ctctgctcga ggcaccccca 180
aactacctat gtatccagcc ccagagggcc tccattccca ggaagtccct atgtatccca 240
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<210> 346
<211> 300
<212> DNA
<213> Homo sapiens

<400> 346
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tgtgaacagc cagccaccgg agaagcagca ggccatgcac ctgtgttttg agaacctgat 180
ggaaggcatc gagcgaaatc ttcttacgaa aaacagagac aggttcaccc agaacctgtc 240
agcattccgt cgagaagtca acgactcaat gaagaattcc acttatggcg tgaatagcaa 300

<210> 347
<211> 300
<212> DNA
<213> Homo sapiens

<400> 347
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tgtgagttct acttcagcct ggacgccgac gctgtcctca ccaacctgca gaccctgcgt 120
atcctcattg aggagaacag gaaggtgatc agaccccatg ctgtcccgcc acggcaagct 180
gtggtccaac ttctggggcg ccctgagccc cgatgagtac tacgcccgct ccgaggacta 240
cgtggagctg gtgcagcgga agcgagtggg tgtgtggaat gtaccataca tctcccaggc 300

<210> 348
<211> 300
<212> DNA
<213> Homo sapiens

<400> 348
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attggtgctg tcatcttcct gggaatgctt gagaaagctg tcttctatgc ggaatttcag 120
aatatccgat acaaaggaga atctgtccag ggtgctttga tccttgcaga gctgctttca 180
gcagtgaaac gctcactggc tcgaaccctg gtcatcatag tcagtctggg atatggcatc 240
gtcaagccac gccttggagt cactcttcat aaggttgtag tagcaggagc cctctatctt 300

<210> 349
<211> 300
<212> DNA
<213> Homo sapiens

<400> 349
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gcacttcaaa gatcatgaag agcaagataa agtcagacct aaagccaaaa ggaaagaaga 120
accaagctct atttttcaga gacaacgtgt ggatgcttta cttttagacc tcagacaaaa 180
atttccaccc aaatttgtgc agctaaagcc tggagaaaag cctgttccag tggatcaaac 240
aaagaaagag gcagaaccta taccagaaac tgtaaaacct gaggagaagg agaccacaaa 300

<210> 350
<211> 270
<212> DNA

<213> Homo sapiens

<400> 350
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gcaatanggn gggcttcctg tccccaggnc caccccacag tgctntntgg cactggnaac 120
tctgctangg agngantgna nnnnaccant aannnnnnan nnatcnacan nnnnnnnncn 180
nnnnnncntn tnnccnannn ntannctncc ntannnnanc cnnccannan cactcncnat 240
naacgnnnnn ttantgagan nttctcaact 270

<210> 351
<211> 300
<212> DNA
<213> Homo sapiens

<400> 351
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atctatgcac tctatcagcc agaatttggc atttagctct tagttaaatc tagtaaagga 120
cagtctattg tttaaagaga aggtgcattt gttcctcaat caagcaagag cacctgtgtt 180
gtactgcttt atatctcatg tatatttata gtaatgaaaa gacttttttaa attgtacacg 240
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<210> 352
<211> 300
<212> DNA
<213> Homo sapiens

<400> 352
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atattttccc cacaaaagaa acacttaaca gaggcaagtg caatttataa atttatatct 120
aaaggggaat catgattata agtccttcag cccttggact ctaaattgag gggattaaaa 180
agaatttaaa ataatttga acgaatttat tttcccctca gtttttgagg gcattaaaaa 240
ggcattaaat caagacaaat catgtgcttg agaaaaataa aattaatgaa aacacagcac 300

<210> 353
<211> 300
<212> DNA
<213> Homo sapiens

<400> 353
cccacactcg gacactgtgg aattctacca gcgcctgtcg accgagacac tcttcttcat 60
cttctactat ctggagggca ctaaggcaca gtatctggca gccaaggccc taaagaagca 120
gtcatggcga ttccacacca agtacatgat gtggttccag aggcacgagg agcccaagac 180
catcactgac gagtttgagc agggcaccta catctacttt gactacgaga agtggggcca 240
gcggaagaag gaaggcttca cctttgagta ccgctacctg gaggaccggg acctccagtg 300

<210> 354
<211> 299
<212> DNA
<213> Homo sapiens

<400> 354

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atttcagagt ccaggcccta ggttgggacc cactccaaat aatctcctcg gtgtgggtgg 120
tggttctata gagggataaa tgaataataa acattgttaa aatatacgaa aaaaaaaaaa 180
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 240
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaacnncn ncnananaaa aaaaaaaaa 299

<210> 355
<211> 300
<212> DNA
<213> Homo sapiens

<400> 355
actgttcatc ctaagttcca ctataaacag gctcatgact cgggcacaga cacttcttgc 60
gtgacttttt cctatgatgg taatgtcctt gcctctcgtg gaggtgacga ttcattaaaa 120
ttatggacaa tccgacaatt taataaacca cttttttcag cctcgggtct tcccaccatg 180
ttcccaatga ctgactgctg tttcagtcca gatgataagc tcatagtcac tggtacatct 240
attcaaagag gatgtggcag cggcaaactt gttttctttg agcgtaggac tttccaaagg 300

<210> 356
<211> 300
<212> DNA
<213> Homo sapiens

<400> 356
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agcaagacaa gatggtggat ccccatgcca ttacctgcta gactcagggt ttatatactg 120
tagtggagag gtgattccga aggaatgttg taagacaatt gaagagcagt aacatcaaag 180
ttatttgacc taagggcagg agttacagta agtatccact tttatacaag aaacaataga 240
taaactggaa atcttggagc ccttcctgga actggggtta atgagaagtc aacatggtgg 300

<210> 357
<211> 300
<212> DNA
<213> Homo sapiens

<400> 357
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tattttgggg agtaaagtca attgggcaga ggatcctgcc cttaaggaaa ttgttctgca 120
gcttgagaag aatgttgaca tgatgtaata agaattcatt tctgacatat tttacatttc 180
tggcaatctc aactcttatt tggaatactt ctgtgcattt gtctgtccac cgtaatttta 240
gaaaagcata tccataacgt ttacagttgt agtacagttg tggttagtta tttgtagtgg 300

<210> 358
<211> 300
<212> DNA
<213> Homo sapiens

<400> 358
ggtgattaca gaagcccaga aggttgatac cagagccaag aacgctgggg ttacaatcca 60
agacacactc aacacattag acggcctcct gcatctgatg gaccctgcac ttgatggacc 120
agctggcacc acccagatca ataaactggc ttatttgaat ttgcggcccc ccacccagga 180

actgactcag tgcaagaaga cagcttcgac tccctgtgat ttcatctctg accaatccgc 240
actcctggct cactggcttc cccaacccat gaagttttcc ttaaaaactc tgctcccgaa 300

<210> 359
<211> 300
<212> DNA
<213> Homo sapiens

<400> 359
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aaagggtcag ttatgtgacc taaatgcaga actaaaacgg tgccgtgaga ggactcaaac 120
gttggaccaa gagaaccagc agcttcagga ccagctcaga gatgcccagc agcaggtcaa 180
ggccctgggg acagagcgca caacactgga ggggcattta gccaaggtac aggcccaggc 240
tgagcagggc caacaggagc tgaagaactt gcgtgcttgn gtcctggagc tggaagagcg 300

<210> 360
<211> 300
<212> DNA
<213> Homo sapiens

<400> 360
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tgagtggtaa attccaattc tgcagcagat cagtaaactc acagtatttt tcctgtggaa 120
atctattcaa taaggaaacc aagacaggat aataaaattt aaaaaaaaac aactttgaat 180
tcccctgcct aggtcttcca gttgttttcc agcgcatacc tcaggtatga ctttgctagc 240
cggggacaaa attagcacct tccgattctc tagtccaaat gaactttgtg ctaaataaaa 300

<210> 361
<211> 300
<212> DNA
<213> Homo sapiens

<400> 361
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tctagtattg aagaactgga acttgaaagt cctccttcta ccaactccac ctccaccccc 120
tcattcccct tctcccaaag tactactgct gttgcatgac aaccccaaat atgttctgtc 180
aacacaaacc tgcctttggt gtataaacag ggcattacag aatggtacac cctatatatt 240
tctgttcagt atccattcac tagttcttca tttataaata tcatcttccc cattctgctg 300

<210> 362
<211> 300
<212> DNA
<213> Homo sapiens

<400> 362
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aaacgggcct ggacgcctcg cccctggccg cagatacctc ctactaccag ggggtgtact 120
cccggcccat tatgaactcc tcttaagaag acgacggctt caggcccggc taactctggc 180
accccggatc gaggacaagt gagagagcaa gtgggggtcg agactttggg gagacggtgt 240
tgcagagacg caagggagaa gaaatccata acaccccac cccaacaccc ccaagacagc 300

<210> 363
<211> 271
<212> DNA
<213> Homo sapiens

<400> 363
ggcaattagc ctcgcttaag ttgccttttt tacacaccaa aactttttac atgaagggct 60
ggtttcacat gaatactata ctgaaatctg tgctctcaag atctagcagt gaccagggct 120
gccccggcggg ggctctcctg gcaagtcagg aaggtnnnnn nnnnnnnnnn nnnnnnnnnn 180
canattantn nctgatcntc tntnangaan nnngantngc tctnttggnc nttgtnnnnn 240
gncntnnnnt naantntttn ntnatgtngc t 271

<210> 364
<211> 300
<212> DNA
<213> Homo sapiens

<400> 364
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tcagggattc tcccgccgct gcttcctgag tagctgggac ctcaggcttc cgcctcgtgc 120
ccgcatccct gctgtgttta ggcagcaggt ggtgacctca ctcctccctg gcctgagctc 180
tccgtcccgc atcccaggcg gaggccctag ggaacacttt gaagctgagc acggggtgga 240
ccctccctcc tgagtgaatg gagaatagaa agggagagga tttctgttct gttctgtggg 300

<210> 365
<211> 300
<212> DNA
<213> Homo sapiens

<400> 365
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aagccagagt tgtttatgct agtgcaactg gtgcttctga accacgcaac atggcctata 120
tgaaccgtct tggcatatgg ggtgagggta ctccatttag agaattcagt gattttattc 180
aagcagtaga acggagagga gttggtgcca tggaaatagt tgctatggat atgaagctta 240
gaggaatgta cattgctcga caactgagct ttactggagt gaccttcaaa attgaggaag 300

<210> 366
<211> 300
<212> DNA
<213> Homo sapiens

<400> 366
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gcctcctgcc tccggtccag gtgtactggg gtctgtgtgt tgtgtttctg cgtgttctcg 120
gcagaaagtg gcatgctgtc ccgcctgggt gatttgctct tttacactat tgctgaagga 180
caggaacgaa tccctatcca caagttcacc actgcactaa aggccactgg actgcagaca 240
tcagatcctc ggctccgaga ctgcatgagc gagatgcacc gcgtggtcca agagtccagt 300

<210> 367
<211> 300
<212> DNA

<213> Homo sapiens

<400> 367
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gaagtccatg tggggtcagt tctggtctgc tcaccagagg ttcttcaaat acttatgcat 120
agcatccaaa gttaaaaggg ttgtgcaact agctcgagag gaaatcaaga atggaaaatg 180
tgttgtaatt ggtctgcagt ctacaggaga agctagaaca ttagaagctt tggaagaggg 240
cgggggagaa ttgaatgatt ttgtttcaac tgccaaaggt gtgttgcagt cactcattga 300

<210> 368
<211> 300
<212> DNA
<213> Homo sapiens

<400> 368
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aggaaaaagg gcgggcgggc ggctgtcctc tcaccgtcct caccccgcga ggcccggccc 120
gctcctccgt cgtggatttc gcggcgatcc ccccggcagc tctttgcaaa gctgcttgaa 180
acttctccca aactcggcat ggatacgact gcggcggcgg cgctgcctgc ttttgtggcg 240
ctcttgctcc tctctccttg gcctctcctg ggatcggccc aaggccagtt ctccgcaggt 300

<210> 369
<211> 300
<212> DNA
<213> Homo sapiens

<400> 369
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cagagtgcat cattttcaga ctctactatt tccgtcaagt attctgtttg atttggatca 120
tctcaggatc ggattctgtt ttagagtgtt tctgggccag gatccgggcc cctgccctcc 180
tctgcacctg accacactcc ctactcaggg ctagtctgtt cttcccggac atcttctggt 240
agccgtgcag gagagggctg ggtggggcag aggccacaga ggggacctgg tgtgtcacct 300

<210> 370
<211> 273
<212> DNA
<213> Homo sapiens

<400> 370
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tggaggggaa gaagcccagg gtgatggcag gcaccttgaa gctggaggat aagcagcggc 120
tggcccagga tgaggagagt gaggcctagc gcctggccat tatgatgatg aagaagctnn 180
nnnnnnnnnn nnnnnnnnnc atcatgtccn ntgcatggct acctatccca tatttnatnt 240
ccctnncgtt gnttcnaatt ncacattntc ttt 273

<210> 371
<211> 300
<212> DNA
<213> Homo sapiens

<400> 371

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gttgtgggtt ctaacttaag ttccagacca gctagtccaa attcttcctc aggacaggct 120
tctgtaggaa accagactaa tactgcttgt agtcctgaag agtcatgtgt tttaaaaaaa 180
cctatcaaac gagtatataa aaaatttgat ccagttggag agattttaaa aatgcaggat 240
gagctcttaa agccaatttc cagaaaagta ccagaattgc ccttaatgaa tttagaaaat 300

<210> 372
<211> 300
<212> DNA
<213> Homo sapiens

<400> 372
gggccccaat gcagctgccc tctccagata cctggcagcc tcatatatca gccaaagcct 60
ggctcggcgg caggggcctg ggggaggggc ccccgcagcc tcccggggct cctggtcctc 120
tgctcccacg tcacgggcat cttcgccgcc cccccagccc cagccaccac ctcccgcagc 180
caggcggctc agctatgcca cgacggttaa catccacgtg ggcgggggtg ggcggctgcg 240
gccagccaag gcccaggtcc ggttgaacca ccctgctctc ttggcctcca cacaggaatc 300

<210> 373
<211> 300
<212> DNA
<213> Homo sapiens

<400> 373
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ctagggctgt gctatccaat acagtaacca catgcggctg tttaaagtta agccaattaa 120
aatcacataa gattaaaaat tccttcctca gttgcactaa ccacgtttct agaggcgtca 180
ctgtatgtag ttcatggcta ctgtactgac agcgagagca tgtccatctg ttggacagca 240
ctattctaga gaactaaact ggcttaacga gtcacagcct cagctgtgct gggacgaccc 300

<210> 374
<211> 300
<212> DNA
<213> Homo sapiens

<400> 374
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tggccatggg cccggtcacg aacaaaaacgg gcctggacgc ctcgcccctg gccgcagata 120
cctcctacta ccagggggtg tactcccggc ccattatgaa ctcctcttaa gaagacgacg 180
gcttcaggcc cggctaactc tggcaccccg gatcgaggac aagtgagaga gcaagtgggg 240
gtcgagactt tggggagacg gtgttgcaga gacgcaaggg agaagaaatc cataacaccc 300

<210> 375
<211> 300
<212> DNA
<213> Homo sapiens

<400> 375
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aattaagttg ccttcatcag tgtttgcttc agagtttgag gaagatgttg tgattgttaa 120
ataaagcagc tccagtttca ggacctcgac tggattttga tcctgacatt gttgcagctc 180

ttgatgatga ttttgacttt gatgatccag ataatctgct tgaggatgac tttattcttc 240
aggccaataa ggcaacagga gaggaagagg gaatggatat acagaaatct gagaatgaag 300

<210> 376
<211> 300
<212> DNA
<213> Homo sapiens

<400> 376
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ggggccagtt cagagaccca ctcccaggtg tgcattctct ttctcaagga tgttccttgc 120
tgagaaaaag aattcagtga tatttctccc atttgcttgt gaaagaagag aaatgtggct 180
ttgttccacc tggctcaccg gcggtcagaa tttaaggtta tctctcttgt ttcctaaaca 240
ttgctgttat cctgttcttt tttcaaggtg cccagatttc atattgctca aacacacatg 300

<210> 377
<211> 300
<212> DNA
<213> Homo sapiens

<400> 377
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cccacatcat acagtttgaa atgaaacttt gccacaacca gcctttgctg tagcacacac 120
atatatcact gaacctgttt gaaataaagt ttttttttctt tttcctctgg tattctgggt 180
tctgaagtct ggtattctgg tattctgggt tcaaaagtat gacttgagag tgttgctctg 240
gtattctgag agttgctctg tattctgggt tctgaagatt atttgaaaaa taactcctac 300

<210> 378
<211> 300
<212> DNA
<213> Homo sapiens

<400> 378
tcgctgtgat ccaaggataa aaaagttcaa ggaagaagaa aaagccaaga aagaagcaga 60
aaagaaagca aaagcagaag ctaaacggaa ggagcaagaa gctaaagaaa aacaaagaca 120
agctgaatta gaagctgctc ggttagctaa ggagaaagaa gaggaggaag tcagacagca 180
agcattgctg gcaaagaagg aaaaagatat ccagaaaaaa gccattaaga aggaaaggca 240
aaaacttcga aactcatgca agacctggaa tcatttttct gataatgagg cagagcgggt 300

<210> 379
<211> 300
<212> DNA
<213> Homo sapiens

<400> 379
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cgaggcagct tcgagccaat ggtgagctcc ttctggatca gctccttcag ctccttcttg 120
ctcaggatgc tgaaattgca aggctgatgg aagacttgga ccggaacaag gaccaggagg 180
tgaacttcca ggagtatgtc accttcctgg gggccttggc tttgatctac aatgaagccc 240
tcaagggctg aaaataaata gggaagatgg agacaccctc tgggggtcct ctctgagtca 300

<210> 380
<211> 296
<212> DNA
<213> Homo sapiens

<400> 380
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gtgtgtgtcc cctgtttact tttagctgag ctggggttgg gtgtacgggt tctgttcctc 120
tgagccctgc ggcccacctg atgtttacgt gtgtgtgtga gggggggcnn nnnnnnnnnn 180
nnnnnnnnnn ngtnatangc ttaacanatg nanagncnac tnactnctga ttntttatnc 240
atttgtgcat tnnaactatg cttttncgat cttnctgntg nnatnacngg catgat 296

<210> 381
<211> 300
<212> DNA
<213> Homo sapiens

<400> 381
cagaaaagag tatagtaggg atgaccaagg tcaaagtggg taaagaagac tcatcatcca 60
ctgagtttgt agaaaaacgg agagcagctc ttgaaaggta tcttcaaaga acagtaaaac 120
atccaacttt actacaggat cctgatttaa ggcagttctt ggaaagttca gagctgccta 180
gagcagttaa tacacaggct ctgagtggag caggaatatt gaggatggtg aacaaggctg 240
ccgacgctgt caacaaaatg acaatcaaga tgaatgaatc ggatgcatgg tttgaagaaa 300

<210> 382
<211> 300
<212> DNA
<213> Homo sapiens

<400> 382
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tttgcatgtt tcgggagagg tttgctgatt tggggcttat atgtcaggcc tttggtttgc 120
gtcttatttt aggggttgtt tgggggcctg ggtggtcggc ctcacatggg aaggggatgg 180
gtagtggatg ggtttctgt tgtatcttgt gggcgggtga ttttgctttt gtttttgttt 240
cacattcttc cccctccaca agccaaagtc gtttcatttg gtttccactg tgtggactgt 300

<210> 383
<211> 273
<212> DNA
<213> Homo sapiens

<400> 383
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tcggaatcgg cactgtcttg tcaacatgga aacatcgtgc tcttttgatt cttccatctg 120
tagtggagaa ggggatgata gtttaaggat aggtggnnnn nnnnnnnngc cngcnttnac 180
ttnatngcnn ctttttcttg atcnacgncn gnnatncnna nnngtntata ntaatncnga 240
ananttnttt gnnntgcttt atcaantntt cnt 273

<210> 384
<211> 259

<212> DNA
<213> Homo sapiens

<400> 384
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tgttggccca gaaggctgag gaaaaggaga accattgtcc cacaatgctc cggccccttt 120
cacatcgcac agtcacaggg gcaaagcccc tgaaaaaggc tgtggtgatg cccctacagc 180
taattcagga gcaggcagca tccccaaatg ccgagatcca catcctgaag aataaaggcc 240
cgaagagaaa gctggagtc 259

<210> 385
<211> 296
<212> DNA
<213> Homo sapiens

<400> 385
agagcctgca agtgacaaag gaagtgaggc agaggcccac atgcccccac cgttcacacc 60
ctacgtgcct cggattctga acggcttggc ctcggagagg acagcactgt ctccgcagca 120
gcagcagcag cagacctatg gtgccatcca caacatcagc gggactatcc ctggacagtg 180
cttggcgcat agcgccacgg gcagtgtggc ttgctgcccc ccaggaggcc tgaggctggg 240
tctcactgct ctgaaaaaga cccnnccaaa atgggccttg gggctnnagg cccttg 296

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

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gagatctcct ttgaccccga gaacctcatc acgggcatcg aggtgatcga cgaaggctgg 240
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<212> DNA
<213> Homo sapiens

<400> 387
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gccaccaaga ccagatcttc agcctggcct ggagtcctga tgggcagcag ctggccactg 240
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<210> 388
<211> 300
<212> DNA
<213> Homo sapiens

<400> 388
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aagagaaaaa agtgaccttt catttttttt tcttgaaact tgaggaaaca agatacatac 180
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<210> 389
<211> 293
<212> DNA
<213> Homo sapiens

<400> 389
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agntactcct atggnnttag cnttntanct atnacctgcn cnaactannc tnangtgcta 240
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<210> 390
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<212> DNA
<213> Homo sapiens

<400> 390
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<210> 391
<211> 257
<212> DNA
<213> Homo sapiens

<400> 391
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ctctcctctc tccttctctc tctgcccgga gctggtttcc gtctctcggc tcggggctgg 180
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aagccgccgg ggagccc 257

<210> 392
<211> 300
<212> DNA
<213> Homo sapiens

<400> 392
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<210> 393
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<212> DNA
<213> Homo sapiens

<400> 393
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<210> 395
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<212> DNA
<213> Homo sapiens

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<210> 396
<211> 300
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ncttnataaa anccttngnt natttggaac aacccncann taaanngcag ggaaaaaaag 300

<210> 397
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<213> Homo sapiens

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<210> 398
<211> 300
<212> DNA
<213> Homo sapiens

<400> 398
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gcaatagaac tgaaatcagg gagcaataag aacattcaca ttgctctggc tacattggcc 180
ctgaactatt ctgtttgttt tcataaagac cataacattg aagggaaagc ccaatgtttg 240
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<210> 399
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<212> DNA
<213> Homo sapiens

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<210> 400
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<213> Homo sapiens

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<210> 401

<211> 300
<212> DNA
<213> Homo sapiens

<400> 401
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<210> 402
<211> 300
<212> DNA
<213> Homo sapiens

<400> 402
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caaaggcgac ccgttccaga atgacccctt tgcagaacag cagacaactt caacagatcc 120
atttggaggg gaccctttca aagaaagtga cccattccgt ggctctgcca ctgacgactt 180
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cttaccttcg aagctcgacc cctttgaatc cagtgatccc ttttcatcct ccagtgtctc 300

<210> 403
<211> 300
<212> DNA
<213> Homo sapiens

<400> 403
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<210> 404
<211> 300
<212> DNA
<213> Homo sapiens

<400> 404
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aattaagaga tgctcagcag gatgcaagag ataaaatgga ggatatcgaa cgccaagtta 180
gagaattgaa aacaaaaatt tcagctatga aagaagaaaa agaacagctt agtgctgaaa 240
gataagagca gattaagcag aggactaagt tggagcttaa agccaaggat ttacaagatg 300

<210> 405
<211> 856
<212> DNA
<213> Homo sapiens

<400> 405
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<210> 406
<211> 843
<212> DNA
<213> Homo sapiens

<400> 406
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ncn 843

<210> 407
<211> 743
<212> DNA
<213> Homo sapiens

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<210> 408
<211> 746
<212> DNA
<213> Homo sapiens

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<210> 409
<211> 761
<212> DNA
<213> Homo sapiens

<400> 409
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naaacttntg tccccctgnt tccacttcca aaaanaactg g 761

<210> 410
<211> 748
<212> DNA

<213> Homo sapiens

<400> 410
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gaaaaancag ctttgtcctg ggtgaaaaag gatgccaaaa ttgcctggaa aagagcagtg 180
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gcccnaagng ggaaaaaaaa aaaaaaaa 748

<210> 411
<211> 773
<212> DNA
<213> Homo sapiens

<400> 411
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<210> 412
<211> 774
<212> DNA
<213> Homo sapiens

<400> 412
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      <210> 413
      <211> 773
      <212> DNA
      <213> Homo sapiens

      <400> 413
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atcggaactt ctaattatta ttgggctttt ccaagtaaag ctcttcatgc aaggaaacat      360
aagttggagg ttctggaatc tcagttgtct gagggaagtc aaaagcatgc aagcctacag      420
aaaagcattg agaaagctaa aattggccga tgttgaaacg gaagagcgac caggcttagc      480
aaaagacttt cttcacttcg agaccaaang ggaacagcta aaggcagaag tagaaaaaat      540
ncaaagactg tgatcccgca agttgtngga agaaatcgcc aagcaaatna agtagcccaa      600
ggaactgctt acagatggac tgattacata ttcgcaataa aatcttnggc ccaaagaaaa      660
atttngggtt tgaaggaaaa ttaaattggt tngaaccttt tggaatttcc cgaaagactt      720
ttgcctncnt ngacttaaaa tatttccatg gnggtgaaag gttgtccaan ctt             773

      <210> 414
      <211> 755
      <212> DNA
      <213> Homo sapiens

      <400> 414
gnagnnnnnn nttctaatgc ttggggnnnn nngtcaatnc ctnnganona ggcggntcgc       60
tcatccagaa angtcagatc ancaaagaag tccangaaaa antgcgaccc agctngaccn      120
tttgatccca ggcttagcac acgattgcat ggcntcccct ttagccactt naaccactgc      180
agacntccag gaagctggac tctctcctca gtccntccag acttctggcc accacagant      240
gaaaacccca ttttcaactg agctatcttt gctccagcct gatactccag actgtgctgg      300
agatagtcat accccactgg ctttttcctt caccgaggac ttggaaagtt cttgtttgct      360
agaccgaaag gaagaaaaag gggattctgc caggaaatgg gaatggcttc atgagtctaa      420
gaagactatc agagtatgga gaaacacacc aaactacctg gggacaaatg ctgtcagccc      480
ttaggcaaga ctaaattgga aagaaaggtg tctgccaaag aaaacaggca ggcccctgtc      540
ctccttcaaa catacaggga atcctggaat ggagaaaaca tagaatcagt gaaacaaacc      600
cgtagtccag ttctgngttt tcctgggata tgaaaagaat gaccanggac tnctggagtc      660
aacttttcac ttgaagaatc tcaaggccac cggtcattgg ccacacactn gaactccttt      720
ttaagatgta cccattactg gaattgggct taggg                                 755

      <210> 415
      <211> 852
      <212> DNA
      <213> Homo sapiens
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<400> 415
gnagnaannn ttctaatgct tgggnnnnnn ngtcaaacct tannaacctg gcntgncgaa 60
ttcggcacga ggtcacaggc aggtttantg gccagtttaa aacttatgct ntctgcgggg 120
ccnttcgtag gatggtgagt gtttccctgg gctttgctca tcacttcggg acatcgtgga 180
ctttaccgtg cgcnttggag tgtgtgatgg tgcctgagta gatctgctgg cagagtagtt 240
tgagccagct ggactgggct ggccgcctgc cgcttcttga gggtggaaga ggggtgctct 300
gagaagacac tcaggcagca gactctgcct ctcactagga ggtgcccccc cgaccccgtt 360
ccaccatagt caaggctgca ggctgccccg ggagaagtgg ctccccttct tgcgcctgtc 420
ttccattcgc ttcaccgggg gganaagacn ttgggcttgg ttggcacagc ntgaccccttc 480
tgcccatctt naaggcagnc ccggaantgg gaaaaatatt tctttaaatg gtggcctttn 540
nttttttttt nctttnaaag gggttgaagt tccannaatg natttcccaa tttccttccc 600
gaattgggnc ccaaagggcc ccaatggggc antcggtcct ttaaaaagna acctttttgg 660
acctgggaag aagaaaatca cccagattgt tgggaaatat tttggncatt aaaataaant 720
aatggaaaac ctnaaaaaaa aaaaaaaaaa aaaactcgag cccnttaaaa acttttagtg 780
agtcnnatta ccnttanatc canacnttga tangaanctt tggataattt tgggncaaac 840
cnnaacttng at 852

<210> 416
<211> 754
<212> DNA
<213> Homo sapiens

<400> 416
ggnnnnnnng tnaaaccttc cnaannaggc tnggcgtcac tgnccccggt caacaaaccc 60
acttttatga cagttttctt ccgcagcttg gctnttaaat tttactggca ggtgtatggt 120
tgttggaggg ttcctagtga gttgggggac ctggcantan agctgcttgg ttggaggaag 180
tgaanctggc ttantaccag cagctgatct cttccacgtg ctgctgcttt ttttgccact 240
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tgggtggcaa tgagaaagag tcacagtgtg ggttaaaggg atctgcagtg gggccaagga 360
tgccacccca ccctcagctg tangcaagct tgcacataaa taaccccgt cagtggagtg 420
ttcgggatgc agggggcant atagtgttct tggactttgt ccgtcctggg gcagttttta 480
agttctttat atttaagtgg ggtcagtgcc aagtgctacc actttcccaa taaangaatg 540
ggggacccan aaggctgggg tccctggcta ccttgttatg aaggttttgn tntttctctg 600
acaaganttg ctttggaaag ancctgtttt taggggatta ttttttgnat accccgatgg 660
gganccaggg ttctnctcaa aacccttaca acccttagga tcatagggaa aaggggcccn 720
tnttttnctg ctggcttncc caacttaaaa acnt 754

<210> 417
<211> 755
<212> DNA
<213> Homo sapiens

<400> 417
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agtctntcgc gacaccctgt acgaggcggt gcgggaagtc ctgcacggga nccagcgcaa 120
gcgccgcaag ttcctggaaa cggtggagtt gcagatcagc ttgaagaact ntgatcccca 180
naaggacaag cgcttttcgg gcaccgtcag gcttaagtcc actccccgcc ctaagttctc 240
tgtgtgtgtc ctgggggacc agcagcactg tgacgaggct aaggccgtgg atatccccca 300
catggacatc gaggcgctga aaaaactcaa caggaataaa aactggtcaa gaagcttggc 360
caagaagtat gatgcgtttt tggcctcaga gtcttttgat caagcagatt ccacgaatcc 420
tcggcccagg tttaaataag gcaggaaagt tccctttcct gtnacacaca acgaaacatg 480

gtggccaaag tggatgangt gaagtncaca atcaagttnc aaatgaagaa ggtgttatgt 540
ctggctgtan cttgttggtc acgttgaaga tgacnngacg atgaancttg ggtataaca 600
ttcacctggc tgtcaacttc ttggnggtca attgcntcaa agaaaaaact tgggcagaaa 660
tgttccnggc cttatnttnt caagaaccnc catggggcna agccccaacg ccctttnttt 720
aaaggcncat ttggaattaa attcntnttt ncccg 755

<210> 418
<211> 757
<212> DNA
<213> Homo sapiens

<400> 418
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ganccentcg attcgaattc ggcacgagga aaggtggcgc gcttctcacg gctgagttgc 120
tgcgcctgca gacggaagct ccccacaggc agagctgctt ggatgtgtga gtcatgaagc 180
cagagaagcc ccgctccatg agcagtgact ccccaggccc tgtgacctcc ctcctgtctt 240
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tggaaattcc tcgtggacct cgagatcttt accctaaaat agttctgttg aatttcaccc 360
tggcaatgta aattgatagc ttatcttcac agatgccaga caatggacaa ctcaccatca 420
gtcctctgct cacctgagac aaatgcatgt ctgattgctt cctctgccct attgnttatg 480
tgaaaatgca gattcactga gccagactaa ggcatcagtg actgttcctc tactgcctct 540
cacatggaga ttgtgtattc agtgaaaggc tgatcaaaga ccccaaagga atgcaccagt 600
ttatctctta tctacctatg acctgcgagc tgnccaccac ccccagttgt tgcgcctttc 660
cagacagaac cagtgtcatc ttacacgtat taattggatg tcctgngnct tccttaatat 720
gtatcaaaac aagctngcct tgaacacctt gggcacn 757

<210> 419
<211> 738
<212> DNA
<213> Homo sapiens

<400> 419
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ggcacgagac tgttcatcct aagttccact ataaacaggc tcatgactcg ggcacagaca 120
cttcttgcgt gactttttcc tatgatggta atgtccttgc ctctcgtgga ggtgacgatt 180
cattaaaatt atgggacatc cgacaattta ataaaccact tttttcagcc tcgggtcttc 240
ccaccatgtt cccaatgact gactgctgtt tcagtccaga tgataagctc atagtcactg 300
gtacatctat tcaaagagga tgtggcagcg gcaaacttgt tttctttgag cgtaggactt 360
tccaaagggt gtatgaaata gacatcacag atgcgagtgt tgttcgctgc ctgtggcatc 420
caaagctgaa ccagatcatg gttggaactg gaaatggatt ggctaaagtc tattacgacc 480
ccaacaagag tcagagggga gcaaaattat gtgtggttaa aacccancgg aaggcaaaac 540
aagctgagac tctactcagg actacatcat cacccctcat gccttgccta tgttcccgtg 600
agccccgnca acggagtaca aaggaaacag ctggagaagg acagactgga tccctgaagt 660
cgcattaacc tgaacctcct gtancangcc cangtcgtgg tggccgattt ggaacccacg 720
ggggcactnt tttttcct 738

<210> 420
<211> 739
<212> DNA
<213> Homo sapiens

<400> 420
gcgntnntat tagcgtgggc tcgntctcgc tcnacncanc nngngctggn cgaattcggt 60
acgagaatca gaggaggctt cttcatcctt caactccatg atgaactcct atatgaagtg 120
gcagaagaag atgttgttca ggtagctcag attgtcaaga atgaaatgga aagtgctgta 180
aaactgtctg tgaaattgaa agtgaaagtg aaaataggcg ccagctgggg agagctaaag 240
gactttgatg tgtaactgtg ctgttgatga agtcctccca gggaagcctg tgcagatgca 300
gtcacctgga aagaacagag attccctttc acctacctca gcaaaacaaa ctttcaagtc 360
ttgatagact tagcctagta attttatagt gagagtttca aactatatat caagtgtcta 420
tagcatcaaa aacttctggg ggcgtggggg aaagtagaat accaagtata atagttacat 480
tcactttcaa agagcatcta tgaatttgcc ttttgtaact tactgtggct ttaaacatat 540
tcagaacaga tgcttgaaat atgcacttag cactttggtt ccacatctgt ctgggtaaac 600
catgaagaaa atgaagctgc tgcctcaatc ganccccagac agcagccata ggcagataaa 660
gatttnggtt caccccttggt ggtgggaggc atcgtgtgtg cctttttttc ctctaatatc 720
aattttacag tccgggaan 739

<210> 421
<211> 727
<212> DNA
<213> Homo sapiens

<400> 421
gtgatctttn tgagtggggg ccntnctngc tctannanat aggttnggng ggctagcgat 60
ttctacctgc gctactacgt agggcacaag ggcaagtttg ggcacgagtt tctggagttc 120
gaatttcggc ccggacggaa agcttagata tgccaacaac agcaattaca aaaatgatgt 180
gatgatcaga aaagagctta tgtgcacaag agtgtaatgg aagaactgaa gagaattatt 240
gatgacagtg aaattacaaa agaagatgat gctttgtggc ctcccctgat agggttggcc 300
gacaggagct tgaaattgta attggagatg agcacatatc ttttaccaca tcaaaaatag 360
gttctcttat tgatgtaaat caagtcaaag gatcctgaag gccttcgagt attttactat 420
ttggtacaag acttgaaatg tttagttttc agtcttattg gattacactt caagattaaa 480
ccaatttaaa ttgtatgttt tcaagctggt tgnatattta attaaaggga tgggaagggg 540
ttatttgtca tttacagtat tggggtttta tgaatgtgaa gcaaccaaaa aaaattnnaa 600
tgtaaaactg gaaaatagga aaattcatta ncagcttaat gggtatcctt acttgatncn 660
ctgggtttgg aagtccccac acacattaaa tctgtaatga aancnctttt ggttaaaatt 720
tctctat 727

<210> 422
<211> 753
<212> DNA
<213> Homo sapiens

<400> 422
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aacttgattg ggttctcctt caggtttgaa gcgccctcna gaagtgtcta aaggagacag 120
ttgatagcca aacaacagtt ttggattcac tgactgatta tgaaagaagc agtagactgg 180
tatcaagaat cagtcagcaa ggaggccctc accagacgcc agtgccatgt tcttggactt 240
ctcagcctcc atattcatga actaagtttt tggaatcctt aggcttccac gtgtggaaag 300
cctgagctaa cctactggag gatgagccat cacctggagc agattcaggc catcctagtt 360
gaagcctccc taggccaagc aaccgtccaa ctaccagaca ttgaccattc agccttgaac 420
attcagcaca aagacaaaac agaccagacc agaagagtcc cacagaatag gggaaactat 480
tcagagaaaa cttaagccac taagttttat ggtgttttgt tcttgtagcc agaagcatag 540
gcatactggc caatacaaac cgaaatcctt ctaacgtant ggaccctttt caggccagca 600

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tttttccct tgaaaacctg ggagccttgt attccatctt attagcagaa gatcactttc     660
accaatggtt tgggctcttg atttggaatt gatgatgtaa tgagcctnta ttcnanatgn     720
gacttaatac ctctgcgaat tgactggatt ccn                                  753
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<210> 423
<211> 844
<212> DNA
<213> Homo sapiens

<400> 423

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nggnnnttnn nnnnnatncc ntgatcgtgt ntcgttcttt ctncaggatn nnntcgtttc      60
gaattcggca cgaggaaaag ggagccgcgc agngcctacg ggagtncggc ggcagcagcc     120
ggtaccggca accacgggca gctctcaggg aatctccgtc gttgaggcca naggctccag     180
tccccgcgag tccagatgcc tgtccagcct ccaagcaaag acacagaaga gatggaagca     240
gagggtgatt ctgctgctga gatgaatggg gaggaggaag agagtgagga ggagcggganc    300
ggcagccaga cagagtcaga agaggagagc tccgagatgg atgatgagga ctatgagcga     360
cgccgcancn agtgtttcag tnagatgctg gacctggaga agcagttctc ggaagctaaa     420
nggagaagtt gttcaaggga acgacttgan tcanctgccg gnttgcggct tggaaggaaa     480
ntgggggggc ttgaanaaga agcccctgga atnccaccgg aagccccctt ttgggggggg     540
gccttgcaaa ccgggaancc ctttnaaagg aatttcngcc antttcaang gttgggccaa     600
ggggaatcnt accnaagggg ccttctnggc cttggnatgg tgaatccang gnaaattaag     660
gtncccaatt gntgaancct tccaanggga ancccaaacc agcacccttg naanaagttg     720
agaaaacttg cttgcntctt ntgacacccc tncnaggggg aacttcaagg aaccggttcc     780
tnaggcttgg aaggaggacc cccananccc tgganc ctaa attnttaaat gggtnggacc   840
accn                                                                  844
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<210> 424
<211> 799
<212> DNA
<213> Homo sapiens

<400> 424

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ggagnnnngn ntccnaattn nntgggnnnn nnngtcaaan nctngctact cgttctttcc      60
gcaggatccc atgcgattcg aattcggcac gagcccagac ctatggagtc agacagtagg     120
tttgaggccc agcaatctat ggtttaacaa gccatccagg tgtttctgat gcacagtgaa     180
attggggtac cactggtatt aggtttggta tggcaacttt ttcatcactt gttttatgta     240
gttgtctgat caattgtgaa aacataatga atgttggaaa tggaacagta aaataacgaa     300
agccaacttt tttttttttt tttgagacgg agtcttgctc tgtcgcccag gctggagtgc     360
agtggcgcga tctcggctca ctgcaagctc cgcctcctgg gttcacgcca ttctcctgcc     420
tcagcctccc gagtagctgg gactacaggc gcccgncacc acgcccggct aatttttgn     480
atttttagta gagacggggt ttcaccgtgt tagccaggat ggtctcgatc tcctgacctc     540
gtgatccacc cgcctngggc ttccaaagtg ctgggattac aggcgtgagc caccgggccc     600
gggccaaaag ccaactcttt atgcctagaa aatattgtgc accctatgac ccaagcccat     660
tgaatttttn cngggaaatt tatggtaaat tattgaaatg gatggtacct ttaaaaagtt     720
atttggcaca ttccccttgg gttacctttg gnatggtttg ccagggaatt naaaactttg     780
ggntnaaacc ttttttann                                                  799
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<210> 425
<211> 750
<212> DNA
<213> Homo sapiens

<400> 425
gangccggat tccaattntc nggctnctct naaanmctgt ntaatgcttg gtccgcanga 60
ncccatgcga ttcgtggagg tctcctttcg ccccagccca ggtggccaag cccatcctgg 120
cctcagaaca tgctgagcac atttgtagg gtggcacctt tttatccaag ttactagcta 180
cacatcagtg tttaaagaga aaaaagtgac ctttcatttt tttttcttga aacttgagga 240
aacaagatac atactactga tttttttttt cttaaaacta aatgcatgac tgcagagcgg 300
tagaggtgta tatttttcat actgtggggc aaagtatttg tgctgctttt tggagatgga 360
ctggaacgtc tggtttctgt ccccgggccc ggcagctacg tctattttct gtagaaggtg 420
ccacagtgag acctggagcc accccttcct gcctggcgcc gtttanagct gggagcccgt 480
ggactccggc ctgtttctac cttctattca accactctga cgtgggggaga caagaagaaa 540
tagaactttt tgatagtgtg gtaaaaacat tggattttga actattttag taaaaggagt 600
taccaacaag aatgtnatag gtgctacttt gagctagata aataaaggct ctttgtgagc 660
ctcctgaaaa aaaaaaantt nnnnnnnnnn atnannnnnn annaaaaaaa ctggnccttt 720
aaaactttan gggncgttta cctanaccct 750

<210> 426
<211> 819
<212> DNA
<213> Homo sapiens

<400> 426
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anganmnnnt gcganncgaa ttcggcacga agggggggttc ccaatagtag aaaagggtcc 120
ccattcctgc tcagcaccgc acctctctac ccccccacag acacacatgc agacacacac 180
atgcagacaa cacgcagaca cacacatgca ggcactcaca tgcaggccca tgcacacaca 240
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cgcatgcagg cacacgcaga cgcacacaga gacacacatg cagatcacat gcacacacac 360
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ccaccttcca ctaaaacctg ggccttaatt tctctcccgt ccccacccct aaattcctga 480
tggatgaacc tagagctgtc ctgtccactc caggccggac tgacgtancc tatgggccca 540
gcaggtccag ggcccacgtt ttaatttctt tttnaaaagc tttaggtctt ggccnggccg 600
ccggtggttc acgccttggg agttcccagc atttttnggg aaggccnaag gccgggttgg 660
attcacaaag gtcaagcaag tttcaaggaa ccaagccttg aaccaggcca ttgggtgagg 720
aaccctgggc ttnttactng ggnaaattcc caaaaaaaaa ttggccttgg gccnaagggt 780
gggcaagggc acccttgttg gggtccccaa antttacct 819

<210> 427
<211> 750
<212> DNA
<213> Homo sapiens

<400> 427
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nntgcgattc gaattcggca cgaggtccaa ggacaacttc gagacatttc tttttgccac 120
cgtatctaac agggagcagg aagatctctg ccgaggaatt gtccagctct gcttcaatga 180
gcaaagccaa cagctgctag cagaggtcca gccctctgac tctttcctca tggtagagac 240
aactgcatac tttgaggcct acaggcacgt cctggaagga ctccaggagg tccaggagga 300
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cttgctaatg gggggcagat atgactttac ccccttaata gagaatcctt cagccactgg 420
ggaatttcta agaaatgtcg agggtttgag acatcccaga attaatgtct tagatcctgg 480
ccagtggccc tcaaaagaag ccctgaactg gatgactcca gatggaagcc ttgcagtttg 540

ctctcacaag ggaactggct attattcaag gaccttctgg aacaggcnaa acctatgtgg 600
gtctnaaaaa ttgttcaagc ccttctacca acgagtcttg tttggcaaaa ttaaccttca 660
gaaattccca tcttggttgn gtgtatacta atcatgcttt ggaccanttc tggaangctt 720
ttccattgtc agaaaaccan atttggccgg 750

<210> 428
<211> 943
<212> DNA
<213> Homo sapiens

<400> 428
gnngnccggt ttcctattct cnggcanctc tcttcctncn acctattanc tggactctaa 60
anaaaagnnt gnngcggttg gctcaagggc caccanaaca tttctttatt attattattt 120
tttaacctgn acatgcntta aagggtctat tacctttctt tccgtctgtc tcaacagctg 180
aaatggggcc nccaaggagt gccttccttt tgctccctcc tactgggact gacggntggn 240
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attgacacan tctctttnta agacangaaa taaactaaac cccaccccaa ggnantnatn 480
ncangcngaa aacnncncat ngcccacatt ncctnatccc ntancaccnn ctcnttnttt 540
nncccaanac tncttcccan ntntcnccnt ttacccntan ncntnnttnt atcccnctaa 600
tncctnannn ccntnnttnt ccnnatnctt acncncncnn ntnnnnnccn nntctttnnn 660
cccaaanctn ncctcncnnt tcnnctnaac cntntnnnca nnanacaccc ttctnatnnc 720
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nanancnatc tnntncncnn cnantnnnnt tcanttcacn ctctnnnnnn tntanccnat 840
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canntnnnnt nnnnnncnnt cnanaccntn nnnntctatn ccc 943

<210> 429
<211> 775
<212> DNA
<213> Homo sapiens

<400> 429
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tcncncgcag naangctgtg gcgctccatt gtgaaagatc caggcatttt tccgagccag 120
gaaaagccca agatgactac aggatattag tgcatgcacc ccaccctcct ctcagtgtgg 180
tacgcagatt tgcccatctc ttgaatcaaa gccagcaaga cttctctgct gctgtgatct 240
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cattgtggca ctgttgcccc ccatggcggc atgggcaaga tgaccttcca ttagcttcaa 360
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nnnnnnnnnt ttttttgagc tcaaagaaag ttctcatttt ccctattcaa ctaataccca 540
tgccgngttt tttaccttgg atttaaaggc accttangtt ggggcaacag attctcactc 600
atgtttaana cctggnattc ancttcataa gaccaaagan ggagctttcc ctttctcttt 660
acccctnagg attctcatcc tttacanntn gactttttcc aggccaattt cccatnnaat 720
ctgcnanncc cngccttttg ncccaagctt ttntgntngn ccccccattt acccn 775

<210> 430
<211> 763
<212> DNA

<213> Homo sapiens

<400> 430

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ngggtgnnnn nntttctaat nctggggnnc nntnnncnnn ntttcctaat ncttaggngc      60
tcgttctttc tccangcagn nnngcgtttc gcgacagctc tccaatactc aggttaatgc     120
tgaaaaatca tccaagacag ttattgcaag agtttaattt ttgaaaactg gctactgctc     180
tgtgtttaca gacgtgtgca gttgtaggca tgtagctaca ggacattttt aagggcccag     240
gatcgttttt tcccagggca agcagaagag aaaatgttgt atatgtcttt tacccggcac     300
attccccttg cctaaataca agggctggag tctgcacggg acctattaga gtattttcca     360
caatgatgat gatttcagca gggatgacgt catcatcaca ttcagggcta tttttcccc     420
cacaaaccca agggcagggg ccactcttag ctaaatccct ccccgtgact gcaatagaac     480
cctctgggga gctcangaag ggtgtgctg agttctataa tataagctgc catatatttt     540
gtagacaagt atggctcctc cgtatctcct cttcctagga gaggagtgtg aacaaggagc     600
ttagataaga caccccttaa acccattccc ttttccagga gacctaccct tcacaggcac     660
aggtccccaa atgagaagtc tgctacctca tttctcatct ttttactaaa ctcaaangca     720
ntgacagcag tcagggacag acattcattt cttnatacct tcc                       763
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<210> 431
<211> 761
<212> DNA
<213> Homo sapiens

<400> 431

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tggtgttnnn ntcctaatgc ttggnngnnn ggtnannctt ctaattactt tggggctcgt      60
tctntctcna cnnngcnngg cgttncgaat tcggcacgag cttgaagcgc tggtttttct     120
cgaagcaatc cttattatat tgttaaacaa ggaaagatca accagatggc aacagcacca     180
gattctcaga gattaaagct attaagagaa gtagctggta ctagagtgta tgacgaacga     240
aaggaagaaa gcatctcctt aatgaaagaa acagagggca aacgggaaaa aatcaatgag     300
ttgttaaaat acattgaaga gagattacat actctagagg aagaaaagga agaactagct     360
cagtatcaga agtgggataa aatgagacga gccctggaat ataccattta caatcaggaa     420
cttaacgaga ctcgtgccaa acttgatgag ctttctgcta agcgagagac tagtggagaa     480
aaatccagac aattaagaga tgctcancag gatgcaagag ataaaatgga ggatatcgaa     540
cgccaagtta gagaattgaa aacaaaaatt tcagctatga aagaagaaaa agaacagctt     600
aatgctgaaa gacaagaacn gattaagcag aggactaant tggagcttaa agcccaagat     660
ttacaagatg aactaccggc aatagtgaac aaaggaaacc gtttttaaa agaaangccn     720
aanctgcttg aaaaaaaaaa aaaaaaactc ggcctntaan t                        761
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<210> 432
<211> 748
<212> DNA
<213> Homo sapiens

<400> 432

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gnngantnng tcttattatc gtggngctct nactnnctct aaatanaatt gtgttgnggg      60
aattcggcac gaggccaccg aagcttcagg atgacatctt agactctctt ggtcagggga     120
tcaatgagtt aaagactgca gaacaaatca acgagcatgt ttcaggcccc tttgtgcagt     180
tctttgtcaa gattgtgggc cattatgctt cctatatcaa gcgggaagca aatgggcaag     240
gccacttcca agaaagatcc ttctgtaagg ctctgacctc caagaccaac cgccgatttg     300
tgaagaagtt tgtgaagaca cagctcttct cacttttcat ccaggaagcc gagaagagca     360
agaatcctcc tgcaggctat ttccaacaga aaatacttga atatgaggaa cagaagaaac     420
agaagaaacc aagggaaaaa actgtgaaat aagagctgtg gtgaataaga atgactagag     480
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ctacacacca tttctggact tcagcccctg ccagtgtggc aggatcagca aaactgtcag 540
cttccaaaat ccatatcctc actctgagtc ttggtatcca ggtatttgtt tcaaactggt 600
gtctgagatt tggatccctg gnattggatt tcttaaggac ttttggangg ctcttgacac 660
catgcttcac agaacttggg cttcanaagc ttcanttttt tgcanaggtg ccccaggtta 720
ggaaaacagt tntncttgtt ttgtannt 748

<210> 433
<211> 769
<212> DNA
<213> Homo sapiens

<400> 433
gggnaaaagt ttnnnannng ggnagnnnng ntnnaccntt cctattactt tggagctcga 60
actcgcncca canannnagt gncntgngct gttttgcaga tgaggaaaac tgaggtacag 120
aattcttagg gaacttaccc aaaatggctt ttctgcactc tgccctttgg tattgtccca 180
tgtgaattgt ttaaaactta tgtgtatagt ggcatgagta ggtgatttca gaaacagaac 240
tcacttttgt tgtttggtct taaaattagg aacttttctt catctgggct tcatttccct 300
gcaccttccc agctttctag tcatgcaagc cacatgtctc cacgtgaggg gttcattgga 360
aagcagccac agagccaccc cctggctggg ttcttcccca gctctgcttc ctccttcccc 420
aagtcctgca gctgctctct ccatggcaga accacttctc cccttactgg aggggaggtc 480
cactgaacaa atccaggaga ggaatcattg tgttttccac agaagagaaa gtacactgga 540
ctttctgtgc aacctgttac tacattttca caganactca tatttgtgca ntgtaactca 600
atttgaaacc cagcaaaatt aggctcccgt gtctccataa aaggccacca tgatggtaac 660
cgttggactt caccttgtgt ttnggacana ngctgattgg attttaccca tcatcacanc 720
cgtgtcttac attctcnttt cctgggcttt ggacccctgn tanaaaaan 769

<210> 434
<211> 764
<212> DNA
<213> Homo sapiens

<400> 434
ctanccttcc taaannctng gctactcgnt ctttctnnan ganncnnntg cgatncgaat 60
tcggcacgag caccttgcct ggccaagggg ctagacctcc caggctaagc ctcagattca 120
gtgcaggaca caagctcatg cccccgtctt gccagtgaca cttgaagcct cccgacttcc 180
acagagtgct tcaggacaca ttttgagtgg tattttcttt tctttttttc ttcttttttt 240
tttttgagat ggagtctcgt tctgttgccc aggctggagt gcagtggcct gatctcggct 300
cactgcaacc tctgcctccc aggttcaagc gattcttctg cctcagcctc cagagtagct 360
gggactatag acatgcacca ccacgcccgg ctaattttgt atttttggtc gagacggggt 420
tttgccatgt tagtcangct ggtcttgaac tnctgacctc aagtgatcca ccactcggcc 480
tccaaagtgt tgagatgaca ggcacgagcc accagcccaa cctgagtggt attttcttta 540
gggaccangt agactttaaa acgagggtaa gagaaaaagc ccagtggtct tttctgangg 600
taaataaatt tctgcccagg aaacnttncc aagccccaac cagcaagcca acccttaaaa 660
aaaaaatcac ttcgtgttcc ccaangggan ctttnttaaa gctttggggg cttccaggna 720
aaatcatttc cagtnnaant ttggaagaat tcannagnat ttnt 764

<210> 435
<211> 755
<212> DNA
<213> Homo sapiens

<400> 435
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tncagatncc ntcgattcga attcggcacg agggatcctt tccagacaga agaccccttc 120
aaatctgacc catttaaagg agctgacccc ttcaaaggcg acccgttcca gaatgacccc 180
tttgcagaac agcagacaac ttcaacagat ccatttggag ggaccccttt caaagaaagt 240
gacccattcc gtggctctgc cactgacgac ttcttcaaga aacagacaaa gaatgaccca 300
tttacctcgg atccattcac gaaaaaccct tccttacctt cgaagctcga cccctttgaa 360
tccagtgatc cctttttcatc ctccagtgtc tcctcaaaag gatcagatcc ctttggaacc 420
ttagatccct tcggaagtgg gtccttcaat agtgctgaag gctttgccga cttcagccag 480
atgtccaagg gtgcctgggg aagagccact gcgcatgtta tctttggtgt tactccagtg 540
ttgaacanag agctggtcag aggcagtgca tcgcanagag acattaataa gggaatcctt 600
tgaatcccta ancagcanca gctttnctga nggggccnat gatgccagtg acctnttcan 660
ggnaagtctg ggacattggg accaccctgg ggggaagaac ttgtgggatg tggcttttct 720
tttatgaata aagtactttg agttggttgn aatcn 755

<210> 436
<211> 760
<212> DNA
<213> Homo sapiens

<400> 436
aaggctggnn nnngnnntgc nnnncttcnt attantctgg gggctcgtnc tctctcnann 60
nagnnaggcg ntgngaattc ggcacgagct caagaaaagg agaaagtttt tttgtatgaa 120
attggaggaa atattgggga acgctgcctt gatgatgaca cttacatgaa ggatttatat 180
cagcttaacc caaatgctga gtgggttata aagtcaaagc cattgtagaa gacttaacaa 240
gctgcagata accatgtgga cttctgtcat aattcttgct gagtcaagag tgtaaataaa 300
agaaatggca ggactcatat tattcagttg tcccaagtat ttaaaaatga ctctcttaag 360
ccttaaaaag tcatagattt gtgctgctgc cagaattata ttaattatta ttaatggtat 420
tattagaaaa aaaatttctg gagtgagagt naagangctt aattagtttg tgggcagttt 480
tcatatgctc tgtgaaatgt gtccagatgt gacataagtt tttttttta atatggngga 540
aatgncttct ctttcccatt cttttctcct aaaaatcata tatactggga atatatgcct 600
ctnttacctc tattaccctc ctcacattta ccctttccca gttnggtttt gctttttnac 660
caaaaagatt ccaatnccna ggtattggca agttntnaaa accgcccntt aaacatccct 720
aatttcncag nattccnnnc ttgccaaatn ttngtntcnn 760

<210> 437
<211> 748
<212> DNA
<213> Homo sapiens

<400> 437
ggnnnnngnn ngntnncgtt ccctattant caggngctcg ntctntctcn annnancnng 60
gcgtgtncga attcggcacg aggattttcg aaactcttca gctacttgcc ctttttttatc 120
tgaaaccatc ataccttctg aaagaaaaaa gcatatcttc attgacataa cagaagtgag 180
atggcccagt cttgatacag atggtccatg atatatatgg agagtggcat tgtgaagata 240
acatctttag atggtcatgc atacctctgc ctgcccagat ctcagcatga atttacagta 300
catttttgt gtaaagttag ccagaagtca gactcatctg cagtgttgtc agaaacaaat 360
aataaagccc caaaagataa actagttgaa aaaactggca aaatctgtat acgtggaaat 420
ttaccaggac agagactgaa gaataaagaa aatgagtttc attgccagat catgaaatcc 480

aaagaaactt taaagaagat gagttgtgta aatggaactg aagggagggg aagaactgcc 540
ttcgcctggt acaaagcaca catgtgtata cacatgggtc aagcagtgct ggtctgtggc 600
tgnctgtcca gangaatgga aatatccttg gctttagcac ttcattttca taataaaatc 660
agcaattntg tctaaaaaaa aaaannnana aaaaactnga gcctntanaa ctntagtgag 720
tcgtattacg tagatncnna catgataa 748

<210> 438
<211> 823
<212> DNA
<213> Homo sapiens

<400> 438
taatccttnn tattgntcgg gtactngntc tntctcnaag annntntcgt tncgcccagg 60
tagctgagac tacccacacc ttggtcccag ctacttggga ggctgaggtg ggaaaatcac 120
tttgcccagg aattcaaggc cgcagtgagc tatgattgca ccactgcact ccaggcaaca 180
gagtgagacc ctgtcttaaa aaaagaaggg agaaagtgtc agatggtgat gaggtctggg 240
ggggaaatag agaatgggga tcaggagtgt ggatggtggt attccctcac caagaggtga 300
catgttgagc agggaacttg ggaggtgagg gtgtgacccg tgtggaaatc agggaaaagc 360
attncagcct gagggacagc caatgcanag gccgtgaggt ggccagtgcc actgagcagt 420
gagcttggga tagggggcan gtgangaggc tggagagcgg ggtcagacaa accaatatgc 480
ttatttaaaa caaggttgtt ncagcaccct tgccttaaag ccttgagcct gnaanctnga 540
aaaatttggg cacnttcaaa agcanggang gaaaccaaaa gaagattggg agggaaaagc 600
ccttncnttc ccttancagg aaatgaagtt nccacccttn aaaacaggnc caggaccttt 660
ttgggaccct tttggccttt tggttcctta gaatcctctt ggtngcttnn gaatnaaaag 720
gnaaaagggg cctttaaggg gggatcccat tntttccaaa attcaaaggg ggctttccct 780
gggcttaccc aaaatttctt ggncttaant aaaaaaattt ntt 823

<210> 439
<211> 767
<212> DNA
<213> Homo sapiens

<400> 439
gnnnnngntt ctaatgctgg nnnnnnnngg taccctttcc aaaacctggg ctctcgntct 60
ttctncangn agccnngcga ttcgtctgtc tggtgatttt tattttaagt gaacctttgg 120
atctatcttt aactctcttt attgtgagtc taaattccaa ttctgcagca gatcagtaaa 180
ctcacagtat ttttcctgtg gaaatctatt caataaggaa accaagacag gatantaaaa 240
tttaaaaaaa ancaactttg aattcccctg cctaggtctt ccagttgttt tccagcgcat 300
acctcaggta tgactttgct agccggggac aaaattagca ccttccgatt ctctagtcca 360
aatgaacttt ggctaaataa aaaattatta tactacataa taaagttnca gatagcagga 420
aatgcaagag ctaggagatt cctagattat atctggccaa gccaaatacc ttaaacatcc 480
acctggaaat cctctacccc ctcttctgag ataatttgcc cagccctttc ttcccacaca 540
ctcactcaat gtcacccccct tctaatcccc aaaactgttt ttgtggcctt ggtagcctat 600
agtagtttct cacatctttt cccctanact tttctgtttt cagtttcaga ccaaaaaaac 660
tcttcaactt ttttccagtg ggtcttcct taccagtaac tttaccactt gnaatcttat 720
ttcattgaaa aaaccttaaa tgggntggga aaaggcttgc cnncann 767

<210> 440
<211> 752
<212> DNA
<213> Homo sapiens

<400> 440
nagnnnnntt tctaatgctt ggnnnnnnnn tcnatgcttc caaaagcngg gngctcgttc 60
tttctccaag atncnngcgn tncgaattcg gcacgaggat ggatgagact gttgctgagt 120
tcatcaagag gaccatcttg aaaatcccca tgaatgaact gacaacaatc ctgaaggcct 180
gggatttttt gtctgaaaat caactgcaga ctgtaaattt ccgacagaga aaggaatctg 240
tagttcagca cttgatccat ctgtgtgagg aaaagcgtgc aagtatcagt gatgctgccc 300
tgttagacat catttatatg caattcatca gcaccagaaa gtttgggatg tttttcagat 360
gagtaaagga ccaggtgaag atgttgacct ttttgatatg aaacaattta aaaatcgttc 420
aagaaaattc ttcagagagc attaaaaaat gtgacagtca gcttcagaga aactgaggag 480
aatgcagtct ggattcgaat tcctggggaa cacagtacac aaagccaaac cagtacaaac 540
ctcctacgtg gtgtctactc ccagactncg tacgccttca cgtnctcctn catgctgang 600
cgcaatacac cgcttcttgg gtcangaatt agaagctact gggaaaatct accttccgac 660
agaagagatc attttagatn taccgaatga anaaagcttg cattagtgac attgaaaggg 720
aaataaaaat tcctacagtc naaaaaaaaa at 752

<210> 441
<211> 775
<212> DNA
<213> Homo sapiens

<400> 441
gnagccngat tccaaaacct gggnnccgat ccaatgcttn ccaattactt gggagctcnn 60
actngcncna ncaanctngc cntgcgaatt cggcacgaga agnaggcgga gcttgcagtg 120
agctgagatc gcgccactgc actccagcct gggcaacaga gtgagactct gtctcaaaaa 180
aaaaaaaaaa aaatggaacg cagggcaaga actcgtnttt ggaaggagat gggggaaagg 240
ancggtatta tacctatgtt gnatttgcag gcaaatgaga tgganccctc tctgtaaaga 300
agagtcattt gtgcaagtag acggggtctg tgggtgcang ccctggaggg gcacacaatt 360
gcctgnangc ttctgtgana tcgggagang gaggagaagc agtctcttga caaaataaag 420
tatttttatt cattngtatt tattaaatga aaaaacaatc ccatggtgtc ccttgtgtgt 480
ggtggaacct aatgactgtt gaaataaagt ctgngttttc ccttcaaaaa aaaaacncnn 540
anaanaaaaa ctcgagccct ntaaaacctn tngngagtcc gnattaccnt anatcccnga 600
cnttgataag gatccattga tnaantttgn cccaacccca actnngaatg ccnngaaaaa 660
aaattgcttt atttgggaaa tttgcnaatn ctttgcttta ntttgnaccc antttancnt 720
cannnnccaa gttacnancn ncaattgcnt tcatttangg ttcaaggttc aaggg 775

<210> 442
<211> 804
<212> DNA
<213> Homo sapiens

<400> 442
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atctcnaann aaaangcttn cgaattcggc acgaggccac ctgcactgag gtctgggccc 120
ggggacaggg tgctttagcc aggcttgtct gcgcctcagg gaagggtgag cagcccaggg 180
accagatgca agttggtggg cccctccacc cntccnacgc cactccccag tgtgctgggt 240
cctaaccagt cgtcctatgg gagcagtcag ccttcctctc ctcctcaggg cagctctccc 300
acctgctgnt ccccgcacac agaacctcat tgctctgagc agttgcttat tacccagttg 360
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gggangccaa ngcgggtgga tcatgangtc aggagatcaa gaccatcctg gcttaacacn 480
gtgaaaccct gtctctacta aaaatataaa aaagtancca ggcgtggtgg tggcccctgt 540
agtnccaann tacttgggaa gctnangcan gaanaatggc ntgaacccaa gaaggaagaa 600

cnttgcantg aancttaaaa ttgcgcccac tggaatttca aaccttgggc cnanaanaat 660
tgaagaatcc cgtcttaaga aaaaaggaaa aaantttncc nttntnaaag gcccggccac 720
aantnggctt taacgccctg gtaaatnccc aancactttt tggggaaggc ccaaaggcaa 780
ggccnggatt caattttnna aggg 804

<210> 443
<211> 786
<212> DNA
<213> Homo sapiens

<400> 443
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nnccccaann annnaggngg ggngaattcg gcacgagcac catttttatt ttgatgctta 120
cactcattta ttctgttttt gtaaaacagt ttcaagaatt taaaaatcct tccagttaat 180
agagcttttg ttattatatt ataattttgt aaacccactt tgtttttccc actttaaagc 240
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ttggctgttg ttacagagat gttgggcaga gctatgcagg tgtttcattg ngaactctag 360
ctttgatcat ggtaaaaagt taaccctttc tattttttaa tggatgttat accaactatt 420
cagaggactc atacttcaaa aatattagga aaatctgtct tatagttctc taataaatat 480
ctgaaatctc aagtacgaca tgaaagaatg tcagaccatt gntattggtg aaagtcattt 540
gatgaatggn aaattctatg aaaagtaagt ggatttgcat ggattaatat cagggaaaat 600
ttaagccttc ccaagtgtga ctgggccaaa gagagccaga tgccccccagt gcctgtgccc 660
ataaagttcc cgaatccccc aatggggtct nttttcaaaa acttggncca gacccggaaa 720
ataaaancat tcntcataaa ttcaannggg gncctcanga aacacnttcc cccancaacc 780
cttngg 786

<210> 444
<211> 760
<212> DNA
<213> Homo sapiens

<400> 444
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acnccaggan ncangcgttg cgaattcggc acgaggagga attacaggta gcaaattatg 120
gagttggagg acagtatgaa ccccattttg actttgcacg gaaagatgag ccagatgctt 180
tcaaagagct ggggacagga aatagaattg ctacatggct gtttnatatg agtgatgtgt 240
ctgcaggagg agccactgtt tttcctgaag ttggagctag tgtttggccc aaaaaaggaa 300
ctgctgtttt ctggtataat ctgttgccag tgggagaagg agattatagt acacggcatg 360
cagcctgtcc agtgctagtt gcaacaaatg ggtatccaat aaatggctcc atgaacgtgg 420
acaagaattc gaagaccttg tacgttgtca gaattggaat gacaaacagg cttccctttt 480
tctcctatng gtgnactctt atgtgctgat atnccatttc ctagtcttaa ctttcaggag 540
tttacaatng ctaacactnc atgatngatt cantcatgaa cctcatccat gttcatctgn 600
ggcaattgct taccttgggg gntcttttaa aaagtaccac gaaatcatca tattgcatta 660
aaacccttaa aagttctggt gggnatcaca gaagacaagg ccnaanttna aagnggagga 720
attttattat ttaaaagaac cttttgggtn ggatnaaaan 760

<210> 445
<211> 761
<212> DNA
<213> Homo sapiens

<400> 445

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tggtgccggt tcttantctg ngctctcgtc ttccttctta tacctgggca ncncttggcg     60
gccccnaggn tcccangnag ccnngcngng ncngattcgg cacgagattc caaaggtttc    120
aaagaacttg gtcataaata tgataatgag aagacaaagt atttatatta aaacagttta    180
gtagccttca gttttgtgaa aatagttttc agcacagaaa ctgacttctt tagacaaagt    240
tttaaccaat gatggtgttt gcttctagga tatacacttt aaaagaactc actgtcccag    300
tggtggtcat tgatggcctt tagtaaattg gagctgctta atcatattga tatctaattt    360
cttttaacca caatgaattg tccttaatta ccaacagtga agcactacag gaggcaactg    420
tggcattgct tccttaacca gctcatggtg tgtgaatgtt ataaaattgt cactcagata    480
tattttttaa atgtaatgtt atataagatg atcatgtgat gtgtccaaac tatggtgaaa    540
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cacanccttc tgcctctgna tttggaagtt gtcagtncaa ctcatcaaag aaaactgcct    660
aatntnaaaa tcatattntg ggaataattt ccctcttttg tagtctgccc aagatcctta    720
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<210> 446
<211> 770
<212> DNA
<213> Homo sapiens

<400> 446

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cgaactcgct cnannagnaa ggccgggnga attcggcacg aggccccgct ccatgagcag    120
tgactcccca gctcctcctg gcaccagtcc ccagggctct cctgttggta gttcctgctt    180
ttcttcttgg aaattcctcg tggacctcga gatctttacc ctaaaatagt tctgttgaat    240
ttcaccctgg caatgtaaat tgatagctta tcttcacaga tgccagacaa tggacaactc    300
accatcagtc ctctgctcac ctgagacaaa tgcatgtctg attgcttcct ctgccctatt    360
ggntatgtga aaatgcagat tcactgagcc agactaaggc atcagtgact ggtcctctac    420
ctgcctctca catggagatt gggtattcag tgaaaggctg atcaaagacc caaaggaatg    480
caacagttta tctcttatct acctatgacc tgcganctgc caccaccccc agntggngcg    540
cctttccaga cagaaccagt gtacatctta cacgtattaa atngatgtcc cnggggctcc    600
cnaanangna tcaaacaagc ngggcctcga ccaccttggg cacatatccc nanggacatc    660
annctggagg ctngngncac tggcattggc cctnaccctn ggcaaaataa accttctaaa    720
attggnaaaa aanaaanaan aaaaacctng nnccctntna naacnntacg              770
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<210> 447
<211> 757
<212> DNA
<213> Homo sapiens

<400> 447

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gctctttccg nangatccca tcgattcggt ctgatgcagg agaattgcta aaacccagga    120
gggagaggtt ncattgagcc gagattgcgc cactgcactc tagcctgggc gacagagcaa    180
gactccgtct cgaaagaaag aaagagaaag gaaattcccc agggaagtac ctcggcttat    240
ttcataaaca ggtactgaag gaagcagagg catgtggagg acttccccac ctcgtgcagc    300
tatttgggcc gtggcatctg aaatttctta tttcagagtc acccctttga tgaccttggc    360
agtgaactgc agtcatctgt ttaggccttt ccatggccca cgtcaatgcc ggtatttctg    420
tttgttgcac atttgatttc cttgttgttg gcatttagaa ggccccccgt ttcccagatc    480
acaccacggg catggaccac agagattgca tcttgtgagt ctgtagaaat ggtcaaggcc    540
ttgtcctctc ttaagtccag agctcangtt aatgcaaaat tttnccggnc atctgtgctg    600
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aaatcccttt ggggaagctc ctggctggtt tcctgtaggt aggacagcta cacgtnctgc 660
cctttattgg cttcttttca tgaagctcct gccatntacn aaacatgtct cccttcttga 720
atcacatctc tggtattgna actctanaat cgcccgg 757

<210> 448
<211> 770
<212> DNA
<213> Homo sapiens

<400> 448
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ttggctactc gntctttctn cangnagccc ntcggtncga attcggcacg aggtgtcttc 120
atcttaccca gtggaaccta agaaattaaa ttctccagaa gaaactgctt ttcagacacc 180
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aatgaatcgg atggctggaa tttttgatgt aaacacctgc tatgggtcac cgcaaagtcc 360
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attttctaat ccttctccat ctacctctat tagtgctgag ggtaagacaa tgagacaacc 480
cagtgtgatt tattcatgga ttcagaataa acgtgaacag attaagaatt tcttgtcaaa 540
acgggtgctg ataatgtatt ttttcagtaa gcacccagag gcctncattc aggctgtttt 600
ttcagatgcc caaatgcata tttgggcatt agaaaggtct gtcgcactta gtagcagcat 660
cattttacag aggatagatt tggagttgtc cagacgacac taccagctat ccttaatact 720
ttgttgacac ttgcaagang cagtcngaca agtactttaa cttcctcatg 770

<210> 449
<211> 792
<212> DNA
<213> Homo sapiens

<400> 449
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ganntcgaac tntcncnaca cagnnangcn ntgcgaattc ggcacgaggn cnnctcnatn 120
atnacttgnt cncancggnc tggcatcnac ncgncacacc tacntnagcg cnttgtagcg 180
caatatncac ctnntnaaac ccnnnagtcc cagggctctg ccnnnnnact gntcaactga 240
cnaacnacnn nctancncaa cntnnnntta ngccnctgnc tgnctctatg gcacctnncc 300
tnccntcncn cntnacccnc tacgctcagg gctatataca atgggaacct tnccaacagt 360
aanccntgga tctnaggnat ggcccttgnc tggcggatca cagccttnna gcntatcagn 420
atcttgagga agacaccatt ccgtcccnga ttntgaccaa ncnctcggat gtgnctatgg 480
gctcnattga ggnacaacaa ctnncactgc nnataggcca tcctcnnnan nctacacatg 540
ngactttncn nnncatntna aatgnnnana tgtctctcnc aagcatcacc cnctgtccct 600
ncgncntcnt ggaagacctt ctgnncaact ganctccttc ntgnnncnnn ngattnttnc 660
nnncnnaata tncntncccc aatgnccttg tnnngnattt atnangggnt ttccaatttg 720
ggntaattca ntncccnccg nannctannn ncccatnaac cntcngngcc ttcttgnaac 780
cttttnncct gg 792

<210> 450
<211> 848
<212> DNA
<213> Homo sapiens

<400> 450

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annctgggng ntcgcaactc nctcnanaca gnaaggncgn gggctttgct ctctccattc 120
caagttgntc tctgttctag aaagcagatg tagtagacat ctactgttgt tgcctgaaca 180
gaatcccttt gtcctttttt tgntaaaagt actcatccct aatattcatt gtnctggaag 240
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agcaaacgga gatcganccg aaaagtggaa anatgagcnc ttctttggng ttggcatatg 360
gaccctgaga gaaagaactn tnattntttc tcttggactg caataaagta tagctgccta 420
aaatacgntt cctgacactt ggaggnttgt ccacaatcgg ngaaataaag gcgagaccgn 480
acactggatg aaaaaaanaa gnnnccngnn gaanacccac tnnnccannn nccnnnccnn 540
tncnccanng nnganccnnn tanccgnnan naggccnnng cnntngcnnc nnngccnnnn 600
nnnnnngggn aaacccnnnn gnnnnncnnn nnnnnnnncn nnnnannnnn nnncnncnng 660
nnggnnctnn nnnnannnnc cccnncnncc cnncnccnnn nggnaanncc nnnnnnnann 720
annnngggnn nnnncnannn ccnnnnnnnn cannncnncn cnnnnnggnn nnnnncnnnn 780
nnnnnnnnnn ncnngngnnn acnnnngngn nnnnccnnnn nnnnnnncngg nnnnncnnnn 840
nnnncccc 848

<210> 451
<211> 765
<212> DNA
<213> Homo sapiens

<400> 451
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gcttnggcna ctcgttctnt ctncangcag nnnntgcgtn gncgaattcg gcacgagcat 120
tcctcctttg ttaacgaagc aacatttaca caagatggac attacattat tagtgcatcc 180
tctgatggca ctgtaaagat ctggaatatg aagaccacag aatgttcaaa tacctttaaa 240
tccctgggca gcaccgcagg gacagatatt accgtcaaca gtgtgattct acttcctaaa 300
aaccctgagc actttgtggt gtgcaacaga tcaaacacgg tggtcatcat gaacatgcag 360
gggcagattg cagaagcttc agttctggta aaagagaagg tggggacttt gtttgctgtg 420
ccctctctcc cgtggtgaat ggatctactg tgtaggggag gactttgtgc tctactggtt 480
cagtcagtca ctggcaaact ggagagaact ttgacagtgc acganaagga tgtgattggt 540
attgcacatc accctcatca gaacctgatt gctcctacag tgaagatgga ctcctaaagc 600
tctggaaacc ataattcaac ttttcttttt taaatcaact cgaaagcatg tncttaaatg 660
aacatattca tgtaanggc ttttttttt tgncactttt ctaagcaaat agatggctga 720
attagtcacn gaataaattt gngaaaatca tggttaaatn ccaac 765

<210> 452
<211> 765
<212> DNA
<213> Homo sapiens

<400> 452
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ngcnnnggng ctcgttctnt ctncacgnng ccngtgcggt gncggtctga ttgaaagctg 120
ttcaggttta tcatgcaaat cctcgcctct ggctacggct ggctgaatgc tgcattgctg 180
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agtctattgt tggtcaagct atcatcgtaa aatagttttg gcatcacagt ctatacagaa 300
tactgtttat aatgatgggc agtcttcggc cattcctgta ccagtatgga gtttgcagcc 360
atatgtctca gaaatgcctt gttgctgctc ctgaagaaca gcaagatcca aagcaggaaa 420
atggggctaa aaatagtaat caattaggtg ggaacacaga gagcacgaaa gcagtgaaac 480
ttgcagcagt naaagccatg atggagatna attcattcca gcttcacctt cttctccatt 540

gagaaaacag gaattagaaa acttaaagtg ctccatactt gcttgcagtg cctacgtggc 600
tctggctttt gggtgatacc tcatggcttt gaatcatgcn gatnaacttc ttcagcagcc 660
caagctgcag gatctcttaa gttttgggac atttatatgc tgcagaaccc ttatcttctt 720
cgacngaatn tctgtgccnt tctcacttga ccccgagaat gtnct 765

<210> 453
<211> 833
<212> DNA
<213> Homo sapiens

<400> 453
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ntgcgattcg aattcggcac gagagaaacg ttctcaggtt gaccagctgc tgaatatttc 120
tttaagggag gaagaactta gtaagtcatt gcagtgcatg gataacaatc ttctgcaagc 180
ccgtgcagcc cttcagacag cttatgtgga agtcaagagg ctacttatgc tcaagcagca 240
gatactatgg agatgaatgc actgaggacc catagaatac agattctaca ggggattaca 300
agaaacatat gaaccttctt gagcacccca ggttttggca ttagaaaatg ggtacccctt 360
ggttcaaaaa tgaacaaaga aagccttaga tttggatggg ggaacctgat ctgtccagtc 420
tagaaggatt ccagtgggga aagtgtttcc atttccttng tcccctggct tggccaagga 480
aagcgaaagc cctttcttga anagcaaccg tggatcattn gaccaggaac ttccttctgg 540
ggtattaagc ttctttcaan tggaagggaa aggttccang gccaaaggaa aaatggaagc 600
ccccaaccng atgggtttca ccctaantaa cctcaattgg aagggcttgg accaagaacc 660
cnggaaaggc nanccattgc acccttaaaa ncaaggaaag tggaccacct ttggggcttg 720
ncnttccntt ccgaaccagg ttgaaaangg gcttgaaaaa tggttgctta cccaaaaggg 780
cgnacnttaa tggcaccaat tattcctntg gaccnttttt aatanccttt ngn 833

<210> 454
<211> 737
<212> DNA
<213> Homo sapiens

<400> 454
gnggnnnntt ctaagttcct aatnctgggc tactngttct ttctgcaggn atcccatcga 60
ttcggcaaaa tcaatgtgga ctgaacataa atcacctgat ggaaggactt actactacaa 120
cactgaaacc aaacagtcta cctgggagaa accagatgat cttaaaacac ctgctgagca 180
actcttatct aaatgcccct ggaaggaatn caaatcagat tctggaagcc ttactattat 240
aattctcaaa acaaaagaat ctcgcttggg ccaacctaaa gaacttgagg atcttgaagc 300
aatgatcaaa gcttgaagaa agcagtaagc aagaagagtg caccacaaca tcaacagccc 360
cagtccctac aacagaaatt ccgaccacaa tgagcaccat ggctgctgcc cgaagcagca 420
gctgctgttg ttgcagcagc agcagcggca gcagcagcag cagctgcagc caatgctaat 480
gcttccactt ctgcttctaa tactgtcagt ggaactgttc cagttgttcc tgacctgaag 540
ttacttccat tggtgctact gntgtagata atgagaatac agtaactatt tcaactgagg 600
aacaagcaca acttactagt accccctgcta ttcaggatca aagtgtggaa agtatncagt 660
aatctggaga agaaacatnt taaccaggaa actgtanctg attttacttc caaaaaagaa 720
gaagaggaga gccacct 737

<210> 455
<211> 718
<212> DNA
<213> Homo sapiens

<400> 455
ggnnnnnntt tnnncngttn cntaaaannc tgggctactc gttctttctn cangnagccc 60
ntgcgatncg aattcggcac gaggatgagg agtgtttaat cattgataca gaatgtaaaa 120
ataatagtga tggaaagaca gctgttgtgg gttctaactt aagttccaga ccagctagtc 180
caaattcttc ctcaggacag gcttctgtag gaaaccagac taatactgct tgtagtcctg 240
aagagtcatg tgttttaaaa aaacctatca aacgagtata taaaaaattg atccagttgg 300
agagatttta aaaatgcagg atgagctctt aaagccaatt tccagaaaag taccagaatt 360
gcccttaatg aatttagaaa attctaaaca gccttctgtt tctgagcaat tgtctggtcc 420
ttcagactcc tctagttggc ccgaaatctg gatggccttc tgcatttcag aagccaaaag 480
gacgattgcc atatgaactt caggactatg ttgaagatac atcggaatac ctagctcctc 540
aggaaggaaa ttttggttat aagttattta gcctgcaaga cctgttgttc tcgtcgctgc 600
agtgtncaga ggatagagnc agaccacgtt ctaaaacnga gaaatcagaa gacatttnca 660
gttatgtctc caaaagtgag tntcagctgt atgagttgac tctgctgaaa gtgacttg 718

<210> 456
<211> 739
<212> DNA
<213> Homo sapiens

<400> 456
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ttcgcttggg aggctgagtc aggagaaatt gcttgagccc aggagatgga ggttgcagtg 120
agccaagatc atgccactgc actccagact gggcaacaga gggagactcc gtctcaaaaa 180
ctaaaaaaaa aaatncattt agtataccgg ggggtggggg ggagaaataa tgttatttcc 240
tatgcgaaat gacgtgtatc cctgtaccca tgggtaaatg taaatatact gtgtctcttt 300
tgggagagcc ttttagtaga ggagtcttat atgaagtctc tcataagtag ttcacttgag 360
ttttgcagtt tgaaatctta aaggagcttt aattgacatt tattatacca attaagcttg 420
gaatggggca atggatgcat ttccaaaacg tgtgaaagcc taacagctta tattgctgaa 480
tgagaatctc ctgggtgtaa tttancactt agggaactgc gtgaacactc ccagccatta 540
tgatgctggt accagcttta ntgtntaaat gccatganta ttctttctgn tctgttttgt 600
gctctcttgg tncatttatt ttaccottta cngaataatt tcttgtaaaa tccntaaaaa 660
tntttggcat ttaaaagtcc nntcttggan tnaananann nnnaanaaaa ancttncccc 720
tttanaactt tngngggct 739

<210> 457
<211> 743
<212> DNA
<213> Homo sapiens

<400> 457
gtgnnntnnt tctnnngttt ccaattantc tgggngctcg ttctttctcn anncnnnnan 60
tggttgncga attcggcacg aggnnanagg gnagctacat gnntnaccnt nttngnnctc 120
tcagccangc tcnnctnnnn ctggtcctac tgctacatag aacacttgtt ntncnnggna 180
actnntntat gtnnccnnga ntctctgnna ctngtttaaa tgctanttga taacaggcta 240
tgcaaggnct gnaagtggan agcgtcatca ttcatcatnc ntnttanctn gantnnntgt 300
atcctacatg ctttgattgg taaatgngcn tcagactggg actctcaata aatgnatata 360
ganganсttg ctgtggaaan ctgtcctctc ntatctntnc atgngnaant tccactncag 420
tntgaactcc aaatgcnntn atnggnganc cctncttgta tagtggtgtc cattccaanc 480
tgcnagggnc tagaaaccgt cggctntngg aaacnatggt gnnagttgan ctggtacang 540
cngttntcac ctgcanctac cataaaatgg gnttacccaa gctttatcat ggaatggnta 600
taaaaaacgc attnattgng cctttntaan cccattatnt gttnaatttn acttatggtt 660

ccccccattn aaattatnca attgggnann gangcttcna gtcnccatnt ttnaatggnn 720
ttnncaaaaa aacgnttttt ttt 743

<210> 458
<211> 906
<212> DNA
<213> Homo sapiens

<400> 458
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ttggttaggn gctcgnnctn tctccacnna gnnnngcggt gcgaattcgg cacgaggctg 120
aatcaaggat cacaaactnc acatttngca cnttggtctn cacatncntg gttngggcag 180
tcncagtnaa catggctntg gaaactnatn ttngnctngc ntcaaccatc tcgttcccng 240
gggacccann ntccnnnatc ncgnnttncc tcgnnnatng gagngctnct tngnccannn 300
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nnnnnngccc tnntncctna tggnnngctn catgncccat nnnnnnggnn ancaataann 420
naaanggtct nttcccncga nncccnnnnn ccnctaacan ngnacctcgc aaagggcccc 480
aggcnttnnc tngnaaacca nnttngccaa nggtanttca aaggnngcct tngggacctc 540
ccnannnngc cntggnnnta ccccgggnaa anggtngnaa acccnnccnn ngntgccnnn 600
cccggncnng gaaanaaatt tccnnggnac ccagnntncc nccgnaannn anantannnc 660
ccancccnaa cnttnngccc ncanccnttn gnnnntgnan tcnncnnncc ctttnnnntn 720
nccaanncgg ccnggnnacn nncttnnacc tntttncncn naanngacnc caanntcctn 780
nannaaaggg nggnnnnnnn nnncncttncc nnnggnagcc cnnnnnncct nncntnncnn 840
aaaaattcnn cnntgnancn cccctnnnnt nangngnccc natnnnnnnn nnngnaaanc 900
nnaccc 906

<210> 459
<211> 765
<212> DNA
<213> Homo sapiens

<400> 459
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ctaggngctc gntctngctc cacgcagncn gggcgtgggc gaattcggca cgagcttctg 120
ttgattggtt tgtttaaagt acctaagtac taccctttga ctccctacca aaagttcttt 180
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cataaaatag tggtagcagc ttatttctta agtncttnat tattggggct ttaccattca 300
ggtcttatct ttaaccctta tttactcagt tttccatctg aatgatccta tctctaaatn 360
aaggatttaa taaatgctgc aaattgtcca ctttgcaaat ngtccaaaag ctttagtttt 420
ggaccttgng aacttttttt ttaataacac attatttggg cccggtcgtg gtggctcaag 480
cctgtaatcg cagcactttg gaatgcctag gcagacagat cacttaangc ctggagttcg 540
agaccagcct ggccaatgtg gtgaagacct ccggttctat tactaaaaat nctaaaaaat 600
tancaaggca tggnggtgca cgcctgnaat ctcagctact tgagangcaa atcnggagaa 660
atgcttgacc ngggangcan anatganccn anattgcacc actgcattcc acctggggan 720
nanantgaga anctggctca aaacccaaaa acccaaaaaa aaaan 765

<210> 460
<211> 677
<212> DNA
<213> Homo sapiens

<400> 460
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cctgaaacct ggctgatggg agaggtctca ttttgtgtct gagaatgtcc aggttgtctg 120
cagaccacag cactgatttc ccattagcag ttattatttc ctggccattt cttcctgaag 180
gttttgtggt taaactccct gtcctcaata ttttatcagc agtagggctg tcattcttct 240
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aaacggttcc tatccaatcg aacacaaaaa cgggtattga gaaggaattg gcagggctca 360
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gaacttctaa ctgaccactc acccccaccc actcttatgc agtctgttca ttcctgaaaa 480
caccactttc atccctcctg cacacaaccc atgagggatt gctacttcct ataagattcc 540
tcagtgagcc ttatagagtt gctgcgagaa ttacatttgg tcatgatgtc aagtgtctgg 600
tatgtagctn atgcttattg aacacatagt aatttattgg aataattgnc atgatcactg 660
gatgagaata tagcccn 677

<210> 461
<211> 787
<212> DNA
<213> Homo sapiens

<400> 461
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ntgggnganc gcnncgcccc ancagnaagg cgggggaang cggcacgagg acatcatcnn 120
cttattctag taagagaaag tacacagatt caactttaga gaggacnggg gggnnnncng 180
gagcnaaatc aaggaaggan tatcacgngg ccncccnnga atataannnn gaagctgnga 240
acagnaccat cagnaacann nnatggacag ctctgatggg gnnnatacca cggcactctn 300
cnnaccnnng gnggaagcna tccggagnna tgactgangn gnaaagnggn nnactgnnag 360
aanccnggng ngctaggann ctgggagagn cactttcang aagnnaccng gcgangagnc 420
atcanaagaa cccgganaag ngagaagacn ggaaaaagnn cncancgnac ngagcccagn 480
nannnncnct gagccanggg ctncgaaang ccccaccnga agcnccatca canggnacaa 540
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nngcccncnc gcccaaagaa nacnggacng cnggcncnna ncanaaggag cncnanggcc 660
cnnggnaang aaactncnag nagcccaanc ccaaaggccc cnanggannn ccnncaaggg 720
gaaaacanna nncacccaag gggcctgggc naanaaggcn ncccacncng gcccnccnnc 780
nnnaccg 787

<210> 462
<211> 747
<212> DNA
<213> Homo sapiens

<400> 462
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ccannnagnn nntgcgttng cgaattcggc acgagcctca gccccacacc agctctattt 120
caggggtgag agtcagagag cactgcaata tgtgcttcat gggatttcga ttcgaagatc 180
ctagaccagg gagacactgt gagccaggga tacaacaaaa tactaggtaa gtcactgcag 240
accgacctcc ctgcagtttg ggaaagaagc tgggtttgtg gagaatcaga gcatcttgac 300
atgactgctg acctaaagat ccctggcatt ggccagggat cctgtggaac ctcttctagt 360
tcaggggtgt gagcattaga ctgccagttg tctagtgaca tctgatgctt gctgtgaact 420
tttaagatcc ccgaatcctg agcacctcaa tctttaattg ccctgtattc cgaagggtaa 480
tataatttat ctggatggaa attttaaaga tgaatccccc ttttttcttt tctnctctct 540
tttctttcct tctccctttc ttctttgcct tctaaatata ctgaaatgat ttanatatgt 600

gtcaccaatt aatgatcttt tattcaatct aagaaatggn ttaagttttt ctctttagct 660
ctatggcatt tcactcaagt gggacagggg aaaaagtaan tgccatnggc tccaaagaat 720
tnntttatgt tttagctatt taaaaaa 747

<210> 463
<211> 750
<212> DNA
<213> Homo sapiens

<400> 463
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gtggaggtga tcagccggca cttgcccgcc ttggggctta agaaccgggg caagggcgtc 180
cgagccgtgt tgagcctctg tcagcagact tccaggagtc agccgccggt ccgagccttc 240
ctgctcatct ccaccctgaa ggacaagcgc gggacccgct atgagctaag ggagaacatt 300
gagcaattct tcaccaaatt tgtagatgag gggaaagcca ctgttcggtt aaaggagcct 360
cctgtggata tctgtctaag taaggattcc atatggctct catatcattc cattccatct 420
ctgccaagat ttggataccg caaaaatttg tgttngngga agattctgnc tgaactcttt 480
cattcaagga actactacca tgaatctgca ttctgntgcc cacactgagg ncttagtaga 540
taattgggtg gtctgaaaca cctattatct cttatntctg gtctctangc tggnatgtta 600
attcctctga aatgntaaaa gtaatgggtg anaccngaaa aagaaatttc aatnacagat 660
caanntgggg ngcatgtatn attttcaagc gtcaaaatgg aataagggaa gantnctgga 720
tacctgcttg gaaaaggaag natgtgtatn 750

<210> 464
<211> 748
<212> DNA
<213> Homo sapiens

<400> 464
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tacgcagnnc ccatcgattc gaattcggca cgaggccggc cggcgacgct ggcgacgctt 120
tcgcccctga ggtagtttgg cgaccgcgaa gaaggaaaaa gggcgggcgg gcggctgtcc 180
tctcaccgtc ctcaccccgc gaggcccggc ccgctcctcc gtcgtggatt tcgcggcgat 240
ccccccggca gctctttgca aagctgcttg aaacttctcc caaactcggc atggatacga 300
ctgcggcggc ggcgctgcct gcttttgtgg cgctcttgct cctctctcct tggcctctcc 360
tgggatcggc ccaaggccag ttctccgcag gttggntgct tctttcgttc tctcctctgg 420
gggctctgaa gtttcaccag gtggacgctg gggagcgggc tcccgagcac ttgtctacct 480
nccgccagtc ctgacaactt ttctggccaa cctacccagc ttcgcttggc tggcgagcgc 540
atctgctgct ggggttcgcg gtgcaaatgg agacgcagtg gtggccagag ggtgatggag 600
aagacgggaa aagcgacagc cacgctnctg gcttgaagcc gcaggacgca aataacttac 660
tttggacctg acagttctac gttgntgtgg angccctgtt tcctggaaat aaaactcaaa 720
atggtggttt tttggaaaaa aaaaaaat 748

<210> 465
<211> 863
<212> DNA
<213> Homo sapiens

<400> 465
gggnnnnnnn aanggnnnnn ggnnnnngtc ccgttccaan gaccnngaga tcgnngncgc 60

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accggcgtga tgagctgccg gtgtttgaac gcngcctatg cngggacttt cccggcanan     180
nggcnngaan atggccncca tncaggaagc cgcccagaac ctcctnggnn acacnacttn     240
agngccttcn agtccgntgg nacccggncc aagccccggc aancnctgcc ccgggtcncc     300
gttcccaagg ccaaccagcc ctgggnaccc ccggggagcc gaaacnctgg ggctnggana     360
ccgngantga gagncncact tttcnntgta nacacgggcc cagganacan ctntgctcgt     420
ggccccgggg naaannnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     840
nnnnnnnnnn nnnnnnnnnn ncc                                              863

      <210> 466
      <211> 713
      <212> DNA
      <213> Homo sapiens

      <400> 466
ngtctttcga gcntggngnt cgttctngct cnannanatt ggttgnggga attcggcacg      60
agcctcagcc ccacaccagc tctatttcag gggtgagagt cagagagcac tgcaatatgt     120
gcntcatggg atttcgattc gaagatccta gaccagggag acactgtgag ccagggatac     180
aacaaaatac taggtaagtc actgcagacc gacctccctg cagtttggga aagaagctgg     240
gtttgtggag aatcagagca tcttgacatg actgctgacc taaagatccc tggcattggc     300
cagggatcct gtggaacctc ttctagttca ggggtgtgag cattagactg ccagttgtct     360
agtgacatct gatgcttgct gtgaactttt aagatccccg aatcctgagc acctcaatct     420
ttaattgccc tgtattccga agggtaatat aatttatctg gatggaaatt ttaaagatga     480
atccccettt tttcttttct tctctctttt ctttccttct ccctttcttc tttgccttct     540
aaatatactg aaatgattta gatatgtgtc aacaattaat gatcttttat caatctaaga     600
aaatggttta attttttctc tttactctat ggcanttcac tcaantggac aggggaaaaa     660
agtaattgcc atgggcttcc aaaagaattg ntttatgntt tagctatttn aaa            713

      <210> 467
      <211> 732
      <212> DNA
      <213> Homo sapiens

      <400> 467
gnnnggtnnt ctaatncttg nnnnnnnntc ncccttctaa gccntggnct cgnctnnccn      60
acnancnggc ttncgaattc ggcacgaggc gagatgaact acactgtgag gtggaggtga     120
tcagccggca cttgcccgcc ttggggctta ngaaccgggg caagggcgtc cgagccgtgt     180
tgagcctctg tcagcagact tccaggagtc agccgccggt ccgagccttc ctgctcatct     240
ccaccctgaa ggacaagcgc gggacccgct atgagctaag ggagaacatt gagcaattct     300
tcaccaaatt tgtagatgag gggaaagcca ctgttcggtt aaaggagcct cctgtggata     360
tctgtctaag taaggattcc atatggctct catatcattc cattccatct ctgccaagat     420
ttggataccg caaaaatttg tgtttgtgga agattctgtc tgaactcttt cattcaagga     480
actactacca tgaatctgca ttctgntgcc cacactgtgg tcttagtaga taatttgggt     540
ggtctgaagc acctattatc tcttatttct ggtctctagg ctggtatgtt aatcctctga     600
tatgttaaaa gtaatgggtg agaccngaaa aagaaatttc aatacngatc aantttgggg     660
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tgcatgttga atttgcaacc tcaaattgga gtaagggaan attctggata cttgctggaa 720
aggaggaatg tn 732

<210> 468
<211> 748
<212> DNA
<213> Homo sapiens

<400> 468
gnnagnnttc taatngcttg tnnnnnnnna gacgttctaa nnctttggcn atcgttnttt 60
ctncagnann ccntcgattc gaattcggca cgaggccggc cggcgacgct ggcgacgctt 120
tcgcccctga ggtagtttgg cgaccgcgaa gaaggaaaaa gggcgggcgg gcggctgtcc 180
tctcaccgtc ctcaccccgc gaggcccggc ccgctcctnc gtcgtggatt tcgcggcgat 240
ccccccggca gctctttgca aagctgcttg aaacttctcc caaactcggc atggatacga 300
ctgcggcggc ggcgctgcct gcttttgtgg cgctcttgct cctctctcct tggcctctcc 360
tgggatcggc ccaaggccag ttctccgcag gttggttgct tctttcgttc tctcctctgg 420
gggctctgaa gtttcaccag gtggacgctg ggagcgggc tcccgagcac ttgtctacct 480
tccgccagtc ctgacaactt ttctggccaa cctacccagc ttcgcttggc tggcgagcgc 540
atctgctgct ggggttcgcg gtgcagatgg agacgcantg gtggccagag ggtgatggag 600
aagacgggaa aaagcgacag ccaagctcct ggctgaaacc gcaaggacgc aaaataactt 660
actttgnacc tgacagtttc tnacgtttgt tgtggangcc ctgtttcctg ggaaataaac 720
tcaaattggt ggtttcttgg aaaaaaaa 748

<210> 469
<211> 776
<212> DNA
<213> Homo sapiens

<400> 469
gggngntcta atgcttgnnn tgattctccg tctataacng gntaatnctt ggncctacna 60
aaaggctang ngaattcggc acgagacctg taccgcctgg ccactggctg tcaccggcgt 120
gatgagctgc cggtgtttga acgcaaccta tgctggactc tcccggcaga ctgcctggat 180
atggtcgcca tgcaggaagc cgcccagcac ctcctcggca cacacgactt cagcgccttc 240
cantccgctg gcagcccggt gccgagcccc gtgcgaacgc tgcgccgggt ctccgtttcc 300
ccaggccaag ccagcccctt ggtcaccccc gaggagagca ggaagctgcg gttctggaac 360
ctggagtttg agagccagtc tttcctgtat agacaggtac ngaggatgac ngctgtgctg 420
gtggccgtgg ggcttnaann tnannnnnnn nnnccnnnac caantctncn nannannnnn 480
ccnacnnnta aaantnncnn ncnnnnncan nnnnnnnnnc cnnnnanncc nnnncttnnn 540
naancnnnnn nnnnnnnanc nnnncancna nnnnnnnnna nnncnnncnn nnnnnnnncn 600
nnnnnnnnnn nannccnnnn nnnnantnnn nnannnnnnn nnnnnnnnnn aaannnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nncncnnnnn nnnnnnncnn nnnnnnnnnn 720
ccnnnnnnnn nnnnnccnnn nnnnnntnnn nnnnnnnntn nnnnnnnnnn nnnnnc 776

<210> 470
<211> 765
<212> DNA
<213> Homo sapiens

<400> 470
tatgnntttn ctaaaatncn tgggcaanac gtcctcnctt tcctaanagn ttnggcanaa 60
cccttggcaa nacgccngtn acccanacnc agnnnggccg tggcgggcga gcgggcaaca 120

gctcttgagg agtgagactg cnggagatnt gggccgtgcc aaagagatgg atgagactgg 180
tgctgagttc atcaagagga ccatcttgaa aatccccatg aatgaactga caacaatcct 240
gaaggcctgg gatttttgt ctgaaaatca actgcagact gtaaatttcc gacagagaaa 300
ggaatctgta gttcagcact tgatccatct gtgtgaggaa aagcgtgcaa gtatcagtga 360
tgctgccctg ttagacatca tttatatgca atttcatcag caccagaaag tttgggatgt 420
ttntcagatg agtaaaggac caggtgaaga tgttgacctt tttgatatga aacantttaa 480
aaattcgttc aagaaaattc ttcanagagc attaaaaaat gtgacagtca gcttcagaga 540
aactgangag aatgcannct ggattccaat tgcccgggga acacagtaca caaagcccaa 600
ccagtcaaac ctacctacgn gggggactac tccagactcc cgnacncctt cacgtcctcc 660
tccatgctga ggcgcaatca ccgcttctgg gncaagaagt tanaaacnct gggaaaaact 720
acctncgaca agaaggggan catttanatt tacccnaaat gaana 765

<210> 471
<211> 820
<212> DNA
<213> Homo sapiens

<400> 471
cnnnnngggn nnngnggcgn cntccnaaan ccggggcgac agngccnnng ttccaacaga 60
ccnggngngc cgncngngcc ccanacagca ngggnggggc nnnggggnnn cnncgncnnn 120
cnnancnaca aagaactcaa caagaaaaaa acnaacccca caagcgggca aaggacgnga 180
acagacantn cccaaaagaa gacatacaag caaccnaaaa taatcnaaaa taagnnncaa 240
aaagaaaaaa ngcnagacag agnngngana gnactnagna aaaagngana tctagcggcn 300
annagnangn nngnnnacgg ncngnnncna agaaanagnc nctggnnccc aagcnggagn 360
acagcggcgc aagcnnggcn cactgcaacc gcgaacnccc gggctcaagc gaaccnccag 420
cctcagcctc ccaagnagcn gnnaaaggca ngcaccacca cacccgacna aaatancngc 480
nancaanaac ananaanggc nccccngngc nnanncagga aanaaacacn cnnangcnnc 540
ngaaaanaan naancncncn cnnnacaaaa aaacnnnagc cnnagaacaa nnnnggaggc 600
ggaanacggn nnancccgac anganaanga nacnanngan gganganngg gaccaaaccn 660
cancccggga anggcnnngn aaaaaaaang ccnnnaaann gggggaaaan ncggngnang 720
ccnaaagggc cnnaaanggg gaaacccnan naaaangccg ggcanannan aaccnagcnn 780
nancnanccn nccaangggg nannnccncn nncnaggccg 820

<210> 472
<211> 738
<212> DNA
<213> Homo sapiens

<400> 472
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ntcgttcttt ctccacnnac nnngcnntnc gaattcggca cgaggtcaca ganatnaaag 120
tccaatcata ggggctggnc cnacntctnt gctnntccct gcangantca tangatcagn 180
nanaccgtgc gnntttgnaa gcntttcaaa tgtgntacca tcgngttact tncnnnggca 240
cctgntgann tnggttgnac tnnncnggat nctccaaanc caccnnnncn atgggntnng 300
tgngcatgng ntggnncann nacagannna ganactttaa ngaannngnt tntgcaaccn 360
tnggnnctag caancntgan antnccaggg nnggccacna agctgaaaat nnatgttana 420
ncnnatgntg naatctctag natgacttcc ncannnancn aaactnangc anggctgcna 480
tgttagaanc tanaggccna atttcttntc natgnaacca ntntatgctt ttaagaccnt 540
caactgtnnc natgaagccc atntacatna ttncggtaat anggctatnc ttaaannnaa 600
ctgctgaaaa tnatgatnca nctacgaaat cctnncancc ncatntggct naatcattac 660
caaccatttg acaccnncat ngnctaccca cntgcattnc catgaccnan tccantgcca 720

cccgcncaga tntacctt 738

<210> 473
<211> 752
<212> DNA
<213> Homo sapiens

<400> 473
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ggcgctcgtt ctntctncac ncagnnnntg cggtncgaat tcggcacgag gtccttttga 120
accaccccaa agaactcaac atggcaaagc aaatggtaaa agcttcccga ctgttctact 180
ttgggtccgc gcgaagccca ctcacgtgtg atctgtgttg cccctgggag gcccggggcg 240
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ccctgagctt gttcggacgt atggtccaaa ttcagattaa ggtggtcacc caacccgaga 360
tgtcaggaaa ggccttctgc agagaaaatg tccccccacc cgccatctgc agccaggtgt 420
gtgccacacg gcagccttcc cgaaacatag tatggatttt aaaaatgtgt ntatttttgg 480
ttctcaacca ctttataacg tattttttaa tttattttgt aatgtcttgt tttgaagtat 540
tgctgctatc cttggtatcc ttcccactgg ttttatcact ganttatttt gngaaagttg 600
ncactaatgt tctatgtcaa aatcaaaagt atttaatgaa atactanntc tatttaatgt 660
ggntatggaa ccagctggaa acacaaaaca aacagtgatt gacancaagc tgggcccaag 720
agncaggtca ttttgnacat atgccaataa ac 752

<210> 474
<211> 752
<212> DNA
<213> Homo sapiens

<400> 474
ttgcanacnn aatanttgct gtaaaagtcc cnnctttttn ccctttctaa tgnttgngcg 60
ctcgntctnt ctccacnagn nnntgcgttn cgaattcggn tctnagccca tgccgggatc 120
ttcccacacc cgtcctcaca gatccagccc cagcccctgt cttcccaggc catctctcag 180
cagcacctgc aggatgcggg cacccgggag tggagccctc agaacgcatc catgtcggag 240
tctctctcca tcccagcttc cctgaacgac gcggctttgg ctcagatgaa cagtgaggtg 300
cagctcctga ctgaaaaggc cctgatggag cttgggggtg ggaagccgct tccgcacccc 360
cgggcgtggt tcgtctcctt ggatggcagg tccaacgctc acgttagaca ttcatacatt 420
gatctccaaa gagctggaag gaacggaagt aatgatgcca gtttggactc tggcgtagat 480
atgaatgaac caaaatcanc ccggaaggga angggagatg ctttgtctct gcagcagaac 540
tacccgnccg tccaagagca ccancagaaa gancctcanc cccagacagc acggnctaca 600
cgcanctcgt gnacctggat gacntggaac anaatggtan cnaatgtggg accacngnct 660
tgtancccna ggacaaggcc ctncnangct tgntggangg gtcnantcng anaaatggng 720
gccactgccc aacccgcang aaganaacaa nn 752

<210> 475
<211> 742
<212> DNA
<213> Homo sapiens

<400> 475
gntttctntt aatncttttn naaangcgnn ntttaccntt ctangnntgn gnctcgttct 60
ttcccacnna nnnnncggtn cgaattcggc ncgaggtgaa acagaaagtg gagatgcttt 120
ccttgacctg aagaagcctc ctgcctccaa atgcccccat cgctatacaa aagaagaact 180

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cttggatata aaagaactcc cccattccaa acagagcctt catgcctttc tgaaaaatat     240
gacagtgatg gtgtctggga ccctgagaag tggcatgcct ctctctaccc agcttcaggg     300
cggagctcac cagtggaaag tctgaagaaa gagttggata cagaccggcc ttccctggtg     360
cgcaggatag tagatccacg agagcgtgtg aaagaagatg acttanatgt tgttctcagc     420
cctcagagac ngagctttgg agggggctgc cacgtgacag ccgctgtcag ctcccggcgc     480
tcangaagtc cattagagaa agatagtgat gggcttcgtc tgcttggtgg acgtaggatt     540
ggcagtggga ggataatctc tgcccggacc tttgagaagg atcaccgctt aacgataagg     600
acctgcggga cttgagagac agagaccnan anaaggactt caaggacaac gtttcangan     660
anaanttttg gagaaagtaa ncntgtcttt tggtgancgt anaaanaaat gattcttacn     720
cnnaanaaga acccgaatgg tt                                              742
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<210> 476
<211> 1122
<212> DNA
<213> Homo sapiens

<400> 476

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ggctctcgtt ctttctncac gcagcnnngc gnnncgaatt cggcacgagc ctgcagccac     120
taatgcattg tgtatgataa caaaaactct ggtatgacac attttctgng atcattgnta     180
attagtgaca tagtaacatc tgtagcagct ggttagtaaa cctcatgtgg gggtggggtg     240
ggggtgtatn cctngnggga nggnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     300
nnnnnnnnnn annnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     420
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1080
nnnnnnnnnn annnnnnnnn nnnnnnnnnn nnnnnnnnnn nc                        1122
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<210> 477
<211> 747
<212> DNA
<213> Homo sapiens

<400> 477

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gnngtgcctt tgaaannccn tttgnnnnng nggcccttct aatgctnttn cgntcgnggg      60
gtcgaactcg ccccacncng cnaggcgggg gctncaagcg attctaaacc acctatgagt     120
atttctttta gggctcactt aaatacatgt ntgngnntac tgggggctag ccngaataat     180
tttagatctg atcaggtngn ngctnaaatt ngaaaaanac cnnntngatg cttaaagaat     240
tngcntccat ttttgagtct aaatctttta aaatntactg ngatccacat ctagngaaat     300
gtcngtgtca anatattctn gatnatcgct naaatccnca ttaatactcn ttnggggtnn     360
nnnatagngg aacttcntag nnntncnaaa agcacatngn cttcctgnct ccgctgctcc     420
cacagnnggt nttgnaactg ggnaaatcag nnnnnngata gcgngngnnt ntnaganaaa     480
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ntngatncac acatncttnn nnctcagncn ncacatngat tgaacactct ggccaagatg 540
ctgnggngga tgangttgga gttcgannga agaagccngc gctggcctgg cttgnaagac 600
ccnngncttt cccntnccct cnctngaaag ctgcccngac ngaggccnaa ngnaaatggn 660
tgannngnnc gtcnngcccn cttcngncnc ttngaaccnn nnagnggnnc tnnnngnacc 720
cnnngnnntn cgngnaaccg nnccngc 747

<210> 478
<211> 746
<212> DNA
<213> Homo sapiens

<400> 478
gnnnnnngcg cgnccttcta atgcttcnta attnnctngg atactcgttc tttctncagg 60
natcnnntgc gnttcgcaag gagnagagtg atagnaattg gcagtgaaat atacgaacca 120
ccctcctgcc ctctgggttc acaatacgtg tacacttgac tgtgaagtgg ctgtgagagt 180
gggtggagag ttcttctttg accctcagcc tgcggatgcc tctagaaacc tcgtgttgat 240
tgcaggagga gtcggaatta accctctgct ttccatcctg cggcacgcag cagatctcct 300
cagagagcag gcaaacaaaa gaaatggata tgagatagga acaataaaac tattctacag 360
tgcaaaaaat accagcgaac tcctgtttaa gaaaaatatc cttgatttag taaatgaatt 420
tcctgagaag attgcatgca gtttgcatgt tacaaaacag actacacaaa tcaatgcgga 480
actcaagcca tacatcacgg aaggaagaat aacggagaag gagataagag atcatatttc 540
aaaagagact ttgttctata tttgtggccc acctccaatg acagactttt tctccaagca 600
actggaaaac aaccatgtac ccaaagaaca catttgcttt gagaagtggt ggtaggaggc 660
aagaccaaag gcaggaaaaa attaangagg tgagatctac tcaaggagag ctcaaaaaaa 720
aaaaaaaaaa actngggccc tttaga 746

<210> 479
<211> 750
<212> DNA
<213> Homo sapiens

<400> 479
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ggatcccntg cgattcgaat tcggcacgag ggtagactgg ctagggatcc tggacccagg 120
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gagtctggaa agtctgagat cagggttcca gcaggattga gttctttggt gaacatnctc 600
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tttaccttnc caaanggntt ccattttccn 750

<210> 480
<211> 714
<212> DNA
<213> Homo sapiens

<400> 480
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gctaggcttg ngaattcggc acgagataac acacatcaca gtatgctctc agaaatttct 120
ttatttgaac cctataccaa tatctgntga tcaatgacca tttttgctca gcatggagaa 180
acagtgccct gcatgaaggg tagtgagaat aaaaaggatc ttaccacctt tatcatgagg 240
gtggctttgc tctctccatt ccaagttgtt ctctgttcta gaaagcagat gtagtagaca 300
tctactgttt ttgcctaaac agaatccctt tttccttttt ttgttaaaag tactcatccc 360
taatattaca ttgttctgga aggactgaaa ataacagaac tcagcaccat gatcggaccg 420
ggacaatcag attatttcat tcctcancaa acggagatcg atccgaaaag tggaaatatg 480
agctcttctt tggtgttggc atatggaccc tgagagaaag aactttaatt ttttctcttg 540
gactgcaata aagtatagct gcctaaaata cgtttcctga ccttggangt ttgnccacaa 600
tcggtgaaat aaangcaaga cgtacacttg gatgaaaaaa aaannnnnnn naaaaaaaac 660
tcgaccttta nactatnnga gtcgatacnt aatcngactg atagatcatt gnta 714

<210> 481
<211> 742
<212> DNA
<213> Homo sapiens

<400> 481
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nactcgttct ttctncacgc acccatcgnn ncgaattcgg cacgaggcat gaaaggagtc 120
ggaagcggaa gcggtagccc ggacggtgct gtggtgcaag ggcttgtgga aaaattggag 180
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gataggtctt atcagcacag tctccgcctc ctggattcag tgtctcggct tcagggagtc 300
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tcaagcctgg taaccaggca tatggatgag ttcaagcgta cacagaagaa tctgggaaac 420
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cagctgcttt cccgtgccaa tcttgctaaa agcagancac aagaagcact gagtatgggc 540
aatgccactt tttatgaagt tgagagcatc cttaaaaacc tcagagagtt tgacctgcag 600
gtggacaaca gaaaacagaa ctgaagaacc atgaagagac tctnctacat caccagaagg 660
ttcagancca atgacaagac ccancaagca naagagccct ggggagccct ctgctgatcc 720
caaanggcaa aaaatggggc cn 742

<210> 482
<211> 752
<212> DNA
<213> Homo sapiens

<400> 482
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ngctcttgtt ctttntgcag gatcccatcg attcgaattc ggcacgaggc caagcctcgg 120
cctccactgc acctgctgcg gagtggcacc tttgcctgca aggccctcta ccccatggcc 180
cagtgtcatc tcagcagggt ctttggccac tcaggaggcc cttgtggtgg gttgctcagt 240
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tccagaactc aggatacctc agggataggt cacagccaag agtacaaagg aatcttcagt 420
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agancagcct ggcaacacag tgagtgagac cctgtctcta tttaagaaaa aaattattaa 660

gaaattttat taaaaaagga agaatcagga aaccaaagtc aacccaact taaccctcaa 720
tgaaccagcc ctaacacaga tgangggatt tg 752

<210> 483
<211> 849
<212> DNA
<213> Homo sapiens

<400> 483
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gtaacatcng gaaaaaacag ctnngncctg ggngaaaaag gatgccaaaa tngcctggaa 180
aagagcagng gagaggagtc cgggagatgn gngatgcatc gggacgcanc atngntnaac 240
attcactggg tctgccaaaa atgtggattt gngggctgct tagatngtta caaggcaaaa 300
ggaaaggaaa gagttctaga gataaaagaa ctatatgctt ggatgaagtg tgtgaaggga 360
cagcctcatg atcaccaaca tttaatgccc aacccaaaat tataccnggt tctgntttga 420
cagacttcta gatgccatgc acactcttag ggaaaaaata ttgggattaa ancccatngg 480
cattggacta acaaacagga atttacaagg tnggaaantt ttncnaccaa tgaaaggggg 540
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gccctgagtc ttaancagca aaaanactcc tcccgaancc tgnagaaaaa aggggggca 660
gccaggcccn naaanggaan gtnaggcccn agatnaacaa ngtnacctcc ncccagnaaa 720
ccccannccc caactggnac cngggnaacc cacaacnttt gcngaagncc aaaaaagncc 780
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nggcccncc 849

<210> 484
<211> 1098
<212> DNA
<213> Homo sapiens

<400> 484
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cangggatcc ccatntttat ntcggacatt ttcgggccac cggaaggggc cgggggcccc 120
cgggccncca ggnccgggna aaggcccccc ttgggcggcc cccggncggc cccaatgggt 180
tccaaaaagg gaaaaaaaaa aaaggggggaa cctgggaagt tggcccanga aaangnaaaa 240
aaaggnaagn aaaccttccg ccaatgggaa tggggaaaaa taattttttc ttgaaaaacc 300
caaaaaagga atggttattt ttcaaattta aaaaaggaac nttgggaaga aagaattggc 360
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tctgagggaa gtcaaaagca tgcaagccta cagaaaagca tttgagaaag ctaaaattgg 600
ccgatgttga aacggaagag cgaaccaagg ctntgcaaaa agagcttttc tttcactttc 660
gagaccaaag gggaaccagc tnnaagggcn agaaaagttn gaaaaaaatt ccaaaggaac 720
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ngaaactttt ttngggaatt ccccagaaag aacttttgac cttccnttng acctnaaaaa 1020
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naaccttttn tncttacc 1098

<210> 485
<211> 798
<212> DNA
<213> Homo sapiens

<400> 485
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attnggcacg aggaaaggtg gcgcgcttct cacggctgag ttgctgcgcc ttgcagacgg 120
aagctcccca caggcagagc tgcttggatg tgtgagtcat gaaccagaga agccccgctc 180
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gacaaatgca tgtctgattg cttcctctgc cctattgntt atgtgaaaat gcagattcac 480
tgagccagac taaggcatca gtgactgttc ctctacctgc ctctcacatg gagattgtgt 540
attcagtgaa aggctgatca aagacccaaa ggaatgcaac agtttatctc ttatctacct 600
atgacctgcg aactggccaa caacccagtt gttgncgcct tttcagacag aaccagtgtc 660
atcttacacg tattnaaatg gatgtcctgg ngtctnccta atatgtattc aaaagcaagc 720
tggggcctng accacccttn ggcacatatt cctcanggac atcattcctg angctgtgtc 780
actggcatgt ccttaanc 798

<210> 486
<211> 785
<212> DNA
<213> Homo sapiens

<400> 486
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tcgctgacaa cttgattggg ttctccttca ggtttgaagc gccctcgaga agtgtctaaa 120
ggagacagtt gatagccaaa caacagtttt ggattcactg actgattatg aaagaagcag 180
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ttggacttct cagcctccat attcatgaac taagtttttg gaatccttag gcttccacgt 300
gtggaaagcc tgagctaacc tactggagga tgagccatca cctggagcag attcaggcca 360
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ccttgaacat tcagcacaaa gacaaaacag accagaccag aagagtccca cagaataggg 480
gaaactattc agagaaaact taagccacta agttttatgg tgttttgttc tgtagcagaa 540
gcataggcat actgacaata caaaccgaaa tccttctaac gtagtggacc ttttcangcc 600
agcatttttt ccttgaaaac ctggagcatg tatccatctt atagcagaga tcactttcac 660
aatggttggg ctcttggatt tgaattgatg atgtaatgag ccctctttnc ngattgnaac 720
ttaattactc tgggnatttg ntggattccc aaccttctaa tatttacttt tcctctttan 780
taanc 785

<210> 487
<211> 797
<212> DNA
<213> Homo sapiens

<400> 487
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cgaattcggc acgagnnngg actaccttnc aaaaccnggt ngggaagcnt gttacagaan 120
tgatntctan tcccctgnat tctggatgct gcagaccaac acctgccnac aanacncana 180

cacacacann caancantat catgtaagac agnncgntna ntnnnnnatt ntnatncttn 240
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gananangac ganantctga atcttaagca tatgctccat cnttnnatat gctntggtgg 360
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tgggcttcaa gcatncttat ttnnaactcc ctgagtgatg ggtggataaa tcnaacattg 480
nctnagtggn ntcaagacaa ctttgntggt ggttttgntc acaatcatga aaatggttnn 540
gccagataaa tattttgata ttagntttcn tttttnatat anngcggtag gtttgaattg 600
nacnttnaaa tgnntngggt tgtnaagaca ntggnttnca atnnaattta tnacatgaat 660
tggngnctcc cctttggnga aaccttaaag aanttntgna tacttcttca taaaagggtg 720
tgngatttng naantttcgg gggttttnaa tttttnntga agcttatttc ntganaatnt 780
acttggntta ccaagcc 797

<210> 488
<211> 762
<212> DNA
<213> Homo sapiens

<400> 488
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ctcaggttaa tgctgaaaaa tcatccaaga cagttattgc aagagtttaa tttttgaaaa 120
ctggctactg ctctgtgttt acagacgtgt gcagttgtag gcatgtagct acaggacatt 180
tntanngggcc caggatcgtt ttttcccagg gcaagcagaa gagaaaatgt tgtatatgtc 240
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agagtatttt ccacaatgat gatgatttca gcagggatga cgtcatcatc acattcaggg 360
ctattttttc cccacaaacc caagggcagg ggccactctt agctaaatcc ctccccgtga 420
ctgcaataga accctctggg gagctcagga aggggtgtgc tgagttctat aatataagct 480
gccatatatt ttgtagacaa gtatggctcc tccgtatctc cctcttccct aggagaggag 540
tgtgaagcaa ggagcttaga taagacaccc cctcaaaccc attccctctt caggagacct 600
acccttcaca ggcacangtc ccccaaatga gaagtctgnt acccctcatt tcttnatctt 660
tttacttaaa ctcaagaggc agtgacaggn agtcaggggc aagacattac atttttcata 720
ctttcccaca tctgaaaaga tgacagggga aactgcaaag cc 762

<210> 489
<211> 822
<212> DNA
<213> Homo sapiens

<400> 489
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ttcgaattcg gcacgaggat tttcgaaact cttcagctac ttgccctttt ttatctgaaa 120
ccatcatacc ttctgaaaga aaaaagcata tcttcattga cataacagaa gtgagatggc 180
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aagccccaaa agataaacta gttgaaaaaa ctggcaaaat ctgtatacgt ggaaatttac 420
cangacagag actgaagaat aaagaaaatg agtttcattg ccagatcatg aaatccaaag 480
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ctggtacaaa gcacacatgt gtatacacat gggtcaagca gtgctggtct gtggctgcct 600
gtccagagga atgggaaata ttcctttgtc tttagcactt catttttcta aataaaaatc 660
anccaatatg tctaaaaaaa aantttnttn ataataaacc tngaagccct nttanaacct 720
tntnntggag gtcctnnttt accntatgat tcccggaact tggataagga atcccntttg 780

gattgganat tttgggccna aaacccncna nncttggaat cc 822

<210> 490
<211> 789
<212> DNA
<213> Homo sapiens

<400> 490
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accntgcang anggaanaan ggctggccnn cngntgtacn ctnaccgtcc taaccccgcg 180
aggtccaggn ccgctccttt cggngnggat tctcgcggaa natccctccg gcagctcttt 240
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tgctgctttt gtggagctct tgctcctcta tccttggcct ctcctgggat acggcccaag 360
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aaaaagcaac nnncaangct tttggctnaa agccgatang acncaaatta nttnctttgg 660
accttganaa tttcctcaan nnttttnagn anncnctttt ttncttggan aaanacttaa 720
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annaatnnt 789

<210> 491
<211> 790
<212> DNA
<213> Homo sapiens

<400> 491
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tngntngatc ccatcgattc gaattcggca cgaggnaaca aagaaggaat gtcttcctca 120
tgtttnggtc tatagaagac gttaaagaaa acttccagaa agtgggtttg aggcatgagc 180
caccacgcct ggccaaagga tttaatgaat taatggatgt acagtgctgg ggctgttatt 240
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cggtgagctg acatggtgcc actgcactcc ggcctgagtg acagagtgag actctgtctc 360
acaaaaaaaa taatgccctt taaataatga ataatagtga tagaaaatgt catttcttgg 420
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ttcatttgtt gaaagtttga caagtgaatg aagttcacat ctggaaatcg ttgaacattt 540
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gctttggaaa gtnaatgcca tcaacaatgg atacagaang acctggattt ggaataaggg 660
caaaaattta ttttgatggg gctgaattgc tctgccaggg agcattttgg gtattgagat 720
gaaaatggcc tctctttgag actgagctgc cacctggcaa attattgnct gcttaanggt 780
tctctttatn 790

<210> 492
<211> 804
<212> DNA
<213> Homo sapiens

<400> 492
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tgcaggaatc ccatcgattc gaattcggca cgaggtcctt ttgaaccacc ccaaagaact 120
caacatggca aagcaaatgg taaaagcttc ccgactgttc tactttgggt ccgcgcgaag 180
cccactcacg tgtgatctgt gttgcccctg ggaggcccgg ggcgaccgga aaagggctct 240
ctcaagttct gaaaagagaa tctgccacca gatcgaattt cgacccctga gcttgttcgg 300
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ttcccgaaac atagtatgga ttttaaaaat gtgtttattt ttgtttctca accactttat 480
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tgtcaaaatc aaaaagtatt taatgaaata ctagttctat ttaatgtggg ntatggaacc 660
ancttggaaa cacaaaacaa acaggggatt gtacaagcan gcttggggcc caagnaaggt 720
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nnnnnnaaaa aancttggng ggct 804

<210> 493
<211> 800
<212> DNA
<213> Homo sapiens

<400> 493
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aacttttgct ttcaaagttg ggtgggacta gaacacacaa tggaaggatg gagtcaggag 180
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<210> 494
<211> 757
<212> DNA
<213> Homo sapiens

<400> 494
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gtttgtatat actgtattct agccagaata attttagatc tgatcaggta gtagctaaaa 180
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taaaatatac tgagatccac atctagtgaa atgtcagtgt caaaatatta tagattatag 300
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caacacattg attgaacact ctggcaaaga tgctgtggtg gatgangttg gagttcgaaa 540
agaagaagca agcgctggcc tgccttgaaa gaacccgaaa gtctttccca ttcacttctc 600

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tagaaagctg ccaagacaga ngcagaaagg aaatggatga tagttctgtc aagcacactt     660
ctgntctcnt agaacttaga aatggttcta agagaacaga agttatngag aacagttcnt     720
gtggaattca acatcttggg tgggacncat tggcttt                              757
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<210> 495
<211> 756
<212> DNA
<213> Homo sapiens

<400> 495

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aatacgtgta cacttgactg tgaagtggct gtgagagtgg gtggagagtt cttctttgac     180
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cctctgcttt ccatcctgcg gcacgcagca gatctcctca gagagcaggc aaacaaaaga     300
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<210> 496
<211> 744
<212> DNA
<213> Homo sapiens

<400> 496

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<210> 497
<211> 772
<212> DNA
<213> Homo sapiens

<400> 497

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<211> 773
<212> DNA
<213> Homo sapiens

<400> 498
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<210> 499
<211> 735
<212> DNA
<213> Homo sapiens

<400> 499
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tngtgagttn anang 735

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<211> 926
<212> DNA
<213> Homo sapiens

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gatgaaatac gcacaggagg gaaatctact gtgtttaggc acaggcagnc ccagtgtata 240
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<210> 501
<211> 706
<212> DNA
<213> Homo sapiens

<400> 501
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taactgcagt gcgtcccaag cagttatttg tatcagtctt attacagagc tttaagtcca 660
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<210> 502
<211> 784
<212> DNA
<213> Homo sapiens

<400> 502
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gnngaggccn tatttacgtt anattccaga cnttgaatan ggatnccatt tgnattgaaa 720
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<210> 503
<211> 764
<212> DNA
<213> Homo sapiens

<400> 503
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tctaaaaagc tgccggttat ttaaccccaa tgatgatgga aaggaggaac caccaaccac 180
attactttgg gtccagtact acttggcaca acattatgac aaaattggtc agccatctat 240
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<210> 504
<211> 795
<212> DNA
<213> Homo sapiens

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cttggacccc tgncn 795

<210> 505
<211> 774
<212> DNA
<213> Homo sapiens

<400> 505
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agaacttgaa ttgggccttg gaagaagaac agccattcaa atagatagaa ttgtggtagc 180
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<210> 506
<211> 796
<212> DNA
<213> Homo sapiens

<400> 506
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<210> 507
<211> 774
<212> DNA
<213> Homo sapiens

<400> 507

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<210> 508
<211> 724
<212> DNA
<213> Homo sapiens

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<210> 509
<211> 803
<212> DNA
<213> Homo sapiens

<400> 509
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gcagtgaaaa aaatgctttn tttgtgaaat tttgngatgc tnttgctttt tttgtaacca 720
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<210> 510
<211> 789
<212> DNA
<213> Homo sapiens

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gaaaacacgt tgtgcctttg tacccattat aagatggtca taanacccaa gaactgataa 720
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<210> 511
<211> 776
<212> DNA
<213> Homo sapiens

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<210> 512
<211> 917
<212> DNA
<213> Homo sapiens

<400> 512

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tccttaccct ggtccgggtg gaggaggttg gggtagcgga agcagcttcc ggggaacccc      180
gggcgggggc ggaccacggc cgccctcccc tcgagacggg tacgggagtc cgcaccacac      240
gccgccgtac gggccccggt ctaggccgta cgggagcagt cactctccgc gacacggcgg      300
cagcttcccg gggggccggt tcgggtctcc gtcccctggc ggctaccctg gctcctactc      360
caggtccccc gcggggtccc agcagcaatt cggctactcc ccaaggcagg annanaanca      420
nccncanggt tntncaagga catntacacc atttggatca nggcgtntta naaaaaaaan      480
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nttggcctta naaanccaan attntngtng gngggntntt aannccnnnc aantncnnnn      600
nnattncntt naaaacnttt nnnccanggn cnnaaaaaaa nggggnaann aaaaaacttt      660
tttnnttnaa nnanttttt tggaaaattt naaancntng gaaaancntt tnnntngttn      720
ntnangggaa annantnttt tgggnncnaa aaaacntttt naannnntnn nggttnnnan      780
nnnttaaaaa ntttnnnccc ccaannnnnt nnanngnanc ttttnnantt ngggantaaa      840
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<210> 513
<211> 780
<212> DNA
<213> Homo sapiens

<400> 513

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cacgagctgc cctgccgcct gccggagctc caggtctaca cccgcggcaa aaagtaccag      180
cggctggtcc gcgcctcccc ggccttcgac tatgcagagt tcgagccgca catcgtgccc      240
agcaccaana acccgtangt ggtccncggc ggcgcgggga ggcccagggc aatnngacag      300
nccctccgnt tgactccgcc agtgctgcag nccctactct ttcanagttg ggagccctgg      360
gacccaggca ccaattgttc ttgcaaactc accctgcggc acatcaacaa gtgcccanaa      420
cacgtgctga ngcacaccca aggccggcgg taccagcgag cttttgtgta aatatgaaga      480
atgtctnaag caaggggtgg agtacatgcc tgctgcctgg tgcacccgan gangaagang      540
gaaggacaaa tggacngtga acggccttcg cccgcgggaa agcttctggg agcccacatt      600
caatgatgaa gggggagctg caagtgatga cagcatgaca gacctgtncc cctgactttt      660
caccagaagg accttgaaca cngaggatgg ggatggactg atgatttttg acaacaaaga      720
ggttgaaagg caaancccca aaaaaaaggc cttgtgaagg cagganaaan acaacctntc      780
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<210> 514
<211> 793
<212> DNA
<213> Homo sapiens

<400> 514

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atatagccat ttaataacat tgatttcatt ctgtttaatg aatttggaaa tatgcactga      180
aagaaatgta aaacatttag aatagctcgt gttatggaaa aaagtgcact gaatttatta      240
nacaaactta cgaatgctta acttntttac acagcatagg tgaaatcata tttgggctat      300
tgtatactat gaacaatttg taaatgtctt aatttgatgt aaataactct gaaacaagag      360
aaaaggtttt taacttanag tagccctaaa atatggatgt gcttatataa tcgcttagtt      420
ttggaactgt atctgagtaa cagaggacag ctgtttttta accctcttct gcaagtttgt      480
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tgacctacat gggctaatat ggatactaaa aatactacat tgatctaaga agaaactagc     540
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ggcatgaata taaaacattt ttatttcagt aactttnccc cctgtgtaaa gttactatgg     660
tttgggggta caacttcatt ctatagaata ttaagtggga agtgggtgaa ttctactttt     720
tatggttggg gtggaccaat ggctatcaag agtgacaaat naaggttaan ggatgattcc     780
caaaaaaaaa aaa                                                        793
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<210> 515
<211> 770
<212> DNA
<213> Homo sapiens

<400> 515

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tggaattgac agatgagcaa agaaatgaac tgatgaaaaa agaaagcagt cgactccaga     360
agactggaca tcgtgtaaca tactcacctc gtaaagagaa agcactaaaa atatatctgg     420
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ggggagtttt ggttttaatt agatggttca ctaccactgg gtagtgccat tttggccgga     540
catggttggg gtaacccagt gacaccacac tgattggact gccctacacc aatcagaact     600
cagtgcccaa tgggccactg ttttgactcg gaatcatgtt gtgcactata gtcaaatgta     660
ctgtaaagtg gaaanggatg tgccaaaaaa ttaaaaaaaa ccnccaaaaa agcttccaaa     720
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<210> 516
<211> 825
<212> DNA
<213> Homo sapiens

<400> 516

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gcntgctnan tgctntgtag nncctttctg nacnntaggc attgctcttg gagaacnnga     180
tgtgctttnt ntnaaanggc anaccagngn tgnnctgnnt ttaatgatgc agancctnac     240
tttatccaca cctggcccgt ttnacatttn agtaangnac gatatttggc tgatggctga     300
acantttctg aaatacacnt ttagtgtatg gaantacaag accnntaaag gnctgccagg     360
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tcttgatggg gtcttttcaa tcantgtatc tgtcgaaann tcttaganaa anctatgtgn     480
tcncggtgtt gtctaaaaan atnctttcaa anatgacccc tggaattncc tganananngc    540
ttaaacgtga gaagacnggt nggcaaaaca ccctncnaag gttnttggna angcccnant     600
ntgttttgtc tggcccatat aancttngcn ccattnaagc cncgggngag ctttgnatnt     660
atattngngg ngttactttc tttgnncctt tgcggggaac ancttnnata atgcttntcn     720
ncccnanntg gacntttgct ttttgnnncc nnaccccccc aaagggngcn cacctccant     780
gaaaaagtct ttttnnaaaa gggctccttn ctnaaaaaaa nnnnt                     825
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<210> 517
<211> 1444
<212> DNA

<213> Homo sapiens

<400> 517
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ccnctattnt cntnntnntc nntcntcnnn antnctnnnt tctncctnnc canctntcca 180
tnntntactn tcnntnntct ggctnttnta tntgggggt ctatttnttn ncttaaatcg 240
actngttcca agtctcntan cngcntctnt ctnnctntct ntgcnctncn ctggggcntt 300
aattncccnn gctnttatan aagngngnaa ttaaggtntc nnntctanng ctntgcaagg 360
ctaatgntta gatccngnta gaanncgnta catgttggga acngacanct tnctgcncaa 420
agngggctna ggcanngnnn tntgcaaann ctcnnntntc nnancttgnn tcncgtagan 480
cggnnncccc tgaattttnn ancnnggan nttaaatnnt ntngnggtac ganncc ncnn 540
ncgnnnnnnc gnntanncc n canngttaan tgcnccccnna nnnantcaac tctntnntcc 600
tnntnnaacn nnnttantct annatnntta cnnntnagnt tttcctcnct nacnnctctg 660
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tatctnctac nctctnttcc ncttctccct nncntctctc atcatatccc acgcnactna 780
ncccctctnn ctcttacctn nntnctctcn tcntatctcn nnaccctctt tctntntctt 840
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anat 1444

<210> 518
<211> 706
<212> DNA
<213> Homo sapiens

<400> 518
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caagtttgcc ttctcctatg ttttccagaa atgacttcag tatctggagc atcctcagaa 180
aatgtattgg aatggaacta tccaagatca cgatgccagt tatatttaat gagcctctga 240
gcttcctaca gcgcctaact gaatacatgg agcatactta cctcatccac aaggccagtt 300
cactctctga tcctgtggaa aggatgcagt gtgtagctgc gtttgctgta tctgctgttg 360
cttctcagtg ggaacggact ggaaaacctt tcaacccact gctgggagag acttatgaat 420
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tcagtgcatt tcatgctgaa ggattaaaca atgacttcat ctttcatggc tctatctatc 540
ccaaactgaa attctggggg aagagtgtag aagcagaacc caaaggaacc atcaccttgg 600
agctccttga acacaatgag gcatatacat ggacaaatcc cacctgctgt gtgcataata 660
tcattgtggg taaactgtgg atcgaacagt atggcaatgt ggaaat 706

<210> 519
<211> 734
<212> DNA

<213> Homo sapiens

<400> 519
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gagggnaaag cagnaagtaa tgagcttgtc cgtcagctgg tagctttcat tcgtnaaaga 120
gataaaagag tgcaggcgca tcgaaaactt gtggaagaac agaatgcaga gaaggcgagg 180
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agagaacaga gctggatgac tatggccaat ttggagaaag agctccagga gatggaggca 300
cggtacgaga aggagtttgg agatggatcg gatgaaaatg aaatggaaga acatgaactc 360
aaagatgagg aggatggtaa agacagtgat gaggccnagg acgctgagct ctatgatgac 420
ctttactgtc cancatgtga caaatcnttc aagacanaaa atggccatga agaatcacga 480
gaagtcnaan aagcatcggg aaatggtggc cttgctaaaa caacagctng angangaacg 540
aagaaaattt ttcaagacct caaattgatt gaaaatccat tagatgacaa ttcttgagga 600
agaaatgnga aagatgcacc aaaaacaana agctttctac acantnaaat ccnannaact 660
ccatccntct anaactatnn gtgagtcctt nttacntcna tccagacatg antancnata 720
cnattgatgg aacc 734

<210> 520
<211> 701
<212> DNA
<213> Homo sapiens

<400> 520
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cactttagat gaagagttac ccaagagagt gaaagctcga ttttccacag cctctgacat 180
gcgatttgaa gacacgtttt atggagcaga cattatccaa ggggagagaa agagacaaag 240
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gagttttgct ggcataggtg acagggtgtg tctctgacag tggtaaatcg ggtttccaga 480
gtttggtcac caaaaataca aaatacaccc aatgaattgg acgcagcaat ctgaaatcat 540
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gtgaaaggaa atactagtga atcacccaca aggaaaagcc actgccacag aggaggcggg 660
tccccttgtg cggcttangg ccctgtcagg aaacacacgg g 701

<210> 521
<211> 784
<212> DNA
<213> Homo sapiens

<400> 521
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atctctggga tgtcagtgag gctggttgaa gaccagaggt aaactgcaga ggtcaccacc 120
cccaccatgt cccaggtgat gtccagccca ctgctggcag gaggccatgc tgtcagcttg 180
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aagaaggagg aatctgaagc cttgggtaag gatttggggc acagtaccag gaggggggct 600
tggtgccaga cctcatgagg aagaaggatt ttcctatgta cagagaaggg gacccctgtc 660
ctgttgggan gtgctgtgca aacctaacca aagttactaa cccctctggt ttctgnggtt 720
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gagt 784

<210> 522
<211> 719
<212> DNA
<213> Homo sapiens

<400> 522
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ctcatatcaa cattgtcgtc attggacacg tagattcggg caagtccacc actactggcc 180
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gatatgagga aattgttaag gaagtcagca cttacattaa gaaaattggc tacaaccccg 660
acacagtanc atttgtgcca atttctggtt tggaatggtg acaacatgct ggagccaat 719

<210> 523
<211> 710
<212> DNA
<213> Homo sapiens

<400> 523
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cagagagaca agatggtgaa ggaactgagc ctgatgaaga gtcaggaaat ggagcacctg 180
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<210> 524
<211> 730
<212> DNA
<213> Homo sapiens

<400> 524
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agacactctt cttcatcttc tactatctgg agggcactaa ggcacagtat ctggcagcca 180
aggccctaaa gaagcagtca tggcgattcc acaccaagta catgatgtgg ttccagaggc 240
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gtaaaaccta ttttcatttt ggaaaatatt tatgaataaa tagttttata tgaaaaaaat 660
tntngnnntt nnnatnnnan aataaaancn tcgnncctct taaaactata gtgaagtcgt 720
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<210> 525
<211> 711
<212> DNA
<213> Homo sapiens

<400> 525
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gaattcggca cgaggataaa tacctcagcc cctcgccttc ctcaacccac ctggcaagtc 120
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gcccggaata ctggggcctg ccttagcatc ccccatagct tccacagccc cagggtgatc 660
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<210> 526
<211> 692
<212> DNA
<213> Homo sapiens

<400> 526
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gaaaagagtc aaaccttttt gggaaaatca gaggaagtaa ctggaaagca agaagatcat 180
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gtactttgat atgtcacagt ttcatgttta tccagttcaa tgtattttta aatttttcct 600
tgagacttct ttgactgata gattattgtg aatgtgtttt taaatttcca aatgtttang 660
gattttcata tctttcttat gctgatttcc aa 692

<210> 527
<211> 769
<212> DNA
<213> Homo sapiens

<400> 527
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tccactgcac ctgctgcgga gtgggcacct ttgcctgcaa ggccttttnc ccantgncca 120
atggtanttt aaccagggtt tttgncnntt aaggaggcct tngtggtggg tngttaatct 180
ggccnttccn tattgaaaag ctcctgttat tgtccacaga ccagaaggac ttgtaacctt 240
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attccagaac ttaaggatac ctcaagggat agggtcacag ccaagaagtn caaaggaatc 360
ttcagtctgg aacaaaaaca gaaccctttc atgattgaca aangtcactt tctgtttgcc 420
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ttaagaaatt tattaaaaaa gaagaatcag gaaaccaagt ncaacccaac ttaacctcaa 660
tgaaccagcc cctaacacag atgangggat ttgggactga taagctctgt gctgngtcca 720
tggcccgtca nttatcaagg ttgcactttt aaatgnggta tttttatgn 769

<210> 528
<211> 757
<212> DNA
<213> Homo sapiens

<400> 528
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<210> 529
<211> 821
<212> DNA
<213> Homo sapiens

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gaaagcaaag acgcaaacag atgcctgtgc accaaagttc acgggcaagc atccttcggc 180
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<210> 530
<211> 765
<212> DNA
<213> Homo sapiens

<400> 530
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<210> 531
<211> 768
<212> DNA
<213> Homo sapiens

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aatggaaaat gtgtngtaat tggctgcagt ctcaggagaa gctnnaacat tagaactttn 660
gaagaaggcn ggggagaatt gatganttgg ttcaactgcc aaagtgtgtg cantcactca 720
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<210> 532

<211> 761
<212> DNA
<213> Homo sapiens

<400> 532
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tgagccacct tgcccaccca catcatacag ttgaaatgaa actttgccac aaccagcctt 180
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cacattttan gggcattggg taatcctgag attttactca ntaaatcctg atggtactgg 720
gtgtaaaata tctttagtng gattgaaggc cttgnggggg a 761

<210> 533
<211> 735
<212> DNA
<213> Homo sapiens

<400> 533
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cactgtccca ctccatcacc caggctggag tccagtggtg tgatcatagc tcgctgcatc 120
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catagttttg ttagcaatac actgtctttt agtggtgcct aaaataatgg tatagttgtg 540
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aaaaataact tgagc 735

<210> 534
<211> 735
<212> DNA
<213> Homo sapiens

<400> 534
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aactagaccc ccatctctta gcatatacaa aaatcaaaat taattaaaaa gttaaatcta 240
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ggngggngct tgngg 735

<210> 535
<211> 735
<212> DNA
<213> Homo sapiens

<400> 535
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gaggagaggc tgtctgcctt tatgaggagc cagtgtctga attgctgagg agatgtggga 180
attgcacacg ggaaagctgt gtggtttcct tttacctttc agctgaccat gaactcctga 240
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gtttcctcat gactgagaag acacgaacta tattatttta cccttgggag cccaccagca 480
agaatgagtt ggagcaatct tttcatgtga cctccttaac agatatttac tgaaggaatc 540
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aaggcaacag aaacaaggag agaagcccga gagacatgtc tgcgtgctgc cacgcatctg 660
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cnatgtnctn aacan 735

<210> 536
<211> 785
<212> DNA
<213> Homo sapiens

<400> 536
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gngtcatggn tnccangngt gagnttnatc tgccnnacat ngtgacggag tttaggaaga 240
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actnt 785

<210> 537
<211> 967

<212> DNA
<213> Homo sapiens

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atntctttac cccccnannn ncacanatgc agacncacac atngcanncg nacacncaga 180
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aattganatt attncntant ngnncacgaa gctttntggta ncangngncc cgagnnctnt 600
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ggtanggann naattgtncc tgggnatagt tctcacaant natnttnaag gggnnaagng 720
atnngngngg nccntntatg nggcnngcca annaangggg tcgnngttaa natattccaa 780
gntaacanan gnacnatggn accnatccct ntnngaagna aggaactncc tgnncgacta 840
nnnactatgn naaatattct cacatntaca naaaaagnag gnnccnnggt ncttnaagnt 900
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<210> 538
<211> 892
<212> DNA
<213> Homo sapiens

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cgggacaatc agattatcta attcctcagc aaacggagat cgatccgaaa agtggaaata 300
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cttggactgc aatnaagtnt agctgcctaa aaatcnnttt cntgacactt ngnaggtttg 420
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nnangntcnn cnannnnttc tnttatttct annatatntc ntancnttna ctaaaacctc 660
cnctcgtnna nattncnnta taatattntc tctaganntt ntnntntntt gnnncttaaa 720
anctcntcta tccctantat nantnattct taccatnaaa tacactanaa gtnntntcac 780
gagacncgnt atgttantnc anactataat cgcttncatn tanntatatn taaaantgct 840
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<210> 539
<211> 751
<212> DNA
<213> Homo sapiens

<400> 539
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gtgagtccnt attacgtaga tccagacatg atnagatcat tgatgaattt ggaccaaccc 720
aactagaatg cagtgaaaaa aatgcttttn t 751

<210> 540
<211> 761
<212> DNA
<213> Homo sapiens

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agcctgcagc cactaatgca ttgtgtatga taacaaaaac tctggtatga cacattttct 120
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cagctttgaa accaaatctg tgtatctaat actaaccaat ctgttggatg tgggttttaa 540
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gtacatgcnt atncccttct ggttaaaact naaaaaaaaa t 761

<210> 541
<211> 748
<212> DNA
<213> Homo sapiens

<400> 541
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ggactgncat ttagtggacc ccgaatcc 748

<210> 542
<211> 784
<212> DNA
<213> Homo sapiens

<400> 542
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ttgctcaang agcagacccg actccntaag gtcatcattg aatgggcatn atangtttga 120
anactgtcca ananantang ngtcaataca tcaacnnctt tanntgcttg atattgnnat 180
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<210> 543
<211> 764
<212> DNA
<213> Homo sapiens

<400> 543
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<211> 755
<212> DNA
<213> Homo sapiens

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tttcagtgac aatttcgtgg tctttttaga ggtatattcc aaaatttcct tgtattttta 120

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aaattcaaag aagcttaata taaaaggttg cattctctca ggaaaaagcc atcttcttgn     600
atatgtcnta aatgtatttt tgncctcata taccggaaag ttcttaattg gattttacca     660
gctgnaatgc tttganggtt ttaaaaataa taacattttt aataattttt taaaaggaca     720
aactttcata atnatcccgg ngntcctttn ccnnn                                755
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<210> 545
<211> 767
<212> DNA
<213> Homo sapiens

<400> 545

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attcgtaaaa tgaatatttt ctgttttgtt ctgttnnatt tttttgagac aagtcttgct     180
ttgttgccca ggctggagtg caatggcatg atcttggctc actgnaaccc ctgccttgcg     240
agttcaagtg attcttctgc ctnagnctcc tgagtagctg ggattacagg cgctcaccac     300
cacacccagc taatttctgt cttttnagtn gacacagggt tttaccatgn tggccaggct     360
ggtctcaaac tnctgacctg aaactnctca caccngtnat ctcagcactt tgggaggctg     420
angtggaaag gatcacttga agccatgagt ttgagaccag cctgngcnac acagcngaga     480
ccccngtgnt gtacaaaagc ttncnacatt tanctggctg aggagtnnct caccentaac     540
ttccancnan tcnnttaagc nnanncatnt tgaacacntg agcccannta nggtcgatgc     600
tnntagtnaa ccgtgactgg accacttaca gtccaagccc gggtngcctt ataaaagaan     660
cggaaaacat ttcnttaatt cgggttnnag cnttanctat ttcggaatnc cttgngtttt     720
naaaaacttg aatctccaan aaacagggtt ttttcttttg gnccann                   767
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<210> 546
<211> 989
<212> DNA
<213> Homo sapiens

<400> 546

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aagttggggg actgaaggag agggagccac tgcaggtgct agctgcttaa ggggatacca     180
gtcctttttac agatataata gatacagctt ctgaggtgga gggtgatagg agtgtgtatg    240
agaaanttgc agnttnacaa ctgctcntgc ctcctnggca anaggannan cntttcnccn     300
nttncnnccc ttatngnaca cacattgncc tgattggncn tnccncngct agcttncagt     360
cttnantnta ctcannagnn nntnggggaa cncnctntcn nantatgntc ccttttcctc     420
tnncntnncc nnatancacc ccnctcnctt tcctttctaa acttncacan ntccctgana     480
atgncttccg aatggantct tngaatttct ncgcccctnc ntcntcataa tcnttttgct     540
nctccngctc nccctcattt tnctacgtnc cnccttctnn ttnactgnct ttaaatntta     600
ttancnncnt ntncnttncn atctncaant tttcnnnccn acnnnntttt nctnntnnca     660
aatcgcgnna aataagtntt gcncactcnn ntnctancnt attntccctc gcnnttntcn     720
tcatctcccg cnncactcac ntnnncnnnt caattnntnn nnacncncnc tgctctacnn     780
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ncnatntctn tncctncaca ccctntancn tntcnctcan aatgcctttt ctnccttann 840
nctntcnttc ncnnatctan ccaantttnc tttnacatcc cctncnnntc tnncccgacn 900
atatntnacc tcttnnatcn cagngcntan natcnccccn ttntcnctnt cnctctcann 960
cttntnttna tcttcatnna tcanncncc 989

<210> 547
<211> 781
<212> DNA
<213> Homo sapiens

<400> 547
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cggggggcac gtggagtcac tggaacattt gngcaatgct ggtgggaatg tcaacccgng 180
cnggcctctg gaatangcct ggcnnntcct gcnagagtta ccntgtgacc cagcaattcc 240
actcctagct ccacccacag gantngaaag cnaagacgca nacagatgcc tgngcnccaa 300
anttcacggc agcatcctnc gccatantgg cancatccgt cgtnacagcg gcatcatcct 360
tcatcattac ggcancatcc gtcgtaacag cggctacatc acttcgccac agnggcagca 420
tctgtngtca cagnggcngc anccttngcc aaagcggcag cntccttcgt catagcggna 480
ncatnctttg ccatancngc naggtggaaa ccctgnccat ccactgaggc ntncatanac 540
tanncatggn cagtccaggg cactggaanc cangccgtng aacggcgccn acggtnanna 600
ggaatganac cntgatgcnc tggggccana catactggct anacanactt ggagacatca 660
tgcttanttg nannnccant cacacttgcn nncggcgtna tcctgctcac gtgatncgac 720
ccgaatgggc acttcaaatg ggaanaaggg ngatggcact nccggtnncc tnganagggg 780
n 781

<210> 548
<211> 735
<212> DNA
<213> Homo sapiens

<400> 548
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agggcagatt ttccaaatgc tcatcaccac ttggcactgt gtggactata attttggcca 180
gttaggaaat ggcatctcat tgttttcatc ttaatttgcg tcagcctgat tactcattga 240
aacttgtgag gttgagaaac ttttcttaag cttattggcc attcaagttt cctcctttat 300
gaaatggttg ttcatgtcat ttgctcattt ttatattaga ttgtttttct tttttccagc 360
tgacttgtag gaactctaca tcttatcaat attaatcatt tatcgaaaac tatttgggtg 420
ccattatctt ctcctagtca atgtttttttg tttgtgatat cttttataat atataagttt 480
ttaatgttgg cagaagtaaa gttaatcttt ttggctgtgt tgtgtgtctt gtttgatgta 540
aagatagttt ctgtaatagt tttgcagttt gattgntcat ctttaggtct tcaattcaac 600
ctgcacatcc atcccctcta tcctctttct tactctgttt ttctccatac cacttatcat 660
ccaataatat ggtcatgccc tttattnacc ngntttgcat atataatttg gcttgtnccc 720
ggttccttcc ctana 735

<210> 549
<211> 812
<212> DNA
<213> Homo sapiens

<400> 549

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ggaaggagcg ggcgtgaggc cagctgaggc atggtgaccc ctgggaagga gcgggcgtga     120
ggccagctga ggcatggcga cccctgggaa ggancgggcg tgaggccagc ttgaggcatg     180
gtgacccctg ggaaggancg gncgtgaggc cagctgaggc atggtgaccc ctgggtacgg     240
gggacttggg ggccgacctt ggtttgccca gggcccctnc tgcaccacgg ccacatgcgg     300
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tncttggtca aggcttcang ctcttggcag atggggcaag gaaccctgag gcttccgcgc     420
ccttccatgg nctctgatgt gggacacttg aacgangcac gattctgaag gactccatgg     480
atcttgggan gattangccc accttcngtt ggtggncnaa agccgtcctt ncggggcccg     540
gcttgtttaa cnggacaact tttcnggtcg ggcttgttgg gccccaatcn ttgggttggg     600
naanttcncc ttaaaccttg ggcccgncct tttaaccttt tttcccaatc ttttgacctt     660
tttccaaaaa ggggtncccc tgggcttttt ngggncaatt ggttccgggg gccaaaggtt     720
gggaaaaaat gccttncatt gggnaaaacc ctggatccct tgttaancct ttgggagntt     780
aaaatggaat gaattttccc cccgggcttt tt                                   812
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<210> 550
<211> 742
<212> DNA
<213> Homo sapiens

<400> 550

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ggnnantcna tgctggtctt gtctctntct aaaagttggc nattcgaatt cggcacgagg      60
ttctgtggct ggcatggtct gcctgctact ggagagatct cctgagantt cagttttgga     120
ttggtgctgt catcttcctg ggaatgcttg anaaagctgt cttctntgcg gaatttcaga     180
ntntccgntc caaaggagaa tntgtccagg gtgctttgat ccttgcaaag ctgctttcan     240
cagtgaaacg ctnactggct cgaaccctgg catcatagtc agtctgggat atggcatcgt     300
caagccacgc cttggagtca ctcttcataa ggttgtagta ncaggagccc tctatctttt     360
gtnctctgca tggaaggggt cctcagagta ctgggtattt tncttatccc ttgactctga     420
tagtaaacct ggccctntca gcagtttgac gcctgggtat ttatggatat taattagcct     480
gactcaaaca atgaagcttt taaaacttcg gaggaacatt gtaaaactct ctttgtatcg     540
gcatttcacc aacacgctta tttggcagtg gcagcatcca ttgggttaat catctggaca     600
acccatgaag tcaanaatag tgacatgtca ntcggactgg ccggnagctn ttgggtagac     660
catgccatnt ggcgccttgc tggtcttcca tganccctt tggcaatcat gggtcttntg     720
gcgaaccatt ttgcaaacaa ct                                              742
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<210> 551
<211> 736
<212> DNA
<213> Homo sapiens

<400> 551

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taaacctttg accagctgag ctgtgactgg ctgtcacntn tctgagtcct gtgtgcacag     120
tantntcctg ggtcaggtaa aatccaggtn ttcaagtttt aaggnttttt tgaanaattc     180
gggcttnttt aanacgatcc ntgcccaant ccacaagctt gttgacagtg gnttacagtt     240
ngngtggcaa agtccaagtt gttacactgn gctttaaaaa aaatcttatc tgcatgtatt     300
gttaacttag agaccatgag atctatttat caggaccagg aagatncaca cttcaggtcc     360
attgcaactg actttttct tgtttttctt aaaaccctgg tggagcctgg gaagggggcc     420
tccacaattc tgtggctttg atattagccc caattttaca agcacataca agccccataa     480
ttgccgcagg aaaacacaag atggaaaatg caataaccca tgcactgaga cttagaaaat     540
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catccttact aggcaaaatg tattatgatg caataagtgc cactgggnat tttnacgttg 600
ggactggnca ggaactgctg caaagaaaaa taacagctcc ttctccatta tttacattta 660
agatgttggt gggggaagg ttgggagaaa ttagttctga gggtatcata tgcctttttt 720
aaagaaaatg ggaata 736

<210> 552
<211> 733
<212> DNA
<213> Homo sapiens

<400> 552
nagtttaann gtatgtcttg tcttttccaa gatcctatcc gattcgaatt cggcacgaga 60
agtgtcagtt ttcctaatct cagtccaggt aggatttaaa aantntctca agtgttgatg 120
ctntccaagc ntgttggggt ggaagggaat tggtgcccag aaaatgggac tggagtgagg 180
aatatctttt cttttgagag tncccccagt taatttntnc tgtgcttnat tgctnctgtn 240
ctttattgtg aatgttgtaa cattttaaaa atgttttgcc ntagcttttt aggacttggn 300
gttaaaggag ccagtggtct ctctgggtgg gtnctataat gagttattgt gacccacagc 360
ttgtgtggga ccacatcact tgttaataac acaaccttta aagtaaccca tcttccaggg 420
gggttccttc atgttgccac tcctttttaa nggacaaact caggcaagga gcatgttttt 480
tngtnattta caaaatctan cagactgtgg gtatccatat ttnaattgtc gggtgacaca 540
tgttcttggt aactaaactc aaatatgtct ttctcatata tgtgctgatg gttttaataa 600
atgtcaaagt tctcctgtta aaaaaaaaaa aaaaaaaaac tcgagccttt anaactntnt 660
gagtcgtnta cntagatccn gacatgataa gatcatgatg agtttggaca accncactng 720
aagcagtgaa aaa 733

<210> 553
<211> 870
<212> DNA
<213> Homo sapiens

<400> 553
nagttaanag taggtcttgt cttttgcaag atcntancga ttcgaattcg gcacgagtat 60
ataacaactt ttgctttcaa agttgggtgg gactagancn cncantggaa ggntggagtc 120
agganacctg gattnttgng cccgntntgg nttttacagt ntgcctaant ttntgcagtn 180
acttcntgcc ancctgtttc nttacntnca anagggaaag acantccttg gccagcctag 240
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aagtccctga cttctagaga ctgcatgtta gtggcaatcg gcgtntaccc ggccttnaat 420
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tggaattatt cccccggccc cntgcatcca gcagcctgnt gcagggaaac tcctccnaaa 540
ggcttgtaag gcaaggaanc cgggacaatg gcntggctat ttaagcttnc aacaagatgg 600
ttacccctaa gtncctaatt ccctaacacc aagggggccc tttaccagga aaccaaaacc 660
aggttaaaaa accccaaagt tgggnaaaaa gccatttgcc anccggggcc nttttaaaaa 720
aaacctttna aaaacctttc cctttaaaa ctttaccttc aagntaaaan tttaagggga 780
atgggnccaa ntttttaac cancccccaaa aaaaanttng gnaatttttt ttcccnaaat 840
tttttnaant tccccaaatt tnggaaaang 870

<210> 554
<211> 766
<212> DNA
<213> Homo sapiens

<400> 554
tatcaatgnt atgtntggtc tnttcgaaag anctagncgg ntcgaattcg gcacgagcca 60
acacccagtt ctnactctgt catccaggct ggtgtgcagt ggtgcaatgt gggcttactg 120
cagccttgac ctccaggaca agtgatctcc cacctnagcc tccggaatag ctgggactac 180
agntcaacaa cgcccctctg aaagtaggac tcttggaaat gaaccttgtt gggagtaaag 240
ctgaaccttc acctctcctt tccaggattc tactccattc atacggcctc acactgaatt 300
aatgtttnta gcagccacat cacttngtta cccaattgat ctagtagtaa agtcttccca 360
tctnttcatg taaaaaaaaa aannnaaaan gggnnaggaa ccntnangnt nnnaanaaaa 420
aaaaaaanca ggnggngngc ntttttaac ctataacctg ntttnaggcc tttccccang 480
tttntccnaa ncnnggttan taggggccna aagctaaccg natttttgnt cccntnaggt 540
taggccngaa attaaccngg gtttaaagaa cncattgant aaagccttgc ctnggccaat 600
tccgggaaaa gggaanagcc tccttgtttt acanattggg aaaaattggc cccaangggg 660
gttaaccang tttgcccntt aataactnaa anggattttt gncaaaacct ggttccaagg 720
ntttaanccc aanccttttn aaanntnggn cnctttggat gnaann 766

<210> 555
<211> 770
<212> DNA
<213> Homo sapiens

<400> 555
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tctctgagaa aactttggtc acacntccaa agccagggtg ggtgcctccn tgnaggaggg 120
ggctttcctg gttggtggcn cagnaggagt ccaggctttg taccgtggac accatgggct 180
atggcaacac cttcctaacc atccttccat gaggacctcg gnaganagtg gacatgaaac 240
cctttgtgct ctgaancatt caacagaagc tttctggttc tgtgcctatt tctttggcac 300
ttgancgtgt ttgcaggttc attacncaca tgatgaaagc tctggcccat agcactagaa 360
ttcatgtttt nagggtttgt gagtgtgaca ggtgctatgg tttggatgtg gtttgtttcc 420
accaaaactc ttgcttgaag tttaactgcc agcatggcaa ttgttggnag gtggggccta 480
ccgggaggtg attgggtcat gggggcttga accctccgga atagattacn gctgcctcct 540
ganaaagttc tacctgtcat gggggctgga tcagtcaaca ttgannantg ggttgttat 600
aaagcaagac tnactcctta tgcaccgttt ntttgcatat gcccctctgg gggnancttc 660
tttggctgct aacattttg gacccaaccc aatgggcctt nacccagaaa nccggaacaa 720
aatgccnnnn gccattcctt tnngganctt tccaacttnc canaaataat 770

<210> 556
<211> 756
<212> DNA
<213> Homo sapiens

<400> 556
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gcatccgatt tcttcactaa aggagaccaa actggttcct tgcggcctag tnttnaagan 120
ctggancttg aaagtcctcc ttntaccaac tccacntcca ccccntnatt cccnttntcc 180
caaagtncta ctgntgttgc ntgacanccc caaatntgtn ctgtcaacac aaacctgcct 240
ttggngtata aacagggcnt tacagaatgg tncaccctat atatttctgt tcagtatcca 300
ttcactagtt cttcattaat aaatatcatc ttccccattc tgctgctgaa tgccacacat 360
ccatccagtc tgagaaagtg agagaggcaa tcatgccaag aacaagccag caaagctctt 420
tcaccagatg tagactgtag ccctgctgcc ttccctccag cgagtctgcc agcatgcttc 480
ttcatccttt taatatgtcc tttgcttcct acttccctgn cttccaacat actgtcactt 540
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caagctatgt cctatatatg natttctgga cttggcangg atagttcaag gggtcttggc 660
aagtttttat ttaccttcat tatttaaaan gggccttttg gggatgttgg cctntttaag 720
gagccttttt ggggaaatca atacttctct taanaa 756

<210> 557
<211> 742
<212> DNA
<213> Homo sapiens

<400> 557
tcgtcnaaan nnatgtcctg gctatccgca ggatccaggc ggntcgaatt cggcacgagt 60
gattttttg gttttttttt ttgntnttgn caaaagctta ntcntttcan ttaaaantgc 120
cactantttg actttttaag taaaaantgt aggggtttt aaanctactt tcctnctncc 180
aaaaantcag aaagtttcta nctttntaaa ttgggaaagc aagcantgtt ttaaaancac 240
tgaaggaatc tctttnttcg ngnccttttg ttaaactcgg tttaagctgt agaccttntt 300
taaantaaaa tttaccacag aacaggaaat agaanctgtg gaagactcga aatacacctt 360
tgtncttctc tgttcttcac ctgctctctc gctgtctcta cacacacaca cacaaacaca 420
cacacaccta tatttgcatt aaaaatgggt agtaaaagca gtgaagggca aacagaaggt 480
ccattncatc aagtaagagg ttgaatataa actggaccaa gtcttaattt tttatttcct 540
tcattcggat ncgtttacta atttctttgc tagctttaag acttttaaaa cattctttgg 600
ccctgggagg gagttgttta cccctaaact tggagaatcc tggccctaga ataaatgttc 660
cttttaaacc cccanggccg gaaaattgaa tncngctgtg ccaaaaagga aaaaannnaa 720
aaaaaaactc gnggcctnta na 742

<210> 558
<211> 730
<212> DNA
<213> Homo sapiens

<400> 558
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tttaataggg acttncaanc aaataattnt cggtttntca ggtggcagca agacaagatg 120
gtggatcccc atgccattac ctgctagact cagggttnat atactgtagt ggaaaggtga 180
ttccgaagga atgttgtaag acaattgaag tgcagtanca tcaaagttat ttgacctaag 240
ggcaggagtt ncagtaagta tccactttta tncaagaaac antagataaa ctggaaatct 300
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tggagttgct tagtctccca ttcaagatgg agtttcttta gcctccattg atagggagtn 420
tttaacaaaa ncangaaata agtctttgat ccattgaatc tctaagagtg agcccttgat 480
gactcaggtt taaacagtnc tgagacaatt taggagatag ttttgaagnt caatttgaat 540
tgtaaaaggt caggattttt taacttttc acatctttga anaaaagccc atagagcgca 600
agttttcagc aaganctgga aancnatatt nctatggaat taaatagctc ctcagggcaa 660
tcaattnggc ctgggganaac ataatgcttc aanggctgan gnaatctgga atttctatgg 720
gatttcttca 730

<210> 559
<211> 743
<212> DNA
<213> Homo sapiens

<400> 559
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cggcacgaga ggaaacaccc ccttataaaa ccatcatntc aggctgggtg atctgacaga 120
gctagacact gtcaaacaaa caaacaaaca aacaaaaaaa ccccatcaca tctcatgaga 180
cttatttact atcatgagag cagctcagga aacacccact cccgtgattc agttacatcc 240
cactgggtct gtcccacaaa ttgtgggagc tacaattcaa gatgaggttt gggtggggac 300
acagccaaac cctatcacca tgtaaaataa tatctaattt gtagagatta aagaacaaga 360
taacttaaat cttggatgta agttaagaga gtggtggtca gagttaaatc attttaaggt 420
tcatttattg tctggacaag aataaaattt tgattatcag gaaatacaag taaaaccaca 480
gggagacatt gnttatatcc aaattgtcaa aaattacaaa gtcttataat accaagtttt 540
gctganggtg tggagcaaca gaaacttttg ttcactggtg ggtatataaa ttgaataatt 600
tcagcttgga cattacctag caaaattgaa ggctgtatac gtacatacct accaatctag 660
caattcactt ctagatatta agtcttgaaa aactcacatg tttccagaga cgtgttaaaa 720
ggtggttaaa tcattntgng aat 743

<210> 560
<211> 833
<212> DNA
<213> Homo sapiens

<400> 560
atccngttct ntannnngtc tngttctttc tncacgatcn nntgcgattc gaattcggca 60
cgaggggtcc tggtgggagt tccatccagc agtgagtgca ttttttcccc agagcagtta 120
agggtcttat taaaagccac cactttgctg aggcctgtac aggccttggg ggtttgggga 180
agagaantaa ggcaggcact tgtcccttca gggagggact tgtccntact gggaggtttg 240
gggttgacct tggctccagc agagataccc agcctggcnt ggaagggcag gtcttgagct 300
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acaagtagga ccaagaagtc aagggaaaag tgccaagata gatctattcc catttctttc 420
ttccacctgg agaattcctg agctatgctt caaacctctt ttgggccagg gaaagactgg 480
gggacatttt ttagtcaagg atgctttaag aaagtaaatt cctgcttggg ggcccaggcc 540
ttctttttca agggcttgct tgtgaatgcc caaccaaaaa aaaggggccc ccaaggccca 600
atcccttact tcctnggtcc ccccaaaaag ggatnccaan ttggggaatt gggaaaactt 660
gggcanncac ccnaanccca ctttggtagg anttnaccaa cccaaccaac ccaaaaccan 720
cccacccaaa ttnaaaaaaa ggccaaaacc accaaccaac cnaaacccnn annnnnnnnn 780
nannnnnnnn nnnaaaaaaa ctttgangcc ttttaaaaac tntttngngn ggn 833

<210> 561
<211> 773
<212> DNA
<213> Homo sapiens

<400> 561
tagtctaatg tnnnaaantn ngcnctngtt ctttctgcag gatcccatcg attcgaattc 60
ggcacgagga agaggaggct gtgtatgagg aacctccaga gcaggagacc ttctacgagc 120
agccccccact ggtgcagcag caaggtgctg gctctgagca cattgaccac cacattcagg 180
gccaggggct cagtgggcaa gggctctgtg cccgtgccct gtacgactac caggcagccg 240
acgacacaga gatctccttt gaccccgaga acctcatcac gggcatcgag gtgatcgacg 300
aagctggtgg cgtggctatg gccggatggc cattttggca tgttccctgc caactacgtt 360
ggagctcatt gagtgangct ganggcacat cttgcccttc cctctnaaca tggcttcctt 420
attgctggaa gaagaagcct gggaattgac attcagcact cttncaggaa taggaccccc 480
agtgangatg aagcctcagg gcttccttcc ggcttggcag actaacctgt caccccaaat 540
gcagcaatgg cctggtgatt nccacacatn ctttcttgca ttcccccgac cttccagaca 600
gctttggctc ttgcccctga caggatactt gagccnagcc cttgcctgtn ggccaaaccc 660

tgaattgggc cacttgccaa acttgcnggg gaaagggttc cttgaaacaa gggggccatt 720
tttggggaag gcttcttggc ttggcctttt ggcatttnaa tttggccttt ttt 773

<210> 562
<211> 655
<212> DNA
<213> Homo sapiens

<400> 562
nnatanacat taangnnaga ngntgagnan ttnccntcgc tctntganna naaggcgncg 60
cgaattcggc acgaggccac cggtctcttc ctaatctgca cattntattt tgggtatttc 120
tgggcgggca gttcctttgc atgtttcggg agaggtttgt tgatttgggg cttatatgtc 180
aggcctttgg tttgcgtctt atttaggggg ttgtttgggg gcctgggtgg tcggcctcac 240
atgggaaggg gatgggtagt ggatggggtt tctgtcgnat cttgnggccg gtgattttgc 300
tnncgnnctg tttcacattc ttccccctcc acaagccaaa tcgttcattt ggntncactg 360
tgtggactgt ctgagcttgc cctgccagaa aaatttgggg ctaggcaccc aggtgcanac 420
tttggaagaa gcantccacc tgtgggtacc gcatctcgtg ngtcccactg gcaggctgaa 480
cctacttgaa catggaaaca gcatgcccat atggcaaagg ggccnnnacn nnngnnnaaa 540
tnnannannn ncngacannc nncnnaatca ngannntcna cannnatcnn annnnancnn 600
nncaantacn ncnaaaacac accnnccana annnnnaann nnnnnncann nnnac 655

<210> 563
<211> 738
<212> DNA
<213> Homo sapiens

<400> 563
tnntaatgct ggaattcctn atncttgggc tactcgttct ttctncagga tcccntgcga 60
ttcgcagaaa agagtatagt aggggatgac caaggtcaaa gtgggtaaag aagactcatc 120
atccactgag tttgtagaaa aacggagagc agctcttgaa aggtatcttc aaagaacagt 180
aaaacatcca actttactac aggatcctga tttaaggcag ttcttggaaa gttcagagct 240
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agaaaagcag cagcaatttg agaatctgga tcagcaactt aggaaacttc atgtcagtgt 420
tgaagccttg gtctgtcata gaaaagaact ttcagccaac acagctgcct ttgctaaaag 480
tgctgccatg ttaggtaatt ctgaggatca tactgcttta tctagagctt tgtctcaact 540
tgcagaggtt gaggagaaga tagacccagt tccatcaaga acaagctttt gctgactttt 600
atatgttttc agaactactt aatgactaca ttcgcttatt gctgcagtga aaagngtgtt 660
tgccatcgat gaatgctgca gaaatgggaa gatctcaaat tctttgctca aaaacgtgaa 720
cttaaccaaa atgatggt 738

<210> 564
<211> 798
<212> DNA
<213> Homo sapiens

<400> 564
nggggngtct aatgctgcnc nnatcnannc anggnnctcg ctctngctcn acnnanaagg 60
cgntgngtgt gccaccacac ccagctcatt attattatta ttattattat tattttgaga 120
cgaagtttca ctcttatccc ccaggctgga gtgcaatggt gcgatactgg ctcactgcaa 180
cctctgcctc ctgggttcaa gcggttctcc tgccttggca ggcacctgta gtgtcagcta 240

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ctcgaagctg aggtgggaga atcgcttgaa cctgggggc ggagattgca atggtgtggt      300
ctcggctcac tgcactcgag cctggcgaca gagcaagact ctgtctcaaa aaaaaaaaaa      360
aaaaaaactc gagccntnna actattngng aggtcgtatt acgtagatcc agacattgat      420
aagatccatt gatgaagttt gggccaaacc ncaacttgaa tgcnnngaaa aaaagcttaa      480
ttgggaaaat ttgggaatgc ctatngcttt atttggaacc ctttntaagc tgcaantaaa      540
acaagttaan caccncccaa ttggcntcca ttttaatgtt tncagggttn agggggggaag      600
gttttgggaa ggttttttna aattcncggg ccnnggggnc ccaatgcttt ggggccccgg      660
gtncccaann ttttgggncc cttttaangg gngggnttan attggccccc cttggggggna      720
aaancgnggn anatacctng gtcccctgtg nanaaatngg nttcccntta caaaatttcc      780
cacnnanatt tnngnncc                                                    798
```

<210> 565
<211> 744
<212> DNA
<213> Homo sapiens

<400> 565

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ttntnngttt naatnntcnn ggnntcgntc tnnctcnaan nanaataggt ttggcgaatt       60
cggcacgagc atgctggcca gcatccctgc ctgtgcaagc tctggatgag ctgtgtgccc      120
ctgccacnca cacccngcac tccctgccag cctggcctca gggcctctga tccatgtgca      180
ctggagtggt gatgactgac agggccactg gggcatttnc acgttaacag cagctgccac      240
tggcaaaaga agtgactcgc caatggtggc atctcagatg tgggcccagg agtctgggga      300
gctactttga acagggctat ccattcattg tcccaccaaa ggctatggag cccacccacc      360
atgtgctgga gtagtcaagg gaaataagac actctccttg tccttgttaa ctcaatcaac      420
aagcatttgc agagcaccgc ctatatgccg gcgctgtccg aagtgctgaa gatacagcaa      480
tgagctaagt aagcactgac ttcgtagaaa accataacat cggccatctt tggaaaagag      540
aaaaacaatg gagttactta tttaaaaaaa aaagaaagaa agttatctct tccanganag      600
gctagaagta cttttctgct ttttggccag tgcccantgg aatgcctggt ttgggggaag      660
aagaagggac tgggttaact gtggtgcttt tgttgtaaaa aggcanctgg cctttgtact      720
tgaggagaaa natggagcct tggg                                             744
```

<210> 566
<211> 756
<212> DNA
<213> Homo sapiens

<400> 566

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gnagtnntat tgatttntct ccgtgaatcg ttctnnctnn annanaagtg ngttnngccg       60
ctggctatgt ggacgctggg gcagagccag gccggagtcg aatgatcagc caggaagagt      120
ttgccaggca gctacagctc tctgatcctc agacggtggc tggtgccttt ggctacttcc      180
agcaggatac caagggtttg gtggacttcc gagatgtggc ccttgcacta gcagctctgg      240
atgggggcag gagcctggaa gagctaactc gtctggcctt tgaggtaatg gggggtggcg      300
gtggtggggg gtgcttantg gctatgctca ccccgctnca ttangcctat tttggtctgc      360
tgtttccaaa tgcttctana tctaggcatt tggtatccaa cctattgcca cantgcctan      420
aactncanac ccccngccnc tatgntnana cctacttggc acaagaacaa nngnanacnt      480
tgnnnatatn ccanaaangnn naanattaca nantnttata ataccaattn ntnttgangg      540
tgttnnnnnc anaaacnttt gntnacngnn nnnnntatna atnnataatt nnnnnttttgn      600
nancannanc tatgnnnaat taaangnntn tntncnnnnc nnnacnnnna nnnnnnttan      660
nnanttncnn ttnnnntnnn nnnnnnnnnt tnaanaannt nnnnnttnat nnnannnncn      720
nctnnaangt ntntttnnnn nnatnnnnnn nnnncg                                756
```

<210> 567
<211> 746
<212> DNA
<213> Homo sapiens

<400> 567
gnntgtnntt nncnnannnn anganagagn tactcgctct ntctctacga tanantgngt 60
tncgaattcg gcacgagatt tcctccagtc ctgggcccca tccttnaggg ccttcccagc 120
cagccagcag gagaggcaag aactggggga acacaggaac ctaggggagg aggggagcgc 180
tgggcatcct caggctggcg gccaagcctg cccctggagg cactagagga gggcatctgt 240
ctgtgggagc ccagagctgc agggaggagg aggagggagg tatctggtgt gagcgttgcc 300
cctgcgacat ttgggaccac acaggtgggc ttccttattc cctgacaaag cctctgtttc 360
cagctcttcc gccctctctg gatgagggaa cagaagtgga ggaaacaaaa gaagcagcag 420
cacgcacagt cctgtcgctg ggtgcggaga cagcctggca aagtcccact cagccatggc 480
ctgatgcang ccccagccct nctttcttgg gtgtcaaatg actgtgtcct ggacatctga 540
tgcaccacct gccctgcctg ttgcaaacgt gatgctcccg gatggaatgg agaaactagg 600
agactgggac aagcaaaang ctgcaaacaa cccagaaccc attcttagaa nactggagaa 660
atgattgagg aatcattggc accgtggncc tgtgcttcat nacaaacacc tttnagaaca 720
acttgggatt gaaaaaccaa gacant 746

<210> 568
<211> 738
<212> DNA
<213> Homo sapiens

<400> 568
gnnnntngtn gttcttanng ttnggatctc gttctttctn cacgatcncn tcgattcggt 60
ctgggcagcc tacgctttcc ggataaaaat ggcagaatga aagaaattat gagtggaact 120
agagaatagg aaagacatga accaacgccc aaaatgagaa agaaggacat ataaagaaaa 180
agacaaatac aagtgaaaaa aatagactaa tggattaacg tccctgtcgt gtgacatttt 240
ctgctatgga aatgatatta gacaaaaagc acttcaagtg gttttcttat ttgagttcaa 300
aatgggtcat aacgcagcag agataacttg aaacatgaac agcgcatttg gcccaggaac 360
tactaacgaa catacagggc agctgtgatt caagaagttt tgcaaagcag actagagcct 420
tgaatatgag gaacacagtg gccagccatt ggatgcttca cttcttgaag catcttgaca 480
gctttttgca ggtgaaatgc ttncacacca gcaggatgca gaaaaatgct ttccaagagt 540
ttgttgaatn cagaacatgg atgtttatgc tgcaggaatt aacaaattta tttctcgttg 600
gcaaaaaagt gttgattgna atgggtccta tttgattaat aaagatgtgt ttgagcctaa 660
aaaaaaaaan nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnnn nnnnnnat 738

<210> 569
<211> 753
<212> DNA
<213> Homo sapiens

<400> 569
gtttntgant ntgattctta tgcttngnct aatgctttnt ctnnangatc ccnncgattc 60
gctggaggag aggagctcag agttctacag agtctttnct gaacaatatc agaaagctgc 120
tgaagaggtg gaagcaaagt tcaagcgata tgagtctcat ccagtctgtg ctgatctgca 180
ggccaaaatt cttcagtgtt accgtgagaa cacccaccag accctcaaat gctccgctct 240
ggccacccag tatatgcact gtgtcaatca tgccaaacag agcatgcttg agaaggagg 300

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ataaaaactt tcagaatgag caaaacacca tcaacgttaa ttccagagat ggaacatttt      360
ttttcctagt gagaaaacaa cccatttgaa gagaagaccc taatgagaag accctaaaga      420
gagacatcaa gaatggattc agcagaatca tttcacgttt tgaacagcag cagtttgaan      480
ggccaaagcc tttgatcagg gatcccgtca ttaaaggaca ctcttgagta ttagtaaacc      540
ctcttatgat gattaaaaga gaagggcagc cctnttcacc tttttggtct ttctattcaa      600
cttgcctgac cataaaatgg ttctcttctg nacaaagccc catcatttgg tgaacctcac      660
ccttaacaaa gtaggattgg ggttgggggg cttaattaat tggaatgggg ccaaggagaa      720
gagcccgaaa ccttagatnc cangggnana agt                                   753
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<210> 570
<211> 832
<212> DNA
<213> Homo sapiens

<400> 570

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tnatnaataa ggtttgantt cttatgcttn ccaanngctt ggacctannt anccangcgg       60
tgcgaattcg gcacgagcca ggccccaata atctgggntt naaactttga ggaaatgcca      120
gtgacttatt ccagagtgcc tcagttaggg gaacttctct gtaaagaacc ctgggtattg      180
agcaaaaacc ttattatcgt taatgaccta taattggaag cttcctgcct ttttctttgg      240
ttgctcctgt ggaaaatact gaaaagatta ctttgtttta ttttgttgtc tttttataaa      300
aggggaggtg gagagacccc ttcagagcag ggattgtgcc gggagagtgc ctctgacttt      360
gggacatttc atccacagaa atttncaagc caatggtttc ttttgggttt tgggttttta      420
tgtttgnttt ttggggggttt ggaaaaacat gcatttttac cgtgcacgta aaattggtca      480
nagaaaaagg gagcccagaa aangcagcan atgggccatg cccctttgct gggttttcct      540
tttcttttgg gactgtnaag gggaaatggg tttttanaag gtgaaggttt ggtcctgttg      600
gaaggaaaag aantgtctct gttngggggg acaanaaggn acccttgggg gaggtccatt      660
cgcaatggtn cctaccaaaa cnnggntctt taanaacacc ngggcctttg ncccaggnaa      720
aaaaccctgg gcccctttaa naaactttgg nangggaacc ccggaaaacc cccttgggcc      780
ttnccaaatc tttttcccca aagncncccc cgggggggccc aaaaaaaaac ct              832
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<210> 571
<211> 748
<212> DNA
<213> Homo sapiens

<400> 571

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agtnttaatn ntggacttct aanganttng gctnntcgnt tggaannnnn cagtnctcta       60
nnagcccatc gatgcgaatt cggcacgagg ctaggattac aggtgtgagc caccatgccc      120
agccacttat ctttaaagga ttaagtttat gtttcctact atgggaaacc atcccacccc      180
aaacttgatg accgcattat gtgcttttat agaacatggc acttctccag gatagcattt      240
attctgtttt gtaagtgtga atgtaattac cctacacaca gcatacacat aatcttcata      300
ttctttgcct tgtcttgtga aggcaagggc catgtctatc ttattcgtca ttagattccc      360
acatccaaca tagtcctggg gacagcacca atgcactttt ggtgcataag caaatagtgc      420
atttatagct cttacctaca atatctgata gactaatcaa atatagtagg ttatctgggc      480
ctttttgatt catgtctcta gcttaacttt cattttttc ttatttggta tctctcactt       540
tgccttttga tatactctta cagtttcgct cactgagtaa aagaaaatnt aaacagcaag      600
aagtaaactt gtgttttatg gatttngata acatcttcta aaagaccccc caagattgtt      660
gatgtctaaa aaaattaaag ggccttcaac tcataataat acttaatagt tcttaaaata      720
ttacaaactg attggaacat tgcctaac                                         748
```

<210> 572

<211> 755
<212> DNA
<213> Homo sapiens

<400> 572
agtcttatta nnnngttcta atcctttctt aangagnnta ggctactcgt nctttctgca 60
ggtatcccnt gcgatncgaa ttcggcacga ggctgagcac ctttggaaac aacatttaag 120
ggaatgtgag cacaatgcat aatgtcttta aaaagcatgt tgtgatgtac acattttgta 180
attacctttt ttgttgtttt gtagcaacca tttgtaaaac attccaaata attccacagt 240
cctgaagcag caatcgaatc cctttctcac ttttggaagg tgacttttca ccttaatgca 300
tattcccctc tccatagagg agaggaaaag gtgtaggcct gccttaccga gagccaaaca 360
gagcccaggg agactccgct gtgggaaacc tcattgttct gtacaaagta ctagctaaac 420
cagaaaggtg attccaggag gagttagcca aacaacanca aaaacaaaaa atgtgctgtt 480
caagttttca gctttaagat atctttggat aatgttattt ctatctttat ttttttcatt 540
anaagttacc anattaagat ggtaagacct ctgagaccaa aattttgtcc catctctacc 600
ccctnacaac tgcttacaga atggatcatg tcccccttat gttgaggtga ccacttaatt 660
gctttnctgc ctccttgaaa gaaagaaaag aaagaagact gtgtttttgc cactgattta 720
accatgtgaa actcatctna ttaccctttt ctngg 755

<210> 573
<211> 743
<212> DNA
<213> Homo sapiens

<400> 573
cangtctaat gctggctctn atcggttctt nnnantnaag ntactcgttc tttctncang 60
natcnnntgc gntncgctca cacagcatgt gtcagatcca tggggtagga gtcggccaga 120
gacttggtaa cagacagatt gctggatccc acccctagac tctctgattc agttagtttg 180
gggtaaggcg caagactgaa tttttcacaa gtttcccagt ggtgctgata cttctggtcc 240
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ttgtcactgt cacactgcat ccttttaaca atgcattccc tatcctattg caatactgac 360
atctcatcaa tattttaaaa catgcgtttt cagaaacaat attttatatc aaatactcac 420
ttttagtaat atttctgcaa ttttgcccta tggatctgag atctaacaaa tactattctg 480
gacatgggct acaacagttg aggctggaag taaaaatgtt aaaccctgct gaccacgtta 540
ttttaaagtg tattttagtt aagaataata tggcttagga gcagggctaa acagtagcag 600
tcacatgggg aatgatactt tgcttttgca cataaaatgt cctgaaggga aaaaataaag 660
cagaaaattn ncagatgaac tgaaaatctg tacaaatgtt gggctgaata ctgccagcgt 720
tgangtgtag gaaaatgaac cnt 743

<210> 574
<211> 737
<212> DNA
<213> Homo sapiens

<400> 574
ccgtctaatg ctggnttcta atcgctttct taangctcnn gggctcgntc tcnctncacg 60
cagcccggcg gtgcgaattc ggcacgaggg gattacaggc atgacccacc gcgcccagcc 120
tgtnatttct tatactntgt atttggnct tgtattatgc ttctgatacg ctataattat 180
ttatgtccat gtncntttct tcaatagact gtgaactctt cgaatgtngg actcctagag 240
ctagatnctc nattattnnn tattaaattg aatgacttgn aactacagat cctttattta 300
aacttcccaa atttctgctt tatctaggcn actctttaaa ttcttttatc tcatgtagat 360

ttcanaggct gaaataattg agatttttag tttgaagaaa agagaactgn ggatttaatg 420
gcnttattat tatattttta atggctgttt gggagtnagg ttgcagacat tggtcacttt 480
cctcctaaat ncttaaatat ttcctaaaaa caggncattc tttnttttnt tatggagtct 540
ggctctggcn tccaggctgg antgccgngg cccatcttgg cttactgcag ctccccttcc 600
cgattcncgc tggtctcctg nctngctgct cgggaggctn aggccnggga atcgttgacc 660
ccggaggcgg aggttncnan agcctnnacg ggccctnggn ctcccggctg ggtacnngac 720
cggacctccg nctgnat 737

<210> 575
<211> 766
<212> DNA
<213> Homo sapiens

<400> 575
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ggnatcccat cgattcgaat tcggcacgag ctttctccct ctgtgcctcc tgcttccttt 120
ctctctcctg cctctcctct gctccccatc ccactttctc atctgcctcc ttttctcact 180
tctgtcagtc tgtaagcttt gataacctgc ttaatactcc aaagtgtgag ttcctctgat 240
ctcttgattc cttagttcta atctcacgtt ttgtttttaa gagatggagt ctctcactct 300
gtggcccagg ctggagtgca gtggcatgat catagctcat tgcatccttg aaatcctggg 360
ctcaggtgat cctnccgcct gagcctcctg agtatctggg actacagatg cgtgccacca 420
agcctggcta attttgtctc atgtcttcta aaaattattt tgtgaagccc cttcacaaaa 480
aaccttaang gaaatctgat ggtgctcagg aatctaactc tccctaaacc atcctctttt 540
aactgcttct aaaatatctc tggtggcctt tcttagcctt tttctggttc attcaatgct 600
tcaaagcgct ttttgnttct aagttgagtn ctttgggggt ttgacaggta gtgacgtgta 660
gttttgacac tgttaacttg ttnaatacag tgaaaangtt tgtgaagtga aaaatgcttg 720
anaaagaatg gnaatgcctt tntacaaata aaagtnttgt taaaat 766

<210> 576
<211> 761
<212> DNA
<213> Homo sapiens

<400> 576
ggggtnnnna gngnnttgan cccctttctt attatcaagg ngctngcnct nnctnnannn 60
ancacaggcg ntgngaattc ggcacgagaa gataacctct taatgcattc atgttgtata 120
tgaaggaaat gagagcaaag gtcgtagctg agtgcacgtt gaaagaaagc gcggccatca 180
accagatcct tgggcngagg tggcatgcac tgtccagtag tatttattgc tttagagatt 240
gcttgtcgta cctgtatgtc gtcccttttt aaatatgttt tcctttttct tgaaactgta 300
taaagttttt ttccccctta gcataagcat cttatatata acaactcatt tgtacaaggt 360
ttttaagttt atatataaaa tgtgtatata tatttttgnt tccccttttt gacttttttt 420
ttctgtatga aacccagatg tcaccaaatg gacattaata gttgcattaa ggatcagtag 480
cattaacaaa agttgcttta aaagccatta tgtaaaacaa gacttgaaaa tgagtgaggg 540
aattttagcg acactgtctg agcacagtgg gaaccatctt cgtttcccct ttgaactcca 600
antgggatgc cctaccctgg cgccccttag gaccccggac tggcccgngt acaaaacttt 660
accgtgccaa aattcttaag tgaatttacc tttctncctc tttttgaagc tngaaatttt 720
tggtcatcan gntttgcttg tgatngtaca tanggtngaa n 761

<210> 577
<211> 803
<212> DNA

<213> Homo sapiens

<400> 577
gggtngttnn nnngtggnnt tnttnnnngt ttctaatnnt cgnggngntc ganctnnctc 60
nananagaat aggtttgnga attcggcacg aggtctcccg cccggcgccc ccagtgtttt 120
ctgagggcgg aaatggccaa ttcgggcctg cagttgctgg gcttctccat ggccctgctg 180
ggctgggtgg ggtctggtgg cctgcaccgn catcccgcag tggcagatga gctcctatgc 240
gggtgacaac atcatcacgg tccagccatg tacaangggc tgtggatgga ctgcgtcacg 300
cagcctctag aactatagtg agtcgtatta cgtagatcca gacatgataa gatcattgat 360
gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg tgaaatttgt 420
gatgctattg ctttatttgt aaccattata agctgcaata aacaaagtta acaacaacaa 480
ttgcattcat tttatgttca agttcagggg gaggtgttgg aggtttttta aatnnncggc 540
cncngcgcca atgcattggg ccccgtaccc acttttggtn cctttaantg aagggtttaa 600
tttgccccnc tntgccgtaa ttcatgggnc atanncttgn tttcctggng ttgaaaattg 660
gntaatcccc ttcnacaaat ttccnccaca atcatttacc aaaccccngg gaggcctttn 720
aaagnngtna aaanccctgg gggtggccct taatttaagt ggnnccttaa ctcncnttta 780
antgccnttg cccttcactg cct 803

<210> 578
<211> 738
<212> DNA
<213> Homo sapiens

<400> 578
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caagctggca gaagcacaga tagaagagct ntcgtcagaa aacacaggag gaaggggagg 120
agcgggctga gtcggagcag gaggcctacc tgcgtgagga ttgagggcct gagcacactg 180
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atgatttagt acttgttccc tctgttggga tgccagttgt ggcaagggga ggggaacctg 600
tccagtttgt accatttctt tgnatgtatt tctgatgtgn tctcttgatc tgccccccact 660
gtcctgtgaa ggacagctna ngncaaggag tgaaaaactt tacttcttaa aaaaaaaaan 720
nnnnnnnnnn nnnnnnaa 738

<210> 579
<211> 758
<212> DNA
<213> Homo sapiens

<400> 579
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gagaagtgct ccctgcaggc cgaagccatc cttgatgcaa acgacgctca tcaaacagag 240
accttctcct cccaagtcaa agggacaaat aagcctctgg gttgaacggt ttgagacatt 300
ctgccttgga ccttcccttg tcaccaaaca agccaacctt gtgcacttcc accaggcttt 360
cacccattcc ctgcaagcct tggtcttttg acctggccct caaccatgtg gctttccacc 420

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ctttggattc aggagctaac caggctcttn ctcgggggcg ggggagattc tgactcttaa 540
tctggattgt gagaaaaatc cagcaagttc catgatattt aaatccaggt ctgcattggc 600
ccggggcaag agtttaacat cttcgggccc tgcatttcct acatcttggg gtctgtacac 660
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gtcatnctgt cttctgnacc ttctggggaa aagggncc 758

<210> 580
<211> 816
<212> DNA
<213> Homo sapiens

<400> 580
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caacttatcc tatnctggcc aaacatagaa tgctttcggt ttgcaaggta acangatccc 660
ctttacagnt gtacnaaaaa tnancnntaa aaaaactnga gccctntaga acntnntagt 720
ggagtcggan ttaacgttng ancccagacc ntggattang gatncattgg atggagtttg 780
gacataccac cancttggaa tggcnantga aaaaaa 816

<210> 581
<211> 868
<212> DNA
<213> Homo sapiens

<400> 581
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gccttggaat agtaactctt ctcatttgtt tgggatctgg ccaccaagtn ccagaatgat 180
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gtttngtgac acagatgcac agtctgcttg tgaagacctt ctctcaagtg gcatttggga 420
gtccatgcca gancatggtg cttcatgaga gactgacagc tatcaggggt tgnggcactt 480
agngaggact ctcctccccc agtgtgtgct gatgacacat cacacctgac aatagctnga 540
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taaaatatcc aancaatggg gtcatacntg gcccaaatgc cagaantcna gagcctaata 660
ggacttccaa tnattaactt tnccaaannc gaaaaaagna gggcnttccn nttatggcaa 720
aaaaatnaan nnaaaaggan atntggnatn gttngccnaa aaaaaaagcc cnntnngaaa 780
cctaatanga ggaggtccca cttaaccggn cgnanccccca gaacantgga atacaggant 840
accnatngga ntgaanattt ggggancc 868

<210> 582

<211> 745
<212> DNA
<213> Homo sapiens

<400> 582
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agggctgtgc tatccaatac agtaaccaca tgcggctgtt taaagttaag ccaattaaaa 180
tcacataaga ttaaaaattc cttcctcagt tgcactaacc acgtttctag aggcgtcact 240
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attctagaga actaaactgg cttaacgagt cacagcctca gctgtgctgg gacgaccctt 360
gtctccctgg gtaggagggg ggggaatggg ggaagggctg atgagacccc agctggggcc 420
tgttgtctgg gacccttcct ctnctganaa gggaggcctg gtggcttaac ctgggcangt 480
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ntggccatta nctnccntna ccacttgnaa cccanggtcc canctggctg ggaccctntt 600
ntnccccaa ngncctttcc cttgggctnt nttggantga gcaccttctn tgtnngcacc 660
ttttanaant gnnnnnntgn tactgatttt tttgntaaaa agannttaaa anctggnant 720
ttntnaaaaa aaannannaa aannn 745

<210> 583
<211> 748
<212> DNA
<213> Homo sapiens

<400> 583
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ccttgcatgg tgtctaactt ctgcaataaa tgatctgcca gtcctagtgt ctgggcttta 180
tgcaatttgt tttcctttgt ggatgaagtg ggagtaagac ttgttgctgt gaggatcaga 240
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gcaaaggtga cttgcttgat gctttctttg cttgagcaca catctcattc attaaatggt 420
gtctcctttt ttgcacacag gatgcagaac ataattgacc ttttccaagt ctacttagca 480
gaaatgaaaa tggaatcata taaatacagt attatacttt aaaataaaaa ggctgtacaa 540
aagtttggct gacatagctt gcttctagta atctgaatgg cttatttaaa taaagttgga 600
tctatggact cttcacagnc tagatattat cctactggaa gatgtgcctc gaaagctgtt 660
gaaccacngc aaaaaaaccc ttcagtcagc acgtgagaaa acctgcgagc ccacatttcc 720
cccgggacca ttctgaacat cctactgg 748

<210> 584
<211> 773
<212> DNA
<213> Homo sapiens

<400> 584
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gtattgtgtc ctaccatgaa ttcactccat gctagccaca ttggcctgta tggctattcc 120
ttggacacac ctaggatgtt cttgcctctt agcttgccta cctttctctc atcatttggg 180
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ccagcacttc agtcaccctt tatcccatta ctctgctttt tcagaaacat tggtgctccc 300
tgaaacatat ttgtttactt gcttagtgtc ttttctcccg cactaccatg taagcttctt 360

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gtttttgcat tataaatggc tttggtgaaa tccctggcac aaaactaata ataaaagaaa     540
taaacagata atgttgaagt tctgggcctg caaaacctaa ctcttttaaa gcagtcccag     600
taaatgtgtc attgggatcc ataagacttt gtgggaaagt caacataatt ttattnggga     660
aaaagcattg aaccttcaaa agtnaaaact ttatnggncc aaaatctcaa ttactggggg     720
gccgttcttt aagtcatttt aaaccctttg angccnacag ttttacacca aat            773
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<210> 585
<211> 745
<212> DNA
<213> Homo sapiens

<400> 585

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tgggcagtct ttttctttcc ctatcagctg agtgaatgaa gatttagagg gcagcagagt     120
catgacatgg atgacgttgg gtctctggat ggctaaatgg aagacccgcc ccccaacgcc     180
actctacccc cctgctttga actatgcttt gagaaatgag cttatgagac cactgagact     240
tgggggctgt ttgttcagca gttcacctac acttattagg aaaggttgac ttcttgtact     300
acgcctttcc ttaaatcatc ttttgtataa ttctcagaac actgctggtt tgggtggtct     360
cacacatttc tcacatccaa attttaaaga tttcatgaat gttcattaca gtggatttat     420
ttttctcttt ctgcttctcg gcatgccctc tcaatttggg agaaatctct aattggatga     480
ctttggtggg accacaggag tgtaaggatc gtaattccct cacttcatcc cctgcaaatt     540
aaagcctggg cacttaagac tcactcaact gaatcttgat atgtgggact ttanatctta     600
agcaaatgan gcaaaagaag gaaaagacag ttgagaaaat caatctctga agttcagcac     660
ttgatttcca ccgtggaccg gactcctgca nctttgcatt ngccttggtt cctggccatt     720
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<210> 586
<211> 749
<212> DNA
<213> Homo sapiens

<400> 586

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ggggtcctgg tgggagtnnc atncagcagn ganngcattc tttccncaca ncagtnaacg     120
gtcttattaa nagccaccac tttnctgang cctgtacagg ccttgnnggt tnggngaaca     180
gaaatnncgc aggcacttgt accttcaagn anggacttgt gcctnactgn nagggttggc     240
gttgaccttg gctcnacnga catacccant ctgacttnna acgngcncgt ctnagcttac     300
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gtacgaccaa cagtcaanga aaagtgccaa gatatatcta tcccatttct tctacacctg     420
tanattcctn actatgctca aactatgtgg ngcaangaan actggnngac atttttagtc     480
aatgatgctg acaattaatt actggtgngg ccaggcatat nttcacggct gcttgtgatg     540
ccaacnaaga acgggcccca gcccatcctt actcctngnc cccaaanaga tccagtgnga     600
atgggaagct gnnannacca acccaactnn tgatttacca ccaacnccaa anatcacgca     660
tgnnnacagc aaaacaacaa cncnatgcac ttaacaagna nccnaaaant naactcgngc     720
ctctaaaact attngggant cctttanct                                       749
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<210> 587
<211> 783
<212> DNA

<213> Homo sapiens

<400> 587
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ttgctatact caatagaaca agcattttaa ataaatttct cgtaagttgt tgctttcttt     180
atgtggtggg tgtggcttta aagagcacaa aaccacaaca aatcaaagag tagctcgggc     240
ttgtcttttg ctttatggct gagggtttga aggatgattc atggacttgt gaatgccagc     300
cccagtcccg gcttaggtct atctgccaat accaccaggg ccaacaaatt cacgcaacaa     360
attctctcat tttttacagt ttatcagttg cactcatagt tattgtcata atcactcccc     420
acagtaacct gtaaggcata taaagtagct attttagtaa gataaatgat attttatata     480
tgttatgata agataaatct tatcatttta agaagaaact gagctcggag agatgaaatg     540
acttcctcag ttgctgctgt aataaaagtc tactttttgc taaaaaaaaa aaannnaaat     600
atnntntann attnnantaa naanaaaaac ttcgagccnt tttnaaactt tnantggagt     660
cnntttntcc cgtaaaatcc nnnactttgg atnaanannc catttngatn aagtttttgg     720
gacaaacccc ccaacttaga aattgcnntn ggaaaaaaaa ntgcntttta ttttgnggaa     780
aan                                                                   783
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<210> 588
<211> 771
<212> DNA
<213> Homo sapiens

<400> 588
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ctttttaaac ctttttggc agctcagatg gtgtaaattt taaaatttg tataggtatt      120
tcataacaaa aatatgtatt tcttttttgt tattttatct tgaaaacggt acatatttta     180
gtatttgtgc agaaaaacaa gtcctaaagt atttgttttt atttgtacca tccacttgtg     240
ccttactgta tcctgtgtca tgtccaatca gttgtaaaca atggcatctt tgaacagtgt     300
gatgagaata ggaatgtggt gttttaaagc agtgttgcat tttaatcagt aatctacctg     360
gtggatttgt ttttaaccaa aaagatgaat tatcaatgat ttgtaattat atcggttgat     420
tntttttgaa aagatgaacc aaaggatttg actgctaata ttttattcct tacacttttt     480
tctgaataag tctctcataa tgagtgcagt gtcagactgt gcctactctg atggtatngt     540
gccatttgta aaatnanaat aagagcagaa aaaacacaaa nangagaaca ctggnttcag     600
acattcantg ggcaagttta aattatggga ctgcaaaaat aatggatttt ttattcaaag     660
aaaagcttta aaaagtttta ttatccanat ttacaaccca ctanttaagc taaataancc     720
tactttnaaa aatngnaaat ggttnctatc tttataangt gccaanttna n              771
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<210> 589
<211> 844
<212> DNA
<213> Homo sapiens

<400> 589
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tncactnnaa tccttntnta aaaagccttc tgcntgatcc catcgattcg aattcggcac      60
gaggccagag cctagaggag agatcaaaga cnttngccga agtgaagccc attctgcaag     120
caactgggtt cccatggcat gtggtggcct tagaggaggt gttcagcctg ccaccgtcgg     180
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acagcttcct ccagcagcag catgtgctgg gggccggggg tggtcctggc ccgactcaag     300
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ctgcccagac tgaggctctt tcccaactgt tctgctcaat gaggacactg actgccaagg     420
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aggagcttct gcagaccctg cggacccacc tgatcctnca cgtggcccga gcccacggct      480
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tgcnctgggt ccaaagggcc ttcctggcct gggatacngg ctttcttgga tgaaccngna      600
ccgggngaac gtnggtggtn ggtgccggnn cattgcctgg gaaccaccac cccccttnaaa     660
angaangntc gnttatttct aacaaaaccc ggnccttgnt tcntaccntn ttccctntct      720
tggnnnnttt tnaanacncn annncccaat tngnaanaac ccnaaaangg gnccctttgn      780
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tnct                                                                   844
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<210> 590
<211> 767
<212> DNA
<213> Homo sapiens

<400> 590

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ccatagaata cagattctac agggattaca agaaacatat gaaccttctg agcacccagg      300
tttggcatag aaatggtacc ccttgttcaa aatgaacaag aagccttaga tttggatggg      360
gaacctgatc tgtccagtct agaaggattc cagtgggaag gtgtttccat ttcctcgtcc      420
cctggcttgg caagaaagcg aagcctttct gagagcagcg tgatcatgga cagagctcct      480
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gtttcaccta gtaactcatt ganggctgga cagaaccaga aagcaaccat gcaccctcaa      600
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<210> 591
<211> 765
<212> DNA
<213> Homo sapiens

<400> 591

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atgttaagtg gaaaaatata cagtttggta aaataaacta gattctacat ttatttgtgg      180
gtttttttcc cctcctttct ttccacagca cttttgatat caagcaagtg gcttcctttt      240
tgagatatta aaaaaaaaaa gaaaaggaaa aaagtaaatg aagcccaact acctaaccct      300
ttcttatttg tatttgtttt agtattgtga agttgtgtta aatagtacta gctagaaata      360
caaatttctg gttatcattt ctcttccctg tggcacttga cattttaatt gtcttaaagt      420
ttttgaagtc atcttctggc cccttgagta ctgccagagg caaaagatgt ttgtttctta      480
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acttgagaag attggcttga attangatca taatcatgtg tgatcccatc atgaattcat      600
tggaatntgg ggtncatgta angcaatcnt tctggtgtaa atcttccttt ttttaatgna      660
catatanttt tggaaaaaat tttgaattaa ccctgaaaat ttttaaaaaa gccctcttan      720
aactattann ggaggtcnca ttaccctaga atccanacat tnant                      765
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<210> 592
<211> 757

<212> DNA
<213> Homo sapiens

<400> 592
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gccccggccc ctatacccca gtgttctctt tgatccagtc ccgaaacaga gggagccttg 240
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gttttaccag ctcccaaggt ggacttcant gtgtgtattt gtgtaaatga gtaaaacatt 600
ttatttcttt ttaaaaaaaa aaaaaaaaaa actcganct ntanaactat tagtgagtcc 660
tatttacctt agatncagac atgataagaa tncattgatg aattttggac aaaccacaac 720
ttggaatgca ntgaaaaaaa atgctttatt tgtgnat 757

<210> 593
<211> 766
<212> DNA
<213> Homo sapiens

<400> 593
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agaaacatcc agaatgctcc tccccatccc ccaatcccag acagcaatta tgtcagccct 180
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tggtgaaggt ggtgagccct tctgaggccc tgatagaact ttccaggagt tcatggtccg 360
cggctccagc ttctcactgt aaagttgtca tcctggcaga ggcagccaat gcttttcatt 420
ctagggggta gagatttatg ctaatgagtg aatattgcac cactagtgac tttctgttta 480
aagttcagct cttagaaaat ggaatcttac ctgaccccta gtgaattatg tacataagca 540
gggaatgttt ccaactagat ctccttcaga agagtccctg tgctggaata ggtcactgaa 600
tcttatttgg ntttgtnaaa caaaagcttt tgggtctcgt ggggtgtgtg tgtgntttgg 660
ngtgtgttgc cccntntgcc gtttcaaata aaaggtttgg taccaccttt tcaaaaaaaa 720
aaaatantnt anntnanant nntntancnt ttnttnncnt tanant 766

<210> 594
<211> 754
<212> DNA
<213> Homo sapiens

<400> 594
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gcgcgaagtc ctcgtccaga gaaggcaacg gcgagaaaca aatccaacat cctgggctgc 180
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cgtattacgt agatccagac atgataagat acattgatga gtttggacaa accacaacta 420

gaatgcantg aaaaaaatgc tttatttgtg aaattttgtg atgctattgc tttatttgna 480
accattataa agctgcaata aacaagttaa caacaacaat tgcattcatt ttatgtttca 540
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gggccccggt nncccanctt ttggntccct ttaagnngan gggtaaantg ncgcncttgg 660
cntaatcttt gnncatnggt tggnttnctg nggngnaaat tggttttccn ggnnanaatt 720
tccccncatn ttangatccc nggnngntnt aang 754

<210> 595
<211> 767
<212> DNA
<213> Homo sapiens

<400> 595
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aagcttttat caagggtcca ccatgtgcca gccactgaag tagatataaa tacaaggatg 180
tgtaaggtat ggatgatggt atacgaactg tcatcttact ggatttgtcc gctctgttaa 240
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cangatctta tgcaactgtt ggaaagaatg aagcgatgct gcactgtggt catgcagtga 480
tctctaagac atattaactc gaaagcaaaa ggtttaacaa tgtatnacaa actgggctgc 540
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ngtcangagt ttgagaccaa acctggccaa tgttggccna aaccnctgct tctactnaaa 660
ctacnaaaaa ttaacctngg gcntggttgg ctccgtgcct tntaatcccn gcttactcgg 720
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<210> 596
<211> 743
<212> DNA
<213> Homo sapiens

<400> 596
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tgtggntttg tgcttctggt ttcctggcca accccagggt cacttgtctg gagcccagct 540
gggcactaat gtctgccanc gactatntta cagtgtataa atgattcctc tatttgggga 600
gagatcttcc aatccagaag agcccctntt ggactgcctg ggttaaatct gcatagcana 660
agtggttgat gagtcatctg aagaaattca gcccccaactt nncaacctgc ccttcctgnt 720
tcctttttaa tggnggcctn tgg 743

<210> 597
<211> 786
<212> DNA
<213> Homo sapiens

<400> 597
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nanaggcaga ngtggccctg ggaacagagt tttatgacnc ttttnaccat anangaangn 180
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gtggatgtgg agtttggnac ctngggatcg ngnaaagata ccagtgatgt ggagccaact 300
gctccgatgg aggaacccac agtggtggag gagttccant gcanccngga agaggagtat 360
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cacaatccan tgnnccttac taagccgtgg tgattnacaa gtcataaatc cattanatga 540
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acatcacatn tcctnttgga gattaaattt tnggtnancn tnccttcgtc cttgggcatt 660
ngaacncata agaatgcacc cccnggntag gcccngtnna aaggttnatg aaggccntta 720
taanttttgn nnccccaanc attaaantgg ctngattccc ttaatntttt cctcccnaac 780
ccagnt 786

<210> 598
<211> 809
<212> DNA
<213> Homo sapiens

<400> 598
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gcagaggcag aggtggccct gggaacagag tttttgacgc ttttgaccag agaggaaagc 180
gagaatttga aagatatggt gggaatgaca aaatagcagt cagaactgaa gacaacatgg 240
gtggatgtgg agttcgaacc tgnggatcgg gtaaagatac cagtgatgtg gagccaactg 300
caccgatgga ggaacccaca gtggtggagg agtcccaggg caccccggaa gaggagtctc 360
cagccaaagt tcctgagttg gaggtagaag aagaaaccca agttcaagag atgactttag 420
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cagaatccac tgttcttcca aagccgtggt gattcacaag tcaaaataca tagatgatat 540
ggtaaaaaga tgactatgag gaccattccc atgttttccg gaaaaccccc cattgacatc 600
acattccaac ttggagatta aattttgggt aacccttcct ttgtncttgg gccttngaac 660
ccntgaagga aggcaccccn ggtgaagggc ccngggggaa agggattcan ggnaagggge 720
cantaanaaa cctttgggga ccccccttaa nccaataaaa tttggtngaa ttgcnangga 780
atggtttgnc cccccnaaac cccnaaant 809

<210> 599
<211> 759
<212> DNA
<213> Homo sapiens

<400> 599
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gaaacttcaa gcaaattgga aaaagaaact tgtaagaaat cacaccctat tctatatgtg 180
tcttctaaat ctactccaga gacccagtgc cctcaacagt aaagactttt ctttaataag 240
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atatcacctt ctgggttatt tactcattgt gccaggacct ggcattttca tgtgcctttg 360
accaagtgtt cagaatttgc ttgactctaa cctggagagc ttcttaagtg atgccccttc 420
atggagcttc tatgacagtg aataaactat taattgaagg aaaatgttat aattaatgta 480

tctatttgct gcattgtata tggattaaat gataaaaaac aagtaatcta ccctcagagc 540
catgtatttg agaatgcttc aatcatattt tcctatgtac cttttttta taaacttagt 600
tttagactat gttgtaaaaa tggggaaagg ttgtaaacta tgtngtaaaa aatngggaaa 660
tgtggcttta aaatatatnc attatatttg gttcaaggat tttggcaggg gntaaaggaa 720
ncnatggttc aatctttgna tttatatacc ntgatttaa 759

<210> 600
<211> 769
<212> DNA
<213> Homo sapiens

<400> 600
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cggcacgaga gcaattccac tcctagctcc acccacaggt aattgaaagc aaagacgcaa 120
acagatgcct gtgcaccaaa gttcacggca gcatccttcg ccatagtggc agcatccgtc 180
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ggngcccacn gtcaaaagga atgagaccct gatgcactgg gcgacacaga cgggcgacac 480
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cngtgnccgg gacnggggtt gggagcgacc ggttgttggt ttngggtttc tttctngggt 660
gaaggaaatg tttttgatat tggggccgtt tgggtgatnt ttgcattacc ctttgaatat 720
gcttanaacc cnctagaaat tgnnacactt tttaaatngn ttggaaatt 769

<210> 601
<211> 755
<212> DNA
<213> Homo sapiens

<400> 601
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aggaggaaga ggagccactg atggagatgc ggctccggga tgcgcctcag cacttntatg 180
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acaatggaat atgatccctt aactcctgat ttgggatcat ctgaaggacc aaggnnggca 660
gtcttcgaag tggaataaaa tagccccggc ngtngtgact tgcacctata ttcccagact 720
tttgggaggc naannttnga aggattgntt gccct 755

<210> 602
<211> 773
<212> DNA
<213> Homo sapiens

<400> 602
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gagcaaatca agatcttcag gtacagttgg accaggcact ccagcaagcc ttggatccca 120
atagttaagg caactctttg tttgcagagg tggaagatcg aagggcagca atggaacgtc 180
agcttatcag tatgaaagtc aagtatcagt cactaaagaa gcaaaatgta tttaacagag 240
aacanatgca gagaatgaag ttacaaattg ccacgttgct acagatgaaa gggtctcaaa 300
ctgaatttga gcagcaggaa cggttgcttg ccatgttgga gcanaagaat ggtgaaataa 360
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aatctaagcc tttagtcgac tctggtactc tggaanataa cacctattat acagatttac 480
ttcatatgaa gctggataac tnaaaacaat agaaattgaa ngcactaaan gtgaattgtc 540
atacaagcga aatgaaancn ttatttgana gccngcgggc ttctaacata ttgagcgata 600
actttttgca aatgaaagat gcccttcngc tttntgaatt gnaaaatatt gaaacctgan 660
agntnanctt agntgaattg aaacttaaat ttgaaccctg nacnanaccg gttaantgcc 720
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<210> 603
<211> 784
<212> DNA
<213> Homo sapiens

<400> 603
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gattcgaatt cggcacgagg gggacatcag tgatcgtaag tctcctgggn ccgttattct 120
canattaggt gacggagcta agacttcgag accatctcgt cctttntgta tcgcggaaac 180
ctgangaacg agccggcggc ggtgacctgc acgagaagcc aggctaactg ggtgaagtac 240
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aggagtagct gccagtgcng gaagtagcgg agagaacaag aaagccaaac ccgttccctg 360
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antgcttgaa aaaatcttta gaaggnngca natcttccta atctcttgtc ttacggacca 480
cctggaactg gaaaaacntc cactattttg gcagcaaact tgagaactct ttgggcctga 540
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nttcganaag aaagtgaaaa atttttgctc aattaanctn gtgtcaagga aaatngnttc 660
anatgggaaa gccgttttcc nccttttttaa gantgggaat tcttngatga ngncnaattc 720
ntnttganct taactgnntt angcagcttt taaaaaanta ccattggata aangagtccn 780
aant 784

<210> 604
<211> 801
<212> DNA
<213> Homo sapiens

<400> 604
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ccctancggg actccaangn agccacacgc cccttctgga agggtgtgng catgtnaant 480
gtgtgccanc gcgtgggctg gcgtgtgaan atctatnaaa taagtatana tgggngtnta 540

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ctaagncaag agtnnntctn gaaaaacnaa ananagtnct ntntanannt ttacgtaatn     660
atcaatactn tntccacntn accctnctnn tanntntncc natatantcg antaattcnt     720
cactcntnna ttcctngtna acacnaatna atnnaactat naaatatntn tnctnnntan     780
tngacatann catncnnncc g                                               801
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<210> 605
<211> 759
<212> DNA
<213> Homo sapiens

<400> 605

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aggggacttg ttaccaggcc attttctgga tggcctgtga gatctctgcc cctccaagac     180
cctccaagtc tgagcctgac ccacagctgg gacactgaat tcagccctgg gaaccatggg     240
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ggcgggctgt cctccttggt gggagctgtc ctgcacactg taggatgctt aaaggtatcc     360
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gttctnaant gggcagacgc ctgggcaccc cttgggccct gcccaancat ggccatngng     660
cangcttttt naacccgcat nggntttcca ngcctggtga atcttgcttt tccanggacn     720
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<210> 606
<211> 809
<212> DNA
<213> Homo sapiens

<400> 606

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gttgaggcag gagaattgtt gaacccggga ggcggangtt gcaatgagcc aanatagcac     420
cactgcactg catccttggg tgacagaagc gagactccat cttaaaagaa gggctcctgt     480
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gacattttac atntttncnn agtttnctta atttaaagtt gnctaatttt accattatac     660
attttnaatt ggcatttctt ttaccnatnc tttttgtntg aaaatggtan tntttgaaat     720
cngnatcngt tctaatgngn tntattttna ccnaatgcca atnntacctn ctttgnaana     780
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<210> 607
<211> 788
<212> DNA
<213> Homo sapiens

<400> 607

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cacatgaaaa ctcacaggca gcaggaggaa caacagaggc aaaaggctca gaaggcggct     300
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ctgctgcccc tggaccagct gagtctgatc aaacccatca aggatgtgga catcctcgac     420
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ggaatgcctg ctttgttttg taaccccttt ttaaaaccta cctgttttta aaaagtggtc     660
atttttantt nacgntttan aaanaaaaan tcctatttct ttttcctttt nattttaaaa     720
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taaaaaat                                                              788
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<210> 608
<211> 796
<212> DNA
<213> Homo sapiens

<400> 608

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agaatacccc acgtttttat ataaggagga aaaccggnaa aanaatttaa aagttaaaaa     480
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<210> 609
<211> 790
<212> DNA
<213> Homo sapiens

<400> 609

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tttttctctg gcaacaaagc ttgatgtttt cactgcttta gtttcctgtt tgctggtggg     420
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ggttgtgggt tggcacangg aattttgggg cattggggaa ggggntttca aaacttttnc 720
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antcttngnc 790

<210> 610
<211> 786
<212> DNA
<213> Homo sapiens

<400> 610
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gtgcctctgc tgggggagga gaacctctgt ccacgtggag gctaggaggt ctcaggtgct 180
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<211> 938
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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ggtgacanag ctaaaacaan acaagccnaa ccnanaagga aaaccccagc tttagggata 720
ctctgntcat ngaatatagc ctgaaaaatg gntaatcaag aaagtnaacn t 771

<210> 613
<211> 774
<212> DNA
<213> Homo sapiens

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<210> 614
<211> 754
<212> DNA
<213> Homo sapiens

<400> 614
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ggaaaaatgt gttgtaattg gtctgcantc tacaaggaga agctangaac atttagaaag 660
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<210> 615
<211> 774
<212> DNA
<213> Homo sapiens

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gcagtttann atccttatgg aanttttca cantgtnaca nggtnttgta atacnttgga 720
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<210> 616
<211> 769
<212> DNA
<213> Homo sapiens

<400> 616
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cntgtntgaa accccсttaa cttatngccn atttncntna agcaaccctt aggcnanttg 720
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<210> 617
<211> 766

<212> DNA
<213> Homo sapiens

<400> 617
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ccaggtggca atcatgagtg aatggatgaa gaaaggcccc ttagaatggc aagattacat     180
ttacaaagag gtccgagtga cagccagtga gaagaatgag tataaaggat gggttttaac     240
tacagaccca gtctctgcca atattgtcct tgtgaacttc cttgaagatg gcagcatgtc     300
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cccaccatat gggtccacaa naantgcagc atctctaatg aganttattc ttgcccttng     600
ttcaangatc ttattgaaag gacatcttac agcttttccc aatgagaang cccangaagt     660
gttaaacata ctgnnttgaa aaaagcactn tatnttntcc cntnttaana tggtntctaa     720
aatgtanaaa naaannaaaa naaaanctcg atccctctnn aacnct                    766
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<210> 618
<211> 762
<212> DNA
<213> Homo sapiens

<400> 618
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ttcgctcagt gcagcgatca tggctcagtg cagcctcaaa ctcttgggct caagcagtgc     120
tccaacctca gcctcctgag tagctaggac tataggcaca cagcaccatg ccccggctat     180
tttttttattt tgtagagatg gggtctcact atgttgccca ggctagtctt gaactcctgg    240
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gtacctggcc cttggtggaa tctttagggt tttctattca tacatataaa atcatatcat     360
tggcaaacag agataatttt acttcctcct ttccaatttg gatgccttag atttcttttc     420
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aaaanaaaaa atataacnnn ntanttnatn aantnnttaa naaaanaaaa actggnacct     660
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<210> 619
<211> 754
<212> DNA
<213> Homo sapiens

<400> 619
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gccggccacc tggaggggca ttgcttggtt cgcgtggtag cagaggagct tgagaatgtt     180
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gagaagctat tccccaaaca atgccaagtc cttgggattg tgaccccagg aattgtagtg     360
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tntctgcaan aagtangnca gcacttttca gtgatttgaa tatcatcttg gcttngangc 660
cangtggaca accttgtcat aactgacttc tgaaaagaac cctntngata tttgatgcct 720
cnggtgtngg tggaactgtc atttantngg anna 754

<210> 620
<211> 767
<212> DNA
<213> Homo sapiens

<400> 620
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<210> 621
<211> 828
<212> DNA
<213> Homo sapiens

<400> 621
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tncttaaaca tatgtgaaca aaaatttngt gatggaagga ttctagttaa tgagtattgc 180
atcaagattt acatctttct tactaaggaa aagagttaat aaaaatngnt ctttatttta 240
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tannnnttcn ncttttgnnc caananntca ttttaancca ccaaaantcn caattnttnt 720
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<210> 622
<211> 784
<212> DNA

<213> Homo sapiens

<400> 622
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<210> 623
<211> 1164
<212> DNA
<213> Homo sapiens

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<210> 624
<211> 798
<212> DNA
<213> Homo sapiens

<400> 624

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<210> 625
<211> 793
<212> DNA
<213> Homo sapiens

<400> 625
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gnccttgttc aaaccaaaat ttnttggnat ttgccagatt ccttantntt gccatgggcc 720
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<210> 626
<211> 825
<212> DNA
<213> Homo sapiens

<400> 626
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gcctgntcct nnttcacgct tancacttat natatgatcc cactattcac tnantctctg 360
aagcttaaaa cctangattc atgcttgact actgnataat nntacaatct actcctaatg 420
cattagcaat tcttgctagc tctaccttca aaatatattc tgaatagact atntcttgcc 480
gnttcccttg cctncncatt tcccatctgc accccttctc tnctncccaa aatcaataca 540

ctagntgttt ctaaaaaaaa tatnganann tagnnnaaaa ncntaaataa atntaaaana 600
angnntancn tnacanaana ttnctaatat aggnnanntn ntgncaanaa cnntaantnt 660
tnaatacgnn aaaactctct cnaanngann aanntatnnn agttaaaagn naaatannnn 720
aanantncca aatntanaag ataangncat aannntatna gncnnaacgc taantgnnga 780
tganntntaa tnngnatana nnantngtta nnacaaaatn tacnn 825

<210> 627
<211> 772
<212> DNA
<213> Homo sapiens

<400> 627
tttttaatgc ttngtcgnac ttctcccagn aatcgnttng aaactcngcn actcgttctc 60
tctgcangat cccatcgatt cggaaatttg cactgatggc tcanaaggct tacgttttgg 120
agagtatgac ctacctcaca gnagggatgc tggaccaacc tggctttccc gactgctcca 180
tcgaggcagc catggtgaag gtgttcanct ccgaggccgn ctgncagtgt gtgagtgagg 240
cnctgcagat cctcgggggc tngggctaca caagggacta tccgtacgag cgcatactgc 300
gtgacacccg catcctactc atcttcnagg gaaccaatga gattctccgg atgtacatcg 360
ncctgacggg tctgcagcat gccggccgca tcctgactac caggatccat gagcttaaac 420
aggccaaagt gagcacagtc atggataccg ttggccggag gcttcgggac tncctgggcc 480
naactgtgga cctggggctg acaggcaacc atngagttgt gcaccccagt cttgcngaca 540
gtgccaacaa atttgaggag aacacctact gctttanctc ngaccgtgag acacttgctg 600
ntnccntttg gcaaagacca tcatgganga ncanntnggt nctnaancng nntggccaac 660
atnctcatca acctgtattg gcatgnaccg cncttgctgn acnncngngc caaancnctc 720
nantccgcca ttggggcttc cggnaaccac tnnacaccaa ggttctnttg gc 772

<210> 628
<211> 808
<212> DNA
<213> Homo sapiens

<400> 628
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ttcggcacga gatgacatcc tcattatcca cantgcaaag ccaaccatcc ctatgatggg 120
ttcattgtgg atcatgactt antgggtcaa gagtttggaa gtggctcagc tgggcggnct 180
tctgctncat gtggctgcca natggtnccc tgctggtnng cagnctngtc tagagggtcc 240
atgatggctt tactcacatg cctggcatct tgacagggac agctggnang caaagnnnat 300
ctgggactgt ncacagagct ncttcntgtg gcctttccag catggtggtc taagggtagc 360
tggacttnct gcatnacagc tcagggctcc cagagctact gtcccaagag atnnaaagtg 420
gnaactgnca atcttttang ctaangncca gaaaccatta cccctgcacc ncacagtctt 480
tttntanctg ntgaaataaa cattnnnttt atcaattnta ancattcgca aattggaatt 540
aaataccttt tactaatttt gncgtgacca tctgcccctn gttcaagatc taaaaaactt 600
ttatngntca tcntgnngat ntaaaaaact nttgtgttng catttanaac ccntaagcan 660
nttnggcant tanannnaan annttnnnaa acccttntat anaaccttat taagttgang 720
catnngnant ttcnccttna aatccnaggt ccttagggct angnnatacc nttcntatng 780
naactttngg gaacctaaan cctctcct 808

<210> 629
<211> 827
<212> DNA
<213> Homo sapiens

<400> 629
ggccnncttt gaaccttntt caaatcnttt ggcactcgcc nctctctgnt ngntcccatc 60
gattcgctgt gatccaaggc atgaaaagag tgcaaggtaa ncangnggca gcnttnatng 120
aagcatnaaa taangcnaaa gcnnatgctn anctnangga gcangnngct aaagacaacc 180
acannctanc tgnntnctaa tcatgctntg cttnctnang tganettata gnaacgcant 240
nagactncan gcnttgcttg gcncaacaag gnnacctana ntcatnanga agcnnttgaa 300
ctaangagtg gctacnncct ttnntnctca tgcntgacct gtaatnattc ttctganttg 360
aggcaanagc gggtnnaant natngntnan ntgnaaanac tntnnnatcc gnnnntnctg 420
attannttnc attnntntna atgatanann ctcatcnngc tcgncctgna ctttganang 480
ctnnnntcnn anntnnctga ctttaggagn nnacctncag cganatgtna agnanngaaa 540
ttnanntncc tnncgntccn ccttgcngac tnanngtctt gngnaacntn angtanntan 600
tctacngggn gnnacnttgg nnaattgggg ncttataaan tnttcntnna agaatgantg 660
naccaattnt nnaanntcta agnttgggga aatctnngtt tcctgnatnn gnacaaaaan 720
tcgatttann ngncnngntt nnttgggcnt catntgccat tgatgcnatt cnacttatgt 780
cctcntggng cntnttnnaa nnnggnngnn aacatttttt gtgtgcc 827

<210> 630
<211> 793
<212> DNA
<213> Homo sapiens

<400> 630
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tctctgcatg atcccatcga ttcgaattcg gcacgaggcg ngttgttcta cactgcnntc 120
ngaagntttn ntaanaagcc accacttagc ngaggcnnct acangtcttg gggncttagc 180
gaagagaaat cncgctggca cttgncccgt tcacntaagn actnntgnct gantccnagg 240
gtannngtnc accttgngnn ccancagaca nacccaannt gncntaaaan gggcaggtct 300
aagcttacnc tngactncac nggcaagctg nangcctgtn ctgccttccn ctgcnntnac 360
aaatngacag tnngaccaag agtcanagna aaaactncaa ggatacatnt atcccantct 420
nttctacacc tntanattcc ntganctatt gctcanaccn atcgtgcggg caaaggcaag 480
acttgggcaa cattnttnaa tacaatgatg ctgacaanta atttccngct ngttgccagg 540
natntttacn cgagctnttg tgattccaaa ctaaagaatg gngccnnnan gcccntcntt 600
antnctggnc ccccanaang ancctaactn gcgaaaggnn agnatggcat tnacccaaac 660
caacttntng gattacnnca actccanaan atccgacggc atnnaanang caaaacaaca 720
acttcncnan natnnaanna atngnnccnn aaananaacc cgngcntctn aaacnattgt 780
ggacccatnc ccc 793

<210> 631
<211> 752
<212> DNA
<213> Homo sapiens

<400> 631
gnagtnncct tngancctct ntnaaatcgc tttngcnant cgcctctttc tgntngatcc 60
catcgattcg aattcggcac gagatgttac agacatgaaa tatgaacaga atnctaaaag 120
aacataaaag aataagagct ccttaaagat tataaataaa tggtgatgtt aaagtaatag 180
caccattgga cgaagctagg gaatcaacac ttgacagaaa gatacatatt ttttttatac 240
aaactacata tatttgagca atcaagtagt agacatagag aattttcttt ttatggaagt 300
actctaataa gtaaagggct gatagaatta tatcagcatt ttctagctcc tggtgaatta 360
tgcattgggc atccatggct gccttagatc acaaaaatac caccagatat atgcctgtgg 420
atgaaagatc acaccaccac ctgtgaaata gtcttcccca caaaaaatcc aacccaaatc 480

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ctatccagcc tgtagatggt actcgagatc ttctataaga aataaagaga gcangctggt     540
cacggtggat tgtgcctgta atcccagcac tntgggaggc caangcaggt ggatcgcctg     600
angtaaagaa gttcnagacc agcctgccaa catggtgaaa cccccctctn tacttaaaag     660
taccnaggat gagcccggcc gttgtggcaa gcacctgtgg tccccagcta cttgggaagc     720
tgagcangaa aaatcgcttg aanctgggga ng                                  752
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<210> 632
<211> 751
<212> DNA
<213> Homo sapiens

<400> 632

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gnnnnnnttn nnnnnttcta atgcttggct actcgttctt tntgcaggat cccatcgatt      60
cgcaactaga gaagattgga cagcaggtcg acagagaacc tggagatgta gctactccac     120
cacggaagag aaagaagata gtggttgaag ccccagcaaa ggaaatggag aaggtagagg     180
agatgccaca taaaccacag aaagatgaag atctgacaca ggattatgaa gaatggaaaa     240
gaaaaatttt ggaaaatgct gccagtgctc aaaaggctac agcagagtga tttcagcttc     300
caaactggta tacattccaa actgatagta cattgccatc tccaggaaga cttgacggct     360
ttgggatttt gtttaaactt ttataataag gatcctaaga ctgttgcctt taaatagcaa     420
agcagcctac ctggaggcta agtctgggca gtgggctggc ccctggtgtg agcattagac     480
cagccacagt gcctgattgg tatagcctta tgtgctttcc tacaaaatgg aattggaggc     540
cgggcgcant ggctcacgcc tgtaatccca gcactttggg aggccaaggt gggtggatca     600
cctgaggtca aggagctcga gaccagcctg gccaacatgg tgaaacccca ttcttttctt     660
aaaaatacca aaaaatttag cccangtgtt gaatggntgc atgcctgtaa ttcccagctt     720
ctnanntagg ctnanacaag gagcttncnt t                                   751
```

<210> 633
<211> 806
<212> DNA
<213> Homo sapiens

<400> 633

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ttnnannncn ttttnaaaag gcctnnnntt gannctttcn aatgcttggc tactngntct      60
ttctgcanga tcccatcgat tcgaattcgg ctntagggaa ggggagggtt ggtgagtccc     120
agaccttaaa aatacaaggt taagagggac cccaaagcaa aaaattccaa cccttttcct     180
cccagtcatt gaaacaccaa aactattata ccggagggtg taatagtttt gctgcccagt     240
tgtggtaggc cagtagtggc ctcccaagat gcccatgtcc taatcccagg aacctgtcaa     300
aattaccttg tatggccaaa ggggctttgc agatgtaatg aagttaagga tctttcgcca     360
ggaagattat cccagcttgt cangagggct tgatgtcctc acccgggtct gtataacaga     420
agagcaggtg acgggagagg aggttggagg tgtancgatg gacangaaac tggagttata     480
ggagggcagc tnaagccaca gaatccaggc cancttanga gcccaggaaa atgcatttct     540
ttccacaaaa gcccttggaa ggccccaanc cctgcttccc acccttggac tnggcttcaa     600
tgaggcttaa tttttataaa ttcntggctt gattttagaa ctcntaaggg gaaataaatt     660
ttgtgttngn tttaantcan aaaataaatn aattaaaaaa aacttgaanc ctttanaaac     720
tntantggaa ttcntattan cttaaanccn aancttggat taaaggatnc atttgtttna     780
anttttggga cnaaccccca anttnt                                          806
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<210> 634
<211> 775
<212> DNA
<213> Homo sapiens

<400> 634
ngggacttcg cctnacgaac cgctnggaaa tcccntntnt gnaggatccc atcgattcga 60
attcggcacg agtataaact ttattttatt ctcttctggt tttgtgttac atgacaagaa 120
attgaattaa nncaatanaa ttttagttcg ggttgcttag gtttttactg ctcccattct 180
tgcttttact aatttatcca agattagatg tgattactat ttaataataa tttagtcctc 240
acacttacaa accacttaca ataccagcat gcttctatca ctgtaattct attcaattct 300
caggcccatg aggcatgcca gccagacgac cagacagcat ttatagagtg ggcactcaat 360
accagccaca aaagatcctg tgtcagaagg ggaaacaggc ttggaggctt ggagtatgtc 420
gtgatagcct ccctccagtc cacacaactg gtactgctgg ggctgaaact agaactcang 480
cctatgcctc tcaagctcaa gggtcggatg tccatgtnct tcgcctctag aactatannn 540
gagtcgnaat tacgtagatc caagacatgg gtaagataca tnggatgagt tnggaccaac 600
ccaccaacct aagaatgcan tggaaaaaaa tgcttaattt ggtgaaaaat ttgtgatggc 660
tattnngctt aaatttngnn aaccatttna taaagnctng cnantaaaan aaaggtttaa 720
ccaacccaac caattggcaa ttccatttca anggtttcaa gggtccaang ggggg 775

<210> 635
<211> 784
<212> DNA
<213> Homo sapiens

<400> 635
ttgagngtcc tnctttnacc ctttcnaatn gcttggcnac tcgctctntn tgnaggcatc 60
ccatcgattc gaattcggca cgagatatag ctctggaggt caggacatag gagatattga 120
ttcaggactt gccagagtat ggtcttgggg tgtgccctga tattacaaac agggatctta 180
gtggctaggt gatgaggcca tggcaaatgt agatggacca agatcaattt gcctttctag 240
atgaggtttt ctaggtgaaa tgtttttgaa actattttgt agcctagtat aatttataaa 300
agtagagaga aactataaat ataaatttgg aangggttag ctaaaaggag aaaacagcan 360
aatcttcata tatatanaaa tggatattaa tttgctagaa ttaanagact gcaggtaaag 420
atagnttttt ttaatacctc tttttgctgt anaaaggaca ggattaaatg atnaagggat 480
gctggaatga ggaatggtaa ctttaggcaa gatagtcttc tgngacggct gatatgaaca 540
atngagagta anacatttnn aatacaanaa attgtcctgc tgctcaccca tcaagccttt 600
tcangtttct tcccttgcca aaantngtaa naacttntgg tacttttnna ncttgtatnn 660
ttccngttna ttggttanaa ccccttcgat naanaanncc atantttnaa tttgggnttg 720
acccccnagg ttaaaanttn ccntttnctc aatttcccct tttcaaagnt ttaacntaat 780
taan 784

<210> 636
<211> 765
<212> DNA
<213> Homo sapiens

<400> 636
ttnnannctt tcnaatnctt ggcnactcgt tctttctgca ggatcccatc gattcgtcct 60
gcgcaggagc cgcagggccg taggcagcca tggcgcccag ccggaatggc atggtcttga 120
agccccactt ccacaaggac tggcagcggc gcgtggccac gtggttcaac cagccggccc 180
ggaagatccg cagacgtaag gcccggcaag ccaaggcgcg ccgcatcgct ccgcgccccg 240
cgtcgggtcc catccggccc atcgtgcgct gccccacggt tcggtaccac acgaaggtgc 300
gcgccggccg cggcttcagc ctggaggagc tcagggtggc cggcattcac aagaaggtgg 360
cccggaccat cggcatttct gtggatccga ggaggcngga acaagtccac ggagtccctg 420
caggccaacg tgcagnggct tgaaggagta ccgctccaaa ctcatcctct tcccaggaag 480
ccctcngccc ccaagaaggg aagacaagtt cttgctgaan gaacttgaaa cttggcccac 540

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ccaactgaac cgggacccgg tcatgcccgt tccnggaaan gtctattata aaggagaaag     600
cttcgagtca tcanttgang gaanaagaag aatttcaaaa gccttcgctt atnttcngta     660
ttngcccgtg ccaaacnccc cngctttttn ggcttaccgg ccaaaaagaa gccaanggan     720
gcccnnanaa cagggatntt gaaaaagaaa naatnaaacc ctcnn                     765
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<210> 637
<211> 853
<212> DNA
<213> Homo sapiens

<400> 637

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ttttggancc nttctttgan nctttctaat gctgggntac tcgntctctc tgcaggntcc      60
catcgattcg aattcggcnc gaggatcagc ccacctcggc ctcncaaagt gctgggatta     120
caggcgtgag ccaccttgcc cagcccacat catacagttt gaaatgaaac tttgccacaa     180
ccagcctttg ctgtagcaca cacatatatc actgaacctg tttgaaataa agtttttttt     240
ctttntcctc tggtattctg ggttctgaag tctggtattc tggtattctg ggttcaaaag     300
tatgacttga gagtgttgct ctggtattct gagagttgct ctgtattctg ggttctgaag     360
attatttgaa aaataactcc tactacattg aaatgcagac ttaaaaattt aaacattgga     420
ttangcagtc aaaaaaacca agcaagcata aaaggtcaat aagttgtaat cttgatagta     480
aaggtggaaa acttattata aatggnaang aaagttttat ttcctttttt gtttgaatgg     540
gcaagtatgc catattatac ccaaaagttc ttttaaaaaa atatttccca ttcaacccat     600
ttttaattna aaattaaaac cattttgnaa gggaaanttt acccaanggc aanccttttt     660
tttcctccaa aaaggttnac cntgttnatc cttctttttn ggnaaattta nccaccaatt     720
tttttaaagg ngggncaatg gggnttaaaa ntanccctgn aagnnatttt ttnanccttc     780
caggtttaaa antcccccttg gatngggtct taacctgggn gggtngnata naaaaaaata     840
natcctnttt anc                                                        853
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<210> 638
<211> 740
<212> DNA
<213> Homo sapiens

<400> 638

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anttgntctt tntgcaggat cccatcgatt cgcagcaaag actttatttt tgtacagaag      60
atggtgaagt ccaagacggt ggctcagtgc gtggagtact actacacgtg gaaaaagatc     120
atgcggctgg ggcggaaaca ccggacacgc ctggcagaaa tcatcgacga ttgtgtgaca     180
agtgaagaag aagaagagtt agaggaggag gaggaggagg acccggaaga agataggaaa     240
tccacaaaag aagaagggag tgaggtgccg aagtccccgg agccaccacc cgtccccgtc     300
ctggctccca cggaggggcc gcccctgcag gccctgggcc agccctcagg ctccttcatc     360
tgtgaaatgc ccaactgtgg ggctgtgttc agctcccgac aggcactgaa tggccatgcc     420
cgcatccacg gggggcaccaa ccaggtgacc aaggcccgag gtgccatccc ctctgggaag     480
cagaagcctg gtggcaccca gagtgggtac tgttcggtaa agagctcacc ctctcacagc     540
accaccagcg gcgagacaga ccccaccacc atcttccctg caaggagtgt ggcaaagtct     600
tcttcaagat caaaagccga aatgcacaca tgaaaactta cangcagcan gaggaacaac     660
agangcaaaa aggcttaaaa aggcggtttt tcagctgaaa tggcaccnnc aattganagg     720
actacngggc cccgtggggg                                                 740
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<210> 639
<211> 774
<212> DNA
<213> Homo sapiens

<400> 639
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catcgatncn aattcggcac gangtgatgn cagattgnna ntncactaaa ctgggcannn 120
catcaggatc acctgtgggc cttcannaat cananatnca cccccaggcc atgccctnga 180
cccagtgcac caggacaaga aatccacccc aggcctctcc cnagacccac tgnaccagna 240
caagaaatcc acccccangc cangccccnt acncactgcc ctangatntn nnggtgtnaa 300
ccnggtggtg ctttgtaaag acgtgcangt ggtaacccca cgccgncncn ctcnnnacnt 360
tggacacatg atcatccacg tgtctgtgat ttgnttcctc ggnttnnttt gtgaatngaa 420
aataantgtn ncgtttgact agggtttaag agcagcaggc agnccctcag ctcagcaagc 480
ngccctctca gctcagcang cagcccaagt ctcctgtang acttctatgg accatnctgg 540
cgggaatgaa gaaactggtc aagctggatt cgggactgaa agtgtaccnt ggtgacaccg 600
tatgactnan ctgactnana aagatcactn atctttccac acttgnnggg naggagccnn 660
tannangttc aatatgcnnt ggtngantcc catngctaca atttcatgga cacantttga 720
ttacttnnga taannnaggc ccttggaggc cccttntccc cttttaacng gaat 774

<210> 640
<211> 743
<212> DNA
<213> Homo sapiens

<400> 640
ctnnncctcc ttgatccntt cctnctttga anncatnngc tacttgttct ttttgcagga 60
tcccatcgat tcgaattcgg cacgaggctg acctacatca gaagctgctg gatgcagnaa 120
agtgaaaaca gaccaaaaca acacngggcg aatcttnaca ccattntggg tgccnnatnt 180
nnccnnngat atttgcttgc tnagctctac tcctccaaga nannangnnt caaacnctnc 240
agcangntag agcanntnaa gaccgcntnt nctnacctnc tnaagannct ctgngaggan 300
cgcaatcctt tngtggaana tagaatcaac agaccacact gcnctctgga ccatgngctc 360
tcaaangngc tagaaggtgc tgaccttttn agactcttgc agaagaggcg angtggtgng 420
anaccctnna ggaanacttt cccgaactag accncnnctt ncngaacnng ntcaactgtt 480
ggggnngaaa ncntgtgann tgtngncctt cngagagacg gcatattcta tgatggcnga 540
cttnatnctt ctgcggaacc anactngacn tactgaaaga aanctganac caagcgtctt 600
ccttaaggac ccttatatcc agacnatcct ttggataata ccnctnggcc aaaacctnnt 660
aactntgcat acaatcngga tggcaacatt tgaactggng gccttnanna ccnttaccgg 720
cttttcncat tatgnaagag ntn 743

<210> 641
<211> 740
<212> DNA
<213> Homo sapiens

<400> 641
ctttcctttg antcttcttc tannaaacgt tngaacgaan tcngcacgag accactaaca 60
gcatctactt gactactgat actttgatca tggagtttgg gcatgccact tgatagaaat 120
ttgaagagca attatatttt tcaaaaagag ttttgaataa tgttaagata gattgcaaca 180
tgactatcaa ttcttccctt cccatcaaag gagagagtcc gtttatccag cctttgaatc 240
ttgattattc aagtgacttg cttcacccaa tgtaacatta ataagcacaa tacaagcaga 300
ggcttgccaa gaacttggtt tgtttctaat gcttagaaga agaatggtgt atgccatatt 360
tctgcattta gaactcacgt ggagacatgt gtggcccaat tgctcctctt tcatctcagg 420
caataaccag acacgggact gaggccatcc atgaccagcc agccctagtc aacacacaac 480
acacaagctg atcacagatg catgagtaag cctaactgag accagccaag accagcctag 540
aatagaactg ctcagcagca ataaaaacta aataaattgt taccttaagc tacttttaga 600

gctatttgga agtgtatttt tgtgcagcta acatttacta tcagataaaa tggtgattgn 660
ttatctctgn tttaatgatg ntttaaggaa atggttctat taaaaggaaa tatctggggc 720
tttgtcaccg ttaaaaaaat 740

<210> 642
<211> 737
<212> DNA
<213> Homo sapiens

<400> 642
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agatgcagcc accaccagca gaagcgatca nctgacccca caaggttttc gtggctgtgg 120
ccgtgggctc aggtggcagc tatggagccg aggatgaggt ggaggaggag agtgacaagg 180
ccgcgctcct gcaggagcag cagcagcagc agcagccggg attctggacc ttcagctact 240
atcagagctt ctttgacgtg gacacctcac aggtcctgga ccggatcaaa ggctcactgc 300
tgccccggcc tggccacaac tttgtgcggc accatctgcg gaatcggccg gatctgtatg 360
gccccttctg gatctgtgcc acgttggcct ttgtcctggc cgtcactggc aacctgacgc 420
tggtgctggc ccagaggagg gacccctcca tccactacag cccccagttc cacaaggtga 480
ccgtggcagg catcagcatc tactgctatg cgtggctggt gcccctggcc ctgtggggct 540
tctgcggtgg cgcaagggtg ttcaggagcg catggggccc tacaccttcc tggagactgt 600
gtgcatctac ngntacttcc tctttgcttc atccccatgg tggtcctgtg gctcatccct 660
gtgccttggc ttgaatggct ttttggggcc tggncctggg ctgttaaacc gccgggctgg 720
natttaacct ntnggcn 737

<210> 643
<211> 748
<212> DNA
<213> Homo sapiens

<400> 643
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gaagtgtaaa tgaacataca ntttaaggag aaagcctgct gtgtttnnct tgttcagcag 120
ggtattatga attagcacaa gtattgcttg ctatgcatgc taatgttgaa gatcgaggga 180
ataaaggaga cataactccc ctgatggcag cttccagtgg aggttactta gatattgtga 240
aattattact tcttcatgat gctgatgtca actcccagtc tgcaacagga aacactgcgc 300
taacttatgc atgtgctgga ggatttgtat gacattgtta aagtgctcct taatgaaggt 360
gcaaatatag aagatcataa tgaaaatgga catactccct taatggaagc agccagngca 420
ggtcatgtgg aagttgcaag agttctttta gatcatggng caagcatcan cactcattct 480
aatgaattca aagaaangtg ctctaacact ngcttgctac aaangccatt tggatatggg 540
gcgctttcta cntgaagctg gtgcagatca agagcncaaa acagatgana tgcacactgc 600
cttaatggan gcctgcatgg atnggacatg tanaggtggc acgtttgctt tttggatant 660
nggtgctcan gtgaacatgc ctgcataatc atnttgaatc tccattgacg ctagctgcct 720
gtgganggac atgttgaaat tgcngcct 748

<210> 644
<211> 759
<212> DNA
<213> Homo sapiens

<400> 644
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gagggaacca tganancсna gagctagaat tgctattgga tnncgtctat tctctntttg 120
cttattgggn cgngntncgt ggttnctggc ctcangggtn nncccgaang anggggtatc 180
tnngagcnan ttntgcnntt tacnggctag cttgntgggg gcttaanntg ccactnttan 240
acatgctnta ctantcantg agannntncn ntcgaccatn tannacnatn ctgtgnnntc 300
cngtacnctn tggccgnatg gagctattag cttcaanatg nntcgnantg ttacatgcan 360
ncactgannt nactatccan natntaagtn ctcttngctt actgtgaaca nnngctactn 420
ncttggatat tatagnaagg ntcnttgata cncgatnatc ntncntgtca gatcnataaa 480
tancanctat accnactgtn naaatnccat ctggnggnct tncnatccan acataattgc 540
attannncgt cnaattgnga tanagtnttg aaagantctn ggtttagacn ttggatgttg 600
caatgnttgt gncttanaan ttatgtgctg gctactgant aanctggggg catgacntta 660
ctggnttgac ctaagnggng aantcnatgg tccgattgct ggnccctanc cttaagnttt 720
gccatgaata ggncttttgc cctaaaataa naccccttt 759

<210> 645
<211> 766
<212> DNA
<213> Homo sapiens

<400> 645
tnnnnnnntt tcaatntttn ancgtccctt aggatccntc gattcgatcc agatgggata 60
cctctaaaca cgaaaagaaa gaagattcca ttantgaatt tttaagtttg gtttnatcaa 120
aagccgagcc acctangcaa cagtccaccc ccttagtaaa caaagaggaa nagcatgcac 180
cagaatcatc cgcaaatnag acagtcaaca aagatgtgga cgcacaggct gaangagaag 240
gganccgcca tccatggact tattcatggc catctttgcc agttcctcat atgaaaagtc 300
ctnatcctgc gangatganc acggtgacag tnaanatgat caggcacgct ctggngagga 360
caacttccaa agctggnaag acactgactt ggnggaaaca tcatctgtgg ctcacgctnt 420
tgtgccagng ccctaggagc cgtcaccttc cttcccgata caaangatgc agatagatna 480
naganaagag ntcggccngn ngctgcctcc cgtcttatgt nccaatgctc gtcagacact 540
tgaagttnct canaaagaga aacattccaa gaacaaagac nagcacaang gcaatanaga 600
acacaggccn gaaagaattg anangaaatt ggaaacactn gaagcacnaa acacctaang 660
naatccaaaa naattggcaa accaggggaa aagtaggtnc ctncgngaag tttcgacagc 720
cngcggacaa gccanaattg acnatgaaac cgcatacgtg tcttnc 766

<210> 646
<211> 752
<212> DNA
<213> Homo sapiens

<400> 646
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atccacctcg cagcttgtaa atctacagcc tgattacatc aaccccagag ccgtgcagct 120
gggctccctt ctcgtccgcg gcctcaccac tctggtttta gtcaacagcg catgtggctt 180
cccctggaag acgagtgatt tcatgccctg gaatgtattt gacgggaagc tttttcatca 240
gaagtacttg caatctgaaa agggttatgc tgtggaggtt cttttagaac aaaatagatc 300
tcggctcacc aaattccaca acctgaaggc agtcgtctgc aaggcctgca tgaaggagaa 360
cagacgcatc actggccgag cccactgggg ctcacaccac gcagggaggt ggggaagaca 420
gggctccagc taccacagga cgggctctgg gtatagccgt tccagtcagg gacagccgtg 480
gagagaccag ggaccaggaa gcagacagta tgagcatgac cagtggagaa ggtactagtc 540
aaccttcaga aagagtatgg agagaaaaag aggcacacct ggacgcagag ccctgccagc 600
gccctctctg ctgttgcagc tgcaaggaga ccatgcctgt gggagccagg cctcgcttgc 660
atgaanaagg aacgatgcct ttttcaatgg tgtcttcctt ccattgtgca naanaacctt 720

ttggtggctt ctcttccgac ttgtgcctga tt 752

<210> 647
<211> 743
<212> DNA
<213> Homo sapiens

<400> 647
ttaatccttt caattcgttc ntctttggat ccatcgattc gaattcggca cgagccctcc 60
ccggcttccc ccggagtggg tcaccacact gttttttatc atcatgggaa tcatttcatt 120
gactgtcaca tgtggtttgc tggtggcttc ccactggcga agagaagcta caaaatatgc 180
tcgatggata gcattcactg gaaccactat gagaagatta taggaaaaac accaagacta 240
gaggactctg ggttcctttt atgcaaagtc aactcttctg ggtcacagtt acccagcaac 300
aaaaataaag agaggaccag gacgatgcca gcaccccgtt tatcctgagt gaactctccg 360
gaggcctctt caagcttgtg ggttctctgc tgtcttgaag ccatccatcc atttgatagg 420
ttttgcaaag acttggtcct gccaagatgg ttttaatcat ttctgctaaa aggaatggac 480
tcgaggattt gatctcattt tagatgcagt tgtcctcact tggccatttt acagcacttt 540
agtaaatatg gccagtgtat ttggtcacta ttaaatcaat ccccattcat tatctgtcan 600
ggcaactcag tgaactaaat actatgttct gacctctggc actctttctc atgttggtta 660
aatatttaat attgnctaag gcaattcaag tatttttctt aaataaaaaa tatgaaaact 720
caaaaaaaaa aaaaaaaaan ana 743

<210> 648
<211> 759
<212> DNA
<213> Homo sapiens

<400> 648
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ggtgattgga ttaacaattt tattctgnnt ccactacaaa ngggctggtg ttttgttcca 120
aatgtttagc tgggagggct gtagggaccc ctgttacccc cattaaacac agtaaagcat 180
ggatccagtc agccccctgc tggcaggtgt gggcctggca actacacaga tccaacccca 240
ccctcctggg tgcggccaga ggccaaggca gtcgcccgag ctcctgaatc ccaagaatgg 300
ttctggcaag tactgctgtt tgtttgtagg ggcaaagagt taaaataaaa cgaggttctg 360
ccatggctaa gccttgtgga aaccagaccc caaagcccct gccatgccan gggtctcaac 420
nccagacgct tgttatggag gcaccancng gtantggccc ctgtaagcan ggccagagtc 480
gggacaaaga gcaagantga aacanccaag agacanagga ccatgctgga ccattgggca 540
cncangaacc tgcctgggaa aaaccggggg gcaangctgg catgggaatg aacacctgct 600
tgntgacacc tatntgagct tcanttncct taacttgaaa aattgaacan gcccggtncg 660
gtggctcata ccctgtaatc ccancacttt tgggangctt tangccgntt ggatcattga 720
ngttaggaag attaaagaac cancctgggc cnacattgg 759

<210> 649
<211> 746
<212> DNA
<213> Homo sapiens

<400> 649
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ccatcttgac accttctccc tcttcagctt ttccaacagt cactactgtg tggcaggaca 120
atgatagata ccatccaaag ccagtgttgc atatggtttc atcagaacaa cattcagcag 180

acctcaacag aaactatagt aaatcaacag aacttccagg gaaaaatgaa tcaacaattg 240
aacagataga taaaaaattg gaacgaaatt taagttttga gattaagaag gtccctctcc 300
aagagggacc aaaaagtttt gatgggaaca cacttttgaa taggggacat gcaattaaaa 360
ttaaatctgc ttcaccttgt atagctgata aaatctctaa gccacaggaa ttaagttcag 420
atctaaatgt cggtgatact tcccagaatt cttgtgtgga ctgcagtgta acacaatcaa 480
acaaagtttc agttactcca ccagaagaat cccagaattc agacacacct tcaaggccag 540
accgcttgcc tcttgatgag aaaggacatg taacgtggca tttcatggac ctgaaaatcc 600
atacccatac ctgatttatc tgaangcaat tcctcagatt tcaactatca aaactaggga 660
aaactgngag tttaacacca agtnctacaa cacaaggttg gaaacacctg aacttggngg 720
atcatgatac cacttnacca ctccnt 746

<210> 650
<211> 789
<212> DNA
<213> Homo sapiens

<400> 650
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tccctcgttc gctgnacaaa agatgttttt caattaaaag acttggagaa nnttgctccc 120
aaagagaaan gcattactgn tgtgtcagtn aaaggaancc ttcaaagctt tattngatga 180
tgggtttggt tggactgtga gaggatcgga acttctaatt attattgggc ttttccaagt 240
naagctcttc atgcaaggga aacataagtt ggaggttctg gaatctcagt tgtctgaagg 300
gaagtcaaaa gcatgcaagc ctacagaaaa gcattgagaa agctaaaatt ggcccgatgt 360
gaaacggaag agcgaaccag gctagcaaaa gagctttctt cacttcgaga ccaaagggaa 420
cagctaaagg cagaaagtag anaaatacaa agactgtgat ccgcaagttg tggaagaaat 480
ccccaagcaa attaagtagc caaaagaagc tgctaacagg atggactgat taccatattc 540
gcaataaaat cttgggccaa aagaaaattt gggttttgaa agaaaataaa aattgatngg 600
aactttttgg aattccagaa gactttgact acatagactt aaaatattcc atggttggtg 660
aaaggatgta ccaagctttg tgaaatattg taaattttta aacctattat ctactaaagt 720
ngtactggaa ttgtccnttt gcctgttnac ttgnggtnta ntcatttnta tttaatgntn 780
aaattaang 789

<210> 651
<211> 757
<212> DNA
<213> Homo sapiens

<400> 651
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agatatttac tgaaggaatc taggttgttt tttcagtgga caatgggaat aanncatttc 120
taaagcaccg actggagagg aaggcaacag agacaaggag agaagccgag agacatgtct 180
gcgtgctgcc acgcatctga gcgattgctc tgtgaagagt tgtacactga acattttcag 240
gggaggctgt ttacccaggc aatgtcctca aacaagcctg tgccggggtg tcctggaatc 300
tgtgccagga ctgtgttttt agcccttcac ctctcagctt tagcaggaca tgaaccagtt 360
ataacaagat ggccctgcag ctggttacag gaatgtgaca tggcaggatc tatggaacca 420
aatggaaggt tttnaggtga tgtaggtctt tcacagttag ctttggggaa tacagaatac 480
tcaaataaag tgctttgtta ttatttcaga gggaatggcg attgaaatgt tacaacagag 540
atttcttggt ggtagctatt tgggtaaang tatatggata tttntctgta catgtgaaat 600
tatntaaaat aaaagttata taaattacat tgacaaaaaa aanangtana aaaaaaactc 660
gaacctttaa aaactatngt ggagtccgta ttacgttaga tccagacctt gataaganac 720
cattgatgaa ttttggacaa accccactng aatgcnn 757

<210> 652
<211> 759
<212> DNA
<213> Homo sapiens

<400> 652
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gaggctgncc aggcagttnn atggcctnct ggttgtgtgc cttcacaccc gcctacagcc 120
ccacctcacc atcaagcgct gagccaatgc ggntgtggct ggccctgagt tcctgagtca 180
gctccttgcc agggccagag ctggtnacag cggggcanca nggtgggtag cctctaccag 240
ncagggcagt ccctgagggg ccagcanggg ggctgactgc ctagtggctn aacctactga 300
acccacccac tcccagcgat gctacccaga accccaacgg cntgaatcct gcacantgcc 360
gggcantgcc agactcnaaa gggctcgctg tggggacagc cccgtcatgg ccacanactc 420
tgtcctcacc tttgattgtc aggatgacag nccccaccac catgatgagc gtctgcaggg 480
cgtccgtgta gattacagca gccaggcccc ctgccaatgg aagcaaggtt gctggaaggg 540
gccctggtcc agggaggaag gacaccggga ggaacttctg ggcttctgct ggggccactt 600
cctgggctgn tnctcnggnc tgtatgggga agtggccttn tgaccccttt acacgttccc 660
tgggtggacc ttccctgntt gcangcaccc ataccttgcg atggtgtnca nggctnttga 720
tgcccnaaac tttaggattg ttggatangt nnaatctnc 759

<210> 653
<211> 820
<212> DNA
<213> Homo sapiens

<400> 653
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acagtccagg ctctgcagac agcatcccac ctgtcccagn tngctgacct gaggagcatc 120
gtggnggaga ttgaggacct tgtngctcgc ctggatgaac tcgngggcnt gtatctccag 180
ncanaanaan gacngcatac aacagaccat tangangntg tcatctacan tntnanngat 240
catntgngna cngacccatc cattaatgag gatcanggcn tccanctgat gaacgctgat 300
cttctgcaan aagaacgttc tagntctanc nnanngccnt cancctncgn ctcttgagct 360
cagtgngtca ngctcntaan atcttnncac ntgccaanct gtgnggnctg ccttnagnct 420
tccggatagg cactntnatn ngacntgccc tatanttgcc ngcngnnant naaccaantg 480
naccatngtc actctgttga catcanggcn atntgnntaa actaatnnct tngcngcact 540
ctagtnngcg ttgncactgc ccncgtnnnc tancntacca nttcncattn cccntttaat 600
gggnaaagan atnatcccta cnatcatatt ncccntnnaa tggattcgag ncgnaantct 660
tnnntantna tctnaancct aaatgntcac atnnaaactt tanangncat cnnnnatgna 720
accnancnat ggctaaangg cctcattaan gccngntttt tcaaacttga aaantgcatn 780
ccnccattga naaagganta cacgggcccc cntgngnggg 820

<210> 654
<211> 768
<212> DNA
<213> Homo sapiens

<400> 654
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tcgattcgcc acatttaagt gagatatggg aaggaggagc agattgtttt tgaagggagg 120
aagagcagtt acttagggtc aaattaagtt gtaaaatccc ccccgggatt ttgtatgtaa 180
gtcaaagtga attgtatttg gaagaagaac tggggagccc acctctggta ttttttttat 240

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gtccctcata tggacaaata aacctctggt attaaatgaa ttttcttttg ggggattcta     300
tatattcggg atttcaacca ccaacctatc tggtttttcc cgctgaaatg ttgggtgatg     360
gaatcaggag agcagatttg gagactcttt atattttata attgagagag acaaagagaa     420
aaccgtttga tttgaaaaag ttttctaggt tccctcaggt agatggaaat tttcatcaaa     480
aacagtttat tcaaggtaca tagcctacta gtttcccatt tgagagtacc gcagaatgat     540
acgacgtgta ctgcttctct acgcagaatg aagtataaaa ttagcaccna atagtacttt     600
aatttgcagg tgctaaactt tttacatgct tnatctcatt taattcttag aagaaactaa     660
ttttaccaag taaantgtct ggaccaacca tntgcaggtc caaaannctg gaaaaaccgt     720
naggtttgga ctcctacata gcctnttttn taagtnncnt nntaaatn                 768
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<210> 655
<211> 752
<212> DNA
<213> Homo sapiens

<400> 655

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gggtaaacct atttatataa tagaaggatg attataaaca tttaataaat tatatcaaat     120
agatattata tattaaatgg gcagataata gaaatctgtc caagcaaaac tctggataat     180
ttttatgttg ccttattttt tgttttctgt gaactccaag aaaaatgaga taccagtttg     240
gaacagatgt aatattgctg atttaacagt ttagggatac tccccaagtt caataatttt     300
gccaagatac aaatttaaat ggaacctttt atgaagcttc atagtgtgtg aagaacttac     360
cttgtttata tgtttgaaga catacatatt tcacatttca gaagagtcta tacatagctc     420
accaaatatc aaaaccacct tgttagaaaa cattaaggtc tgtcttattt atttgttcat     480
ttgnttatga gacacantct cactctgtaa tctcactctg ttgtagaggt tgagtgcagt     540
ggcacgatca cggctcactg caacctncat ctccctgact caaggaatcc ttccacctca     600
gccttccaag tagcanggac caccaggtgc accccactat gcccagctta atttttttgna     660
ttttattgga cagattgggg ttttgcccat gttattcagg ctggatcctt nnggcctcaa     720
actcctgggg cttcaagcca atctggcctg cc                                 752
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<210> 656
<211> 754
<212> DNA
<213> Homo sapiens

<400> 656

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ttttcctttt natcttgctc nanaanccnt ggatccctcg attcgcagag gctggttcag      60
aaaaggagga agaggcccgg ctggcagccc tggaagagca gangatggag gggaagaagc     120
ccagggtgat ggcaggcacc ttgaagctgg aggataagca gcggctggcc cangaggagg     180
agagtgaggc caagcgcctg gccattatga tgatgaagaa gcgggagaag tacctgtacc     240
agaagatcat gtttggcaan aggcgaaaaa tccgagaggc caacaagctg gcngagaagc     300
ggaaagccca cgatgaggcg gtgaggtctg agaagaaggc caagaaggca aggccggagt     360
gagtgcctgc ggcccctcac agggctgang ccagccccta tcagctggat gtggcagagg     420
catgccanag gacctaagtg tgatggacca gantcacttc tnctcctcct ttctncacca     480
gccctgaccc ctcatgctct ctggctgggc cantgggcaa ccctcgcttc cttggatgga     540
ctgcctgctg gtgcctggtc agagaanagc ctntttttccc agnctgattc tntgctccca     600
ggaaccaatt gaccatnaag gtgcaaangc cnanccaatc cccttacnta ctggccccca     660
ttnattcctg gctttttcan aagccccccnt gccaaacann ttgggacccc ctgattnntt     720
aagggtgcct tttnatnggg gttaaaggtt aant                               754
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<210> 657

<211> 734
<212> DNA
<213> Homo sapiens

<400> 657
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cgcaggagct gtggcggttt tcctaatcct gcgnttatgg gtagtgcttc nttccatgga 120
cgttacgccc cgggagtctc tcagtatctt ggtagtggct gggtccggtg ggcataccac 180
tgagatcctg aggctgcttg ggagcttgtc caatgcctac tcacctagac attatgtcat 240
tgctgacact gatgaaatga ntgccantna aatnaantcn tnngaactan ancgagctga 300
ttganaccct agtaacatgt ataccaaata ctacattcac cgaattccaa gaagccggga 360
ggttcagcag tcctggncct ncaccgnttt caccaccttg cactccatgt ggctctcctt 420
tnccctaatt cacagggnga agccngattt ggtgatgngt tacngaccac gaacatgtgt 480
tcctatctgn gtatctgncc ttatccantg ggatactagg aataaagaaa gtgatcattg 540
ntactttcaa agcatctgcc gggttgaaac gatntncatg tcccnaaaga tttgttgatn 600
tgcagctnct cantgctann gtcggttttg aanaaagttt nccaaatnnn tgtaccttgg 660
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ntccaattng ggng 734

<210> 658
<211> 783
<212> DNA
<213> Homo sapiens

<400> 658
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gagacactgt cccactccat cacccaggct ggagtccagt ggtgtgatca tagctcgctg 120
catcctccag ttcctgggtt caagccatcc ctcctgcctc agcctcccca gtagctggaa 180
ctacaggtgt gtgccatcac acctggcttt acatttttct gtggggtctt actatgttgc 240
ccaggccggt ctcaaactcc tgagctcaag tgatcctctg nctcagcctc cagagtatct 300
gggattacat atgtcggcta ccgtgtctgg ccgttcacat ctttggccac tattngcttg 360
tgaaaaggta tnatgaggtg gtacttatca tngttactgt gtctcatgtt nngtatattt 420
ttgcttcatc aactaagatg cactgtaaca tctgtgaaat ctggatatat tatcaaangg 480
tttatcatag ttttgttaac aatacactgt cgttttactn ggtgcctaan ataatggtat 540
agttgngagg tgatcttaga tttgatgaag cacagtatgc aangtaggcc taatggnggg 600
aaagaatggg naattttcan angcnnggaa gtatttgntn ttttgtaaat ggacttgaaa 660
agcttgttct gnnggattgg acccaacccc tttccctttn aaaccccgaa ttctnatnga 720
ctnttccaac ttngaaaact ttgctcnaac ttaaatacct ttnaaaaatt aaccntgacc 780
ccg 783

<210> 659
<211> 741
<212> DNA
<213> Homo sapiens

<400> 659
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ggataaaaat tgggtaaagg acatttgctt acctgcaaat gaatcactgt ggaaatgtga 120
tcttcccata tcatcaagaa acttgttttc tggatgaata ctgggagaat aaaatgagaa 180
ctctggagtg agctaaattg atcccaatta agtttttctg cttagcagac agaaggtata 240
attttttgac accctttccc acctggtgcc tatgctaggc ttgtcctgag aacatccctc 300

agtaacttga tattcacatg acctacagga tgtcccatct gcagggctga gtcagttggg 360
gaacaccaga ggctacacag tagctcttcc tgctactcgg ttaatgagct tggcaggttc 420
tttgtctcac tgaattctta tcatggaaac agcagcagca gccgctagga aatcttcaag 480
tgtagtgtct gtgctaaccc agtggtaaat cccttagatc ccctgctggt ctctggcagt 540
ctccttgatt ttgggtacca tgtatatttt ccgctttgac tttaacgctt tctaggatag 600
ggtaagcacc cttaattcan gcactgtcca ttagcttcct ttgcaaaagc tacttatggn 660
cggtcacaat ncaacactna nacagagcca aggcaatatc ctcttgccca tggctatgat 720
gtcagacagt ggatggctcn t 741

<210> 660
<211> 734
<212> DNA
<213> Homo sapiens

<400> 660
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taaaaggtgt gagaatgagc ttttccacca gaatcagcag gtttagttaa agcatgagca 660
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acattgcagt ngat 734

<210> 661
<211> 762
<212> DNA
<213> Homo sapiens

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gtnnntgacc tgnagacctc agctgacnct nccttngtan ggttngatnt nggaagcatc 420
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<210> 662
<211> 745

<212> DNA
<213> Homo sapiens

<400> 662
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cagctgggca ctaatgtctg ccaccgacta tgttaaagtg tataaatgat tcctctattt 480
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cctgctccct tttgatagtg gcttctgggt actcgggcnn gtncttggga caccanccctt 660
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ctntattggg aggatngctn ntcct 745

<210> 663
<211> 748
<212> DNA
<213> Homo sapiens

<400> 663
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cctcttcttt atattctgcc acatcgacct ctaaaccgga attgtccttc agtttgccgt 660
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gtcnaactgg gcanacagag tctggatt 748

<210> 664
<211> 785
<212> DNA
<213> Homo sapiens

<400> 664
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cattaaattc ttgaggaang aaaatgacct attatccccc ataaagaacc tgaaacttca 720
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tcctc 785

<210> 665
<211> 763
<212> DNA
<213> Homo sapiens

<400> 665
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ntttttaatt gattagtgtt tttttcctca catttgacat gactgataac agataattaa 600
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gaaacagaaa taaaattttt gcactgctna aannnaaann actttccagc naanctaaaa 720
aactnnancc tttaaactat antgagttcg nanaccnggn ccn 763

<210> 666
<211> 759
<212> DNA
<213> Homo sapiens

<400> 666
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aaaaaaaaan aaaaaactcg agcctntana acttttgng 759

<210> 667
<211> 760
<212> DNA

<213> Homo sapiens

<400> 667
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cggactattt gtaagtcntg tncagaacat gatcaaaggg tgttacactg ggctttccgt 720
tacaaagatg aangtctgng natgcttaat ttccatnaan 760

<210> 668
<211> 763
<212> DNA
<213> Homo sapiens

<400> 668
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tgttattctg atggtcgaag tttacatttg gaaaaaaatg gaaatcacac accatcctcc 180
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gaaagggatt ggaacataat ggggagaaaa gaaagccgta attgacattt tctggcanan 720
tcttgtnanc aagaggggna aagtnaccct tntntgcttg aaa 763

<210> 669
<211> 754
<212> DNA
<213> Homo sapiens

<400> 669
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taattggtat catataatga cccactcttt cttatgttat ccaaacagtt atgtggcatt 540
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taaactctga atcttctcat ctgttnaaat gtgnattaaa gtatctacct aactgagtng 660
tgantgtant gaaagaaagg ncatatntta aacnttgaat ttancaagcc cacnctcgna 720
ttttatgncc tttcttttgc ctngggattg aanc 754

<210> 670
<211> 752
<212> DNA
<213> Homo sapiens

<400> 670
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aagccgaaca tcagacagaa gatgcagcag gtctcgggac cacaaaaggt cacgaagtag 180
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agatcagaca gaggactact gttcgaagat ttttggaaga atactgagaa cggcataaag 600
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aagctcaant agttttttta ttattattat tattaaaagt tattcaggac tgatgtgact 720
ncngatttna gaacatgtgg taatagtnta nt 752

<210> 671
<211> 752
<212> DNA
<213> Homo sapiens

<400> 671
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tggtcttatg actagtagat aaattcattg ccataatgag gctagctccc agataaacag 600
tgtattttct tctttttttt ttttggtgag tggtccaaac tttaagctac tttttccagt 660
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<210> 672
<211> 792
<212> DNA
<213> Homo sapiens

<400> 672

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<210> 673
<211> 755
<212> DNA
<213> Homo sapiens

<400> 673

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ggccccggnn gccaatgcat tgggccccgg tacccaactt ttgttccctt tantgagggt    660
taattgcncc ccttggccgt aatcatggta atagctgttt cctggtgnga aattgtttcc    720
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<210> 674
<211> 753
<212> DNA
<213> Homo sapiens

<400> 674

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aacaaactca aaatggattc ttaggagcat tttaatgttt attaaataac tgaccatttg 600
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gcanaattgt cnactttagn ctgaccataa tnc 753

<210> 675
<211> 760
<212> DNA
<213> Homo sapiens

<400> 675
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<210> 676
<211> 751
<212> DNA
<213> Homo sapiens

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<210> 677
<211> 756
<212> DNA
<213> Homo sapiens

<400> 677

tgctttgaat cctttgtaan cgccctntnt gcatgatccc tcnattcgaa ttcggcacga 60
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aaaagtacca ataatgagta ggaaatcact tctgcagtat ttttggagca ttttccttaa 180
gcatgacata aaagccaaag gtcacaaggg aaaaaactga tagatttgtc tgtgatattg 240
agagatgtat gcacatatac atacaacagt catagtaaga caccgttaga caaaaggtga 300
tgtatgaaaa agaggcaaaa caacaagaag aaaagattga aaaaatgaga gctgaagacg 360
gtgaaaatta tgacattaaa aagcaggcag agatcctaca agaatccagg atgatgatcc 420
cagattgcca gcgcaggttg gaagccgcat atttggatct tcaacggata ctagaaaatg 480
aaaaagactt ggaagaagct gaggaatata aagaagcacg tttagtactg gattcagtga 540
agtttagaag cctgaaactt ttctcgtatg gggtggtttt tgcattaaat nctggggtcc 600
attttacaat ccattatttt tgaccactgc tatgtgttca agtagtatga gaatgtgatt 660
gntnttatct ggntcatata tatttctttg gctaatttaa tatgtcaaat aaatgagttc 720
atttaaaaaa aaaaaaaaaa acccggactg ttttnt 756

<210> 678
<211> 756
<212> DNA
<213> Homo sapiens

<400> 678
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aagccattcc aggaggaact agatccacca cttcctctgc tgggcatgct ccaaaaatgg 180
ttgtggcttc cagagaggac tccaaaagaa agcacaaaaa ctagacagtg ggagggcata 240
cccaaaagcc ctgagtttct gaaaaaatat tgaaagtttc tatggtgaaa taggaagtta 300
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gttttaatgg acatgggagg agccataaaa gtagtctatc tatcatcagt tacatatcta 420
atgaactgtc tatctgggat accctatcct gttttaatct gagtgactct ctctcagctg 480
agagagctgg acagactcca ttttagcctc ttcacttgca gtccccttat ccccctccct 540
taagggaata actagtgcaa gctgacttca agcacattca ggaatgcact tactgataag 600
atattgaggc aagctgtacc agcagcttct gggggacctg ctcantggat ggtcccaacc 660
cctgcattta tctctttggg atagtttaag cccctgnacc tggaactgng tatttttctg 720
tactatctct gtancattaa ttttttttact ttttgg 756

<210> 679
<211> 747
<212> DNA
<213> Homo sapiens

<400> 679
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tatgcactct atcagccaga atttggcatt tagctcttag ttaaatctag taaaggacag 180
tctattgttt aaagagaagg tgcatttgtt cctcaatcaa gcaagagcac ctgtgttgta 240
ctgctttata tctcatgtat atttatagta atgaaaagac tttttaaatt gtacacgttt 300
cagtgccttt cttgtgttat gaaaggcagg tagatattat agccataggt aaaaatccat 360
agttaaattg cacactgacc ttaaatctct ctgtgtatgc ccttgtatct tgcatgttaa 420
aagttggatt attgggcatg tgtggcagcc tgccctgcta catgctagac aagtgtgctt 480
tagtacatag ccacaagttc ttcattcttt aaaatgtttt gacagatcat ctcataataa 540
aaataattca ngaaaactat ggggaaatag ttacatttca caaaagatat tttaaactct 600
ttgtaaaact tagataatag agcctancaa gttactttgn atctaattgg atacatttta 660

tgnttaattt taccaccata cattttatta atcaaaattg gttagcatgt gactcttttt 720
ggcttcanaa gttntcaaaa aaattat 747

<210> 680
<211> 750
<212> DNA
<213> Homo sapiens

<400> 680
ttctaatnct tggctctcgt tctttctgca ngatcccatc gattcgaatt cggcacgagg 60
accggctggg cctacaaaaa gatcgagctg gaggatctca ggtttcctct ggtctgtggg 120
gagggcaaaa aggctcgggt gatggccacc attggggtga cccgaggctt gggagaccac 180
agccttaagg tctgcagttc caccctgccc atcaagccct ttctctcctg cttccctgag 240
gtacgagtgt atgacctgac acaatatgag cactgcccag atgatgtgct agtcctggga 300
acagatggcc tgtgggatgt cactactgac tgtgaggtag ctgccactgt ggacagggtg 360
ctgtcggcct atgagcctaa tgaccacagc aggtatacaa gctctggccc aagctctggt 420
cctgggggcc cggggtaccc cccgagaccg tggctggcgt ntccccaaca acaagctggg 480
ttccggggat gacatctctg tcttcgtcat ccccctggga nggccaggca gttactcctg 540
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attcttgaaa gttgtctccc ttgacccttc tttaatggca acttaactga anaaaggat 660
gtncncttat atccaaaatt cagctatttg gcaaataaac canatggatt aaaaaaaata 720
attntntctt aananaaana actccggcct 750

<210> 681
<211> 748
<212> DNA
<213> Homo sapiens

<400> 681
ctaatncttg gctctcgttc tttctgctng atccctcgat tcgaattcgg cacgagccca 60
gctgctcagg aggctgaggc aggagaattg cttgaaccca agaggcggag gttgtggtga 120
gccgagattg cacctttgta ctccagcctg ggcaacgagc aaaaaactct gtctcaaaaa 180
aaaaaaaaaa aaagaaaaag aaaaatggct tccaggacag agcatgctca tttgctggcg 240
gacagttcca gaaacagacc ctgttagtcc ttctacttac ctgctggatt tttcaagcac 300
taaatttata actttttgaa acaaaataat gtgtaatttt ccatttgggg gcaaactcta 360
ttcttgtgag cattattaaa atcttgtttg taaatatatt gtctttctct taatatttgc 420
tctgggtcan gaagaagctg ttcacggtgt gataatactc tttanattgt gctttcatta 480
ttatagatgc atcatgtctt ctgctttcac gtgtctggga tggggtcaga aatgcatnct 540
ccagntgaca naaaaatccn agnatgagat caanaaggat actggtgttt tctgactttt 600
acaaaaatta ctttgntgtt ttcattaaaa aaaaagcttt aacctantgn ttncntantc 660
cttttagaaa ntattaaatt tnaaaatgaa ttcnatanaa atanaannac naaaaaactt 720
nntnccttta naactttagt gangcgtn 748

<210> 682
<211> 755
<212> DNA
<213> Homo sapiens

<400> 682
ctaatgctng gctttcgttc tttctgcagg atccctcgat tcgaattcgg cacgagcagg 60
agcaatcaat tcctgtcgaa gtgaatacca tgcagctttt aacagtatga tgatggaacg 120

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catgaccaca gatatcaatg cactgaagcg gcagtactct cgaattaaaa agaagcaaca     180
gcagcaggtt catcaggtgt acatcagggc agacaaaggg ccagtgacca gcattctccc     240
gtctcaggta aacagttctc cagttataaa ccaccttctt ttaggaaaga agatgaaaat     300
gactaacaga gctgccaaga atgctgtcat ccacatccct ggtcacacag gagggaaaat     360
atctcctgtc ccctaccgaa gaccttaaga cgaagctcaa ctncccgtgg cgaactnaca     420
tccgagtcca caaaaagaac atgccaagga ccaagagtca tncgggctgt ggggacaccg     480
tanggctgat agatgagcag aacgaggcca gcaagaccaa tgggctgggg gcagcagagg     540
cattcccctt tggntgtcan gcgacagctg ggagagaang caagnaagcc ctgaangcna     600
gtccaggagg accnncnaag ggcagtttcc ggagcccgnt gttccggaga tgctgatgtg     660
ggntgtgtct gcanttcang gccaaanttg gggacccctg ggaactgtac cctangggnt     720
ncttgnagnt taaaacttga ccttaanggn ngcct                                755
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<210> 683
<211> 755
<212> DNA
<213> Homo sapiens

<400> 683

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tcggcacgag aattagtatc aacttacaat ccaagtccaa gtatcatctt ataatcactt     120
ttttctacta tattaagatc taatgaattt gatttctttt ttgaagtttt ttcttgtaac     180
atctgagatt agaagtttaa gatcacttga ccccaaacct ttgtttatgt aagaattttt     240
aaacataaaa gtgtttgttt ctgttatgtt accataattt gatgtatata gtgtccagat     300
ccatttagaa atttaatatt tattaataac tgaaactgtt tgtcttcctt tggtatatag     360
tctcgcatat tatattatag caggccaaga taaaatttg acagctcttt aagcccacat      420
gcagcagtgg gtcagataac cctgtggcag tgacacgggc aaattggcat ttgaataaag     480
ccctgggacc acctcaacat gcgtagcctc ttgtcttaaa tgtactcccc atggcagcat     540
ggaggaggca agacctgtgg gtcaattttg aactggnctt actttgattt taaaacaaga     600
gactcagggg aaagtactaa accaaaaact ctgattntac tttgcgtttt ctggaagtnn     660
ttggtttact gagatgcttt tgtaaaggaa aataatgctt gngacanttt agtaatttct     720
acanaattcn ttaatatttc ttcctcntgg gcttn                                755
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<210> 684
<211> 774
<212> DNA
<213> Homo sapiens

<400> 684

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ggntttnann ctttnnaatn cctttgctnc tcgntctttn tgctggatcc catcgattcg      60
caagatctgg aggaatgcag agaggaactt gatacagatg aatatgaaga aaccaaaaag     120
gaaactctgg agcaactaag tgaatttaat gattcactaa agaaaattat gtctggaaat     180
atgactttgg tagatgaact aagtggaatg cagctggcta ttcaggcagc tatcagccag     240
gcctttaaaa ccccagaggt catcagattg tttgcaaaga aacaaccagg tcagcttcgg     300
acaaggttag cagagatgga tagagatctg atggtaggaa agctggaaag agacctgtac     360
actcaacaga aagtggagat actaacagct cttaggaaac ttggagagaa gctgactgca     420
gatgatgagg ccttcttgtc agcaaatgca ggtgctatac tcagccagtt tgagaaagtc     480
tctacagacc ttggctctgg agacaaaatt cttgctctgg caagttttna ggttgaaaaa     540
acaaaaaaaa tgacatgggt gcagaagctt gtaacattga tcacattctt aatgtaaatg     600
gtgtctttct tctggggttt cagtatttgc aaagaaantg aagaagaatt ctggaaatgc     660
cattcaatta accctnagga aaaaagccga ccttanaaat ttaccttant gcnttgnnnn     720
ttaaaaanaa aaaaaantna aaaaactttn accctttana ccttttgtgg ggnc           774
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<210> 685
<211> 759
<212> DNA
<213> Homo sapiens

<400> 685
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ttcggcacga gagtacccag agttgcgagg agttttttaa ctgatttagc cnnntggcaa 120
tcatgagtga atggatgaag aaaggcccct tagaatggca agattacatt tacaaagagg 180
tccgagtgac agccagtgag aagaatgagt ataaaggatg ggttttaact acagacccag 240
tctctgccaa tattgtcctt gtgaacttcc ttgaagatgg cagcatgtct gtgaccggaa 300
ttatgggaca tgctgtgcag actgttgaaa ctatgaatga aggggaccat agagtgaggg 360
agaagctgat gcatttgttc acgtctggag actgcaaagc atacagccca gaggatctgg 420
aagagagaaa gaacagccta aagaaatggc ttgagaagaa ccacatcccc atnactgaac 480
agggagacgc tccaaggact ctctgtgtgg ctggggtcct gactatagac ccaccatatg 540
gtccagaaaa ttgcagcagc tctaatgaga atattctgtc ncgtgttcaa ggatcttatt 600
ggaaggacat cttacagctt ccaatgagaa gccaagaagt tgtgaacata ctgattgaaa 660
aaagacttta ttttaatccc tcattaaaan ggttttaaat gttaaaaaaa aaaaaaaaaa 720
acttcgagct tttaaactat ngtgagtcga ttcntataa 759

<210> 686
<211> 749
<212> DNA
<213> Homo sapiens

<400> 686
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gaattcggca cgagggcaat tagcctcgct taagttgcct tttttacaca ccaaaacttt 120
ttacatgaag ggctggtttc acatgaatac tatactgaaa tctgtgctct caagatctag 180
cagtgaccag ggctgcccgg cgggggctct cctggcaagt caggaaggtt tctgttgcta 240
atataacata gaaacacatt agtgcactgg gcctctctga ggtcagcata tttgtactct 300
tggaatattt gttttttctt tcagtaacaa cagaaacccc agttgggagt ttaacaaata 360
actgactacc actcactcat gcatttttat ttccaattaa agcaaagcac tgtgctgtgc 420
tcagataata atagtttgta agtaaaagtt tttagttttc agtgttcagg ttatagaata 480
taactgacca taaaaattac ctgcaggtat tttcttttta tgaacttgtt tttaaattac 540
caagtaatta ctggtgtcat tttgttttat gacagacaca cgtatctaac aaacaaacaa 600
acagtgacct tctccatggg tcaaggactt ccttacaatt tctnctgagt taacttttgt 660
gaaaataatc ctaaggtttt ctggcttatt gaggaaattn ctacaaacaa caaaccaaca 720
acngaagaga agatcatcaa ccactgttt 749

<210> 687
<211> 760
<212> DNA
<213> Homo sapiens

<400> 687
ggnnttctaa tgctttctaa taccttggct ctngctcttt ctgcaggatc ccatcgattc 60
gaattcggca cgaggaaatg tgtatttcag tgacaatttc gtggtctttt tagaggtata 120
ttccaaaatt tccttgtatt tttaggttat gcaactaata aaaactacct tacattaatt 180
aattacagtt ttctacacat ggtaatacag gatatgctac tgatttagga agtttttaag 240
ttcatggtat tctcttgatt ccaacaaagt ttgattttct cttgtattac atttttttatt 300

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tttcaaattg gatgataatt tcttggaaac attttttatg ttttagtaaa cagtattttt    360
ttgttgtttc aaactgaagt ttactgagag atccatcaaa ttgaacaatc tgttgtaatt    420
taaaatttg gccacttttt tcagatttta catcattctt gctgaacttc aacttgaaat    480
tgtntttttt tttcttttg gatgtgaagg tgaacattcc tgatttttng tctgatgtga    540
aaaagccttg gtattttaca ttttgaaaat tcaaanaagc ttaatataaa agtttgcatt    600
ctactcanga aaaagcatct tcttggatat gtcttaaaat gtatttctgt cctctataca    660
naaaagttct taaattgatt tttacagtct ggaatgcttg gatgntttaa aatantaaca    720
ttttatattt tttaaaagac aaancttata ttnatcctng                          760
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<210> 688
<211> 752
<212> DNA
<213> Homo sapiens

<400> 688

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aattcggcac gagacaaaac ctacagatgg agataaaaat tactactgtt attcaacatg    120
tgttccagaa ccttattttg gggagtaaag tcaattgggc agaggatcct gcccttaagg    180
aaattgttct gcagcttgag aagaatgttg acatgatgta ataagaattc atttctgaca    240
tattttacat ttctggcaat ctcaactctt atttggaata cttctgtgca tttgtctgtc    300
caccgtaatt ttagaaaagc atatccataa cgtttacagt tgtagtacag ttgtggttag    360
ttatttgtag tgggattgaa agtaattttt ttctttttat atttctatat ttagtttgtt    420
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tggcgcgatc tcggctcact gcaacctctg cctcccgggt tcaagcagtt ctgcctcagc    540
ctnccaagta gctgtgacta aaggtgcacg ccgccatgcc canctaattt tttggatttt    600
aagtagaaac cgggtttcac ccgtgttgcc caagctgctc tnaaaactcc tgagctcaag    660
cagtccaccc gncttngcta ccggantgct aggattcaga cgtaagcccc cgaancctgg    720
ctagtttgcn ttnttttctn tcattttata ag                                  752
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<210> 689
<211> 806
<212> DNA
<213> Homo sapiens

<400> 689

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nnnntgnacn ntannnattg nancanntan tactggnnnt ccntaatncn nttaatgtna    180
cntnttgcaa gnngnnctga tnaaatacac gacaggaggg aaanctantg cgtcataggc    240
acaggcagac ctaccgnnta aggagatnat ntnccnnang gntggctgtt gagnncatgc    300
aactctggna tgtatttccc tttataggac caccttgtnc atngtggata aagcccctaa    360
agnaggatgn naaagatgat cngatccaat acgttacnct gacannaaan nntgtnatac    420
ntcngctgan caatctntcc ancnnntnta atatcgtgna tcacctaggg tgtatgatcn    480
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antangcgna gaanancnnt canncacan ntaaccagat tggtgctgnn anatggtant     600
gcnntttnan cncccacgac ncaataaagn ncnnctntnc cccananccт ntnnagggaa    660
gaaaggaatt ttncatagtg ggctcaatga angggtacc cttggncttt ntaaaaaacg     720
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cgnctatang gggnacnnat ttttnc                                         806
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<210> 690

<211> 772
<212> DNA
<213> Homo sapiens

<400> 690
ntntttgaat ctttgaaata cctttgctat ngttctttnt gcaggatccc atcgattcga 60
attcggcacg agaggttgct cacctgaagg agcacaggag ggttttccag gccatgtggc 120
tcagcttcct caagcacaag ctgcccctca gcctctacaa gaaggtgctg ctgattgtgc 180
atgacgccat cctgccgcag ctggcgcagc ccacgctcat gatcgacttc ctcacccgcg 240
cctgcgacct cggggggcc ctcagcctct tggccttgaa cgggctgttc atcttgattc 300
acaaacacaa cctggagtac cctgacttct accggaagct ctacggcctc ttggacccct 360
ctgtctttca cgtcaagtac cgcgcccgct tcttccacct ggctgacctc ttcctgtcct 420
cctcccactn cccgcctacc tggtggccgc cttcgccaag cggctggccc gcctggccct 480
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cctacgaccc tggagaggag gacccagccc aagacccggg cctttggaaa acttccctgt 660
gggaagcttt aagnnccttc nanangccac ttacccaacc ttgaggggnt ccaaangccc 720
gccanccggt nattaaccaa ggccctggnc aatgcctgaa ggtcaaacaa tn 772

<210> 691
<211> 755
<212> DNA
<213> Homo sapiens

<400> 691
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ttcgaattcg gcacgagaaa aagtaaagct tttcatgagc acaaatncct tgcattgttt 120
gatgttactg atattcgtaa aatgaatatt ttttgttttg ttttgtttta ttttttgag 180
acaagtcttg ctttgttgcc caggctggag tgcaatggca tgatcttggc tcactgcaac 240
ccctgccttg cgagttcaag tgattcttct gcctcagcct cctgagtagc tgggattaca 300
ggcgctcacc accacaccca gctaatttct gtatttttag tagacacagg gttttaccat 360
gttggccagg ctggtctcaa actcctgacc tcaaactcct cacacctgta atctcagcac 420
tttgggaggc tgaggtggaa ggatcacttg aagccagagt ttgagaccag cctgtgcaac 480
acagcaagac cccgtctcta caaaaactta aaaaattagc tggctgtggt gttgctcacc 540
catagttcca gctactcggg aagctgagca ntaagatcac ttgagcccan gaggccnatg 600
cttncantga actgtgattg tttccantac agnccacctg ggtgacanag taaanaaaan 660
gaaacattac ataatttggc tagagcataa taaattgatt tctgggttnt gaaattnnag 720
ttgccataaa aggnntttna atgngcnant tcant 755

<210> 692
<211> 748
<212> DNA
<213> Homo sapiens

<400> 692
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tcggcacgag gtccgaagaa aaagactgtg gtggcggaga tgctctctcc aatggcatca 120
agaaacacag aacaagtttg ccttctccta tgttttccag aaatgacttc agtatctgga 180
gcatcctcag aaaatgtatt ggaatggaac tatccaagat cacgatgcca gttatattta 240
atgagcctct gagcttccta cagcgcctaa ctgaatacat ggagcatact tacctcatcc 300
acaaggccag ttcactctct gatcctgtgg aaaggatgca gtgtgtagct gcgtttgctg 360

tatctgctgt tgcttctcag tgggaacgga ctggaaaacc tttcaaccca ctgctgggag 420
agacttatga attagtgcga gatgaccttg gatttagact catctccgaa caggtcagcc 480
atcacccacc aatcagtgca tttcatgctg aaggattaaa caatgacttc atctttcatg 540
gctctatcta tcccaaactg aaattctggg ggaagagtgt agaacagaac ccaaaggaac 600
catcaccttg gagctncttg aacacaatga ggcatataca tggacaaatc cacctgctgt 660
gtgcataata tcattgnggg taaactgtgg atcgaacagt ntggcaatgt ggaaattnta 720
accncagact ggggacaaat ntgtgttg 748

<210> 693
<211> 881
<212> DNA
<213> Homo sapiens

<400> 693
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aattcggcac gaggcggtga cccacgtgtc cttttgattg ccctactgct gtggagacct 120
cgtgctgacc atctggcagt gntcttcgta ttctctggcc tgtggggcgt ggcaagatgc 180
ccgtctggca gacacaaaac aatgctctct acggcgttct gtttganaag agcaaggaag 240
ctgccttcgc caattaccgc ctgtgggagg ccctgggctt cgtcattgcc ttcnggtaca 300
gcacgttttn gtgcntgcac gtcaagctct acattctgct gggggtccng agcctgacca 360
tggtggcgta tgggcttgtg gantgcgtgg agtcccaaga accccgaatc anacccnact 420
ctttcaggac aggtcaanca agtcagagga tgaagaanat tcanacaaan atgtgatanc 480
cngngaggcc naangaggan naantnataa aagcaccagc cagaagaatt ttcttanaan 540
atgcctnagg gacatatcan ccggggttct cattacccat cttaancncc anatttngnc 600
ccattcttga aataagantc nttgnttnaa ttntcaactt ctttttatgg tnatttcnat 660
ntatctantt antaaaacca caaatntgtt nncnatnacc accanttctt ttaaaccatn 720
tagnaattca aangntgtgt nnttacnaat ntntaanggg ttattcaaan ttcnaaattt 780
taaanattnt tatgcantnc ncacaatnta tataanangg tcctnaaaac gngnnccaat 840
atnncannnc nataatntag nanatntntn nnccntgtan n 881

<210> 694
<211> 742
<212> DNA
<213> Homo sapiens

<400> 694
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agttgatagt agattgcatg gtttcatgtt tcctcatatt ggtttattaa ttctatttaa 180
tcaaggaaaa taacttcaga ttccataaag tttcagttta tttttagttt actactaggt 240
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gggggttttt aaaaactgag gatatcanta ataaattgca gaatattttg caaagctttc 420
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tggaaactcc tcaaangagg ganaaagtna ttttttttcca gacatttttc ctcaattctg 660
ggtctttcac acactanntt tccatagtnc nagaatttct gnntttttac catttgggct 720
gtgaaatgtt cacaatntcn ng 742

<210> 695

<211> 745
<212> DNA
<213> Homo sapiens

<400> 695
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gaggctagac gaagtggtga agcccaaaga cttatttttg agctcgctgt aagactgaga 120
aatcacgtag tccttcctga aaccactaag aggaaaaatg tctgtgacac tgcatacaga 180
tgtaggtgat attaaaattg aagtcttctg tgagaggaca cccaaaacat gtgagatgga 240
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gcctcctggg ttcaagcaag tcttctgcct cagcctcccg agaactggaa gaggaggcaa 360
cagtatttgg ggcaagaagt ttgaggatga atacagtgaa tatcttaagc acaatgttag 420
aggtgttgta tctatggcta ataatggccc gaacaccaat ggatctcagt tcttcatcac 480
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cttaatgatg tacacattaa gggccntaac tattcatgcc aacccatttg ctcagtagct 660
attgatngan ctggacaaat tactttgncc aaattgctng aacacacttt attggggggt 720
taccccgntt ttaattatgt canaa 745

<210> 696
<211> 795
<212> DNA
<213> Homo sapiens

<400> 696
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tttntttccc ttaattcctt caattcaatc cggnctttcc ttaatttccn ggattcttng 720
ggtccaaggg tccccttttt tccccccaa naacaaagaa aaggttgggc ccgaaanggt 780
cccaaccttn ttnnt 795

<210> 697
<211> 734
<212> DNA
<213> Homo sapiens

<400> 697
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cccctgtcaa gtcacttacc atgcaaacca caggctctaa gagtttgtcc ccagggacat 120
ccatccaagt catctccatg gctcctgggt cccctggtga gcatggagtc aggaggtcat 180
caatcatcat gctgggggttg gtgcgagagg ggccacagac ctgaaaccaa atggatctga 240
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ccttgatgtc ttcctcatta acactgtcac gtctcaccag gaatacagtg acattaaaag 480
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gaattcccac atgttgtggg anggacccag gggaggtaa ctgaatcatg gnggctggtc 600
ttttcccgtg ctattctcgt gaatngtgaa ntttnacgag atctgatggg tttatcaggg 660
gttttccaat ttttggttct tatttttctn ttgcaatctg catttaagna antgccnttn 720
ggtctctaac antn 734

<210> 698
<211> 728
<212> DNA
<213> Homo sapiens

<400> 698
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gtcgccgttg aggaatcctc tgttgtcaac atcgagaccc ctggttttcg ggaaacccaa 180
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agaaggggac tggactgtct cccttgaaca tattttagct tcacttctga ctgaacagtc 600
attagtcaac tttttttgaa aagccactgg acatgaaatc caaacttgaa aatgccaaga 660
tcaatcagtn caatctcaaa cttttgaaat gaccncaatc caatctggac ntaagctgag 720
tacttgtn 728

<210> 699
<211> 746
<212> DNA
<213> Homo sapiens

<400> 699
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agacaagctt gtcctatgtc ctatttgagt ggcagcagcg ccagcccagc aagaaggctg 180
ggggttgtca aggttgtccc cagaccttgc ttgcagtggt tggagaaccc agggggctgc 240
cttgggccct ctggccagag ggaagcgggc agctctagcc ctggagattg tggtcacatt 300
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cttcctgtct tcagaatgta aaagggtggg ggaattattg tctctggtta aatntgcacn 660
cccttgactt gtgggggttt tggggcatgt tcanntattt angaatgaat tncaattnga 720
caaaaggggg tttantnaat tgttnt 746

<210> 700
<211> 759

<212> DNA
<213> Homo sapiens

<400> 700
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gattcgaatt cggcacgaga taagggtggg gccttaattc agtagaattg gtggcctcct 120
aagcagagga agagagattt ttctttctct ctctgccatg tgaagacagt gaggagtcgg 180
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tttacctaag atttacagaa tgtatgtcta taaaaggagg gatttctgga ctagatgatg 480
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tgtgggtgtt tgacctttta aaaaataaat ttaagcaaat tgaaatgntt tcctttgaga 720
nttttggcca naaacccaca tnganatttt ncgtctncc 759

<210> 701
<211> 751
<212> DNA
<213> Homo sapiens

<400> 701
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ttcaagctca caatactatt ttgggacaaa cagttgtcta gtgtttggac tcatgaaccc 180
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gtgtcaatta tgtcacttaa ttttcacaac aggtctctga agtgtttctc atctcatttt 480
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tcangaattt ncagttctgg gcctgggctg tgggtctggc agacagacct ctggccctaa 660
ggtttgggtn ccangttctc tgcttccaga atgagaagct ttgctgtgca ccaagnanct 720
gggcccctct ggnatctcnt gaatnaaaan n 751

<210> 702
<211> 748
<212> DNA
<213> Homo sapiens

<400> 702
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attcgaattc ggcacgagcc tgaatataaa gaggaggagg aagaccaaga catacaggga 120
gaaatcagtc atcctgatgg aaaggtggaa aaggtttata agaatgggtg ccgtgttata 180
ctgtttccca atggaactcg aaaggaagtg agtgcagatg ggaagaccat cactgtcact 240
ttctttaatg gtgacgtgaa gcaggtcatg ccagaccaaa gagtgatcta ctactatgca 300
gctgcccaga ccactcacac gacatacccg gagggactgg aagtcttaca tttctcaagt 360
ggacaaatag aaaaacatta cccagatgga agaaaagaaa tcacgtttcc tgaccagact 420

gttaaaaact tatttcctga tggacaagaa gaaagcattt tcccagatgg tacaattgtc 480
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actgcccagt tcaagagacg ggaatcccag atggcactgt taaaaccgta tatgcaaacg 600
gtcatcaaga aacgaagtac agatccngtc ggataagagt taanggcaag gagggtaatg 660
tgctaatgga cccgaactgt gacgatcctc atgtgatcat gaagtaccag tactgacttt 720
ttatgttaaa aaatgtccat ttactgng 748

<210> 703
<211> 769
<212> DNA
<213> Homo sapiens

<400> 703
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ggatcccatc gattcgctca gctgaggcaa ttaaactgga aaagaaatag attgaaaaga 120
tactacagaa gaagcagtac agaagttggg ggactgaagg agagggagcc actgcaggtg 180
ctagctgctt aaggggatac cagtcctttt acagatataa tagatacagc ttctgaggtg 240
gagggtgata ggagtgtgta gagaaattgc agttcagaac tggagcatgc agttaggcaa 300
gaggcatccc atgtgaagat gtcaagcaag tactggaaaa tgctgaacta aaactcaggg 360
atggatatgt agatttagag aacttcattg tagaggcagt cattgaaagc taaaagggct 420
gataataaaa ttgccaagga tggaaatagt aagagggagt cagtgttatt aggattagaa 480
ttctgttttg tttttctttt aaacagattc tcgctctgtc accctggctg gagtgaagtg 540
gtgtgatctc ggctcactgc ggcctcgacc tcccaggctc aagttatcct cccaactctc 600
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tttttgtana aaccaaggtt ttgccatgtt tnccaggctg gnctnngaac ttctgggctt 720
aagccattcc cccacccttg ggtctcccaa aatgctngcc attatangg 769

<210> 704
<211> 759
<212> DNA
<213> Homo sapiens

<400> 704
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aattcggcac gagacccgtc cggggccggc caatttgcat atttggaatg cgccgctata 120
aacccggctg ggttttgca gcgatttctt agatgtaaaa atgagatctc aatagcagcg 180
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cagaaaaagg ggactcaccc tcaagaagtg attggtatgg taatttaaag caacgcgcat 480
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ggaaatgtgt caaggcaatt ccaaaggtga aaacgcagcc aactggctca cggcaaaaga 600
gtggtcngaa aaaagcgctt gccccttaca cgaagcacca gacactggag ctggaagaan 660
ggagtttctg ttcaatatgt accccttactc gaaaagcggn gcctagagaa taacccgcan 720
cgttccacct taacggacag gacaagtgga aaaatcttg 759

<210> 705
<211> 777
<212> DNA
<213> Homo sapiens

<400> 705

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aggtgctcgc cgtgcgcgtg gtcacactgc tctacgacct ggtcacggag aagatgttcg     180
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cangactgga ctgggatgcc cgctagtgaa gcttgaaggg tgccaaccgt gggttgggct     600
ttcttaagca tggaggacat ttttggcaat gcttggcttt gggccattta aatgggaaac     660
cttgaaaggc caaaaaaaaa aaaaaantna tntnaaaaan aaacttnnac cttttaaaac     720
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<210> 706
<211> 760
<212> DNA
<213> Homo sapiens

<400> 706

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tgcacagaac atatattaca tttcagactt ggaaacatgc ttcaattcta attcagcaac     180
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accaaaagct tcagtgggct acaaaaatca tacaagaaaa atatagagca aataaaaaga     420
aacagaaagt atttcaacac aatgaactta agaaagagac ttgtgttcag gcaggttttc     480
aggacatgaa cataaaaaaa cagattcagg aacagcacca ggctgccatt attattcaga     540
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ctattcaaag aagatacaga aaactaactg cagtgcgtcc ccaacaagtt atttgtatac     660
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<210> 707
<211> 856
<212> DNA
<213> Homo sapiens

<400> 707

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ataanancan tannaantta tatttcnnan atantanann nancnnttta naannantta 660
nggnnancan nnattantnn tnnatanntt acattaaant tattnanann anaaannnan 720
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naanaataag nnntanatna nnnnttangn ntnatatann ttnanatann nnnnacnata 840
nnacatnnnn tannga 856

<210> 708
<211> 766
<212> DNA
<213> Homo sapiens

<400> 708
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accaactttt ccaaggtcac acagaggtgg gatccagccc acttccgtct gaccccaagc 300
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tnctacactt gtaggggcaa aaccccggtt tgactctttc cgggttccta cccttaacca 720
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<210> 709
<211> 743
<212> DNA
<213> Homo sapiens

<400> 709
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ggtggaagta gctctcagca gatggctggg gagccagaag gggatagca tgggaaggta 180
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atttgggcaa gaagacagga gtccttgttc tcattaggtc catgggcaca agcctgaggg 480
tggagccctt gccagtgacc ctgcccttct ctacccagca cttccctgtc cccctcccat 540
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gggaagatgc aatcctcttt atgacaagtt tctaanaagt tgataagaaa aatggggacc 660
tgcctaaggg ctagtatctc atttaatact ctatagaata ttatgnggtt ttccctttta 720
ngttttaaat gttgaananc nan 743

<210> 710
<211> 753
<212> DNA
<213> Homo sapiens

<400> 710

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aatattttat attgacttaa ggaaaacctt tcattgggaa ttaattaaat taagtctcta    660
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<210> 711
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<212> DNA
<213> Homo sapiens

<400> 711

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ttgcattact tttcattggg attgaactga gaaataacaa acaagcttta agtgggaaat    180
taaaaaaaag aagtaaccta tgtagatcca aacttaaaat gtgagaaatt attgaaattt    240
catttctac aaacttgaaa ttagcctgct aattgtaaag ttgttttaat aatgctgaca    300
aatgtcagtt acgtttgcaa aggagtgtat ggttctaggt atttgcctac tgttaaccgt    360
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gaaagagagt gacaaaggag gagaaggaat agtatttctt ttttagtatt gntttgaaat    600
taaaactctg ntattttaat atggtaaaga gcaagaattt gggttgggcc gcngtgactc    660
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<210> 712
<211> 783
<212> DNA
<213> Homo sapiens

<400> 712

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aggaattgaa agcaaanacg caaacagatg cctgtncacc aaagttcacg gcagcatnct    300
tcgncatagt ggcagcatcc gtcgtcacag cggcatcatc cttcatcata gcggcagcat    360
ccgtcgtcac aagcggcagc atccttcgcc acagnggcan gcatctgtcg tcacancggn    420
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cggcaaggtg gaaaccctgt ccatccactg aggcgtgcat agactaaaca tgggcagtcc    540
agcactggaa ttccaagccg tacaacggng nccacngtca aaaangaatg aggaccctga    600
ngcacctgng cnganaacaa gaacnngcga nnccaanact tttnagacat tattgcctta    660
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agtngaaaaa cccagngcac caacgggaaa ccngaccgnc ntgnanccct gnttaacntt 720
nantnngttn cccgaaaatg ggggcacntt nccaaaaagg ggaataaaag gggagaattn 780
cct 783

<210> 713
<211> 765
<212> DNA
<213> Homo sapiens

<400> 713
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atgaagagag aggacatcta cactttagat gaagagttac ccaagagagt gaaagctcga 180
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<210> 714
<211> 740
<212> DNA
<213> Homo sapiens

<400> 714
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tgatgatagc caacctgata aaaaagctgt tcttcccact agtaaaagca gccaaatgat 180
caccttcacc tttgctaatg gaggcgtggc caccatgcgc accagtggga cagagcccaa 240
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caattaagct gggtttaact tgttaagcaa tatttttaag ggccaaatga ttcaaaacat 480
cacaggtatt tatgtgtttt acaaagacct acattcctca ttgtttcatg tttgaccttt 540
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agattgtaat tgatgtgcct taatttgcat aaatcataaa tgtatgtcct ctctgtaatt 720
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<210> 715
<211> 708
<212> DNA
<213> Homo sapiens

<400> 715
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actgtgtgac tgagcttgat ggccaagttg aaaatcttca tttggatctg tgctgccttg 180
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gaaagacatt gccaagcccg gtcaccatca cgcccagctc catgaggaaa atctgcacat 540
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tctaatctga tgagttactg agctttggtc ccttaaaaca agctgacttg gtccctaaac 660
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<210> 716
<211> 730
<212> DNA
<213> Homo sapiens

<400> 716
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acctactcga ggctgaaagc agctatagac aatacataaa tgaatgagcg tgagtgtgtt 240
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ntgcttaatn 730

<210> 717
<211> 728
<212> DNA
<213> Homo sapiens

<400> 717
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taccagttga ctatttttag gaaaaaaaca caaatggctt ttaaacatca cagtgtgata 300
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tggatttttg tactaanccc agttgcctct ttnaaaacaa cttgtcaact ttgtctaatc 660
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gncttttn 728

<210> 718
<211> 730
<212> DNA
<213> Homo sapiens

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gtcacatgtg agagggcaga ttttccaaat gctcatcacc acttggcact gtgtggacta 180
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cttcaattac aacctgcaca ttcatccctc tatcctcttt cttactctgg ttttctccat 660
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ngctggtacg 730

<210> 719
<211> 733
<212> DNA
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tcatcagtgt ttgcttcaga gtttgaggaa gatgttggat tgttaaataa agcagctcca 180
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gaggagaaat gaacagcttg accctacatg atgagangtt tgagaaagtt ttatgagcca 600
tattgatgat gatgaaattg ggagctctgg ataatgccag aatttggaaa ggttctattc 660
aagtgggaca gcaattcgct ttcnaggaag ttttgaatga ctactattaa agagaangcc 720
caanaattnt ntt 733

<210> 720
<211> 740
<212> DNA
<213> Homo sapiens

<400> 720
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tcgaattcgg cacgagaaga gaaggaccta gagattgaga ggcttaagac gaagcaaaaa 120
gaactggagg ccaagatgtt ggcccagaag gctgaggaaa aggagaacca ttgtcccaca 180
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caaacattct gggtctcggc ggccgccanc gctntggcgc cttctgaccg tcgctnctac 660
ttncgncttt tcaaattttt ggnataaccc ccgtgtttgn gtaaaatcca gtttttgttc 720
cgntaaaaaa aaaaaaaaat 740

<210> 721
<211> 736
<212> DNA
<213> Homo sapiens

<400> 721
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atgagtgata ttttggtctg ggtttcctct taagatttta gtttgtctga attaaggaaa 120
aatgttttta atatacattc ttattttgtc ccacccctcc agaaataagc tggaaatctt 180
aactttttgg ggggtctttt ttggtgtttt aatgggccca gaactgtggt ttaaattttt 240
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gatatgtgga ccttaaagtt attgagttta agctacaaat tgtaacgtca ttactggaca 420
tgtcagcatc aaccctctca aaatagcttg gtcactttat gaaggggcgt tttaaagttg 480
ttgtttagca gtgacattta atatggtcca attgcttttc tttttaacgt gacaaaaaga 540
gaataaggaa caaacactat tgctgccgaa tgccataaca ctgagttgtc aaattgtgat 600
tgaggaaatg aaaaggttta tactttttaa aaaaaaaaaa cnnaanccaa aaaaccaaaa 660
cttcaaatgg aataaattat tcatgaagcc cttaaaaaaa aaaaaaaaaa aactcgaacc 720
tntaaaactn tngngg 736

<210> 722
<211> 751
<212> DNA
<213> Homo sapiens

<400> 722
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aattcggcac gagattatag agattaatct cctttgctcg aagtctattt aaatattagt 120
cacatctaaa acatactttt acagcaacat ctagactggt gtttgaccaa acaactgggc 180
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gcatcatgtt tgtatttgat ccanctagat gacatgtaag agaaaacttt attgnggact 660
ctgtaaagtg tgacattcgt ttgtgactca atttgctcat gtatttggtc ctggggagtc 720
attacatagc taactttcag ctgctttcaa t 751

<210> 723
<211> 749

<212> DNA
<213> Homo sapiens

<400> 723
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tgctagccaa agcctgctgc cagctccata gcctggacct acagcactcc atggtggagt 120
ccacagctgt ggtgagcttc ttggaggagg cagggtcccg aatgcgcaag ttgtggctga 180
cctacagctc ccagacgaca gccatcctgg gcgcactgct gggcagctgc tgcccccagc 240
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tctgggcctg tatggcacgt cagaccggct gacttttacc aangagggca agnccctttt 660
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agaaagacct ggaacangcc cttgctnct 749

<210> 724
<211> 761
<212> DNA
<213> Homo sapiens

<400> 724
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atcgattcga attcggcacg agcctcagcc ttctaaaaag ctggggctac acccagctga 120
agaaattgta actaaagata gattgtttaa agcaaagcaa gaaacttctg aagaaatgga 180
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cagtagagct tttgaatta tttttgatg atgaaacatt caacttaatt gtcaatgaaa 660
ccnataatta tgcttctcag aaaaatgtca gctttggaag tccagttcag gaaaaaaaan 720
nnnnannaaa aaactcgagc ctntanaact atngtgagtc c 761

<210> 725
<211> 760
<212> DNA
<213> Homo sapiens

<400> 725
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catcgattcg aattcggcac gaggcggact ctcaggacga aaagagtcaa acctttttgg 120
gaanttcaga ggaagtaact ggaaagcaag aagatcatgg tataaaggag aaaggggtcc 180
cagtcagcgg gcaggaggcg aaagagccag agagttggga tgggggcagg ctgggggcag 240
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ctatctcttt taaatttggt gtggccaagt tttagggccn 760

<210> 726
<211> 741
<212> DNA
<213> Homo sapiens

<400> 726
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ggcacgagac aagttctatt gagtgctatt cagaatagga acaaggttct aatagaaaaa 120
gatggcaatt tgaagtagct ataaaattag actaatctac attgcttttc tcctgcagag 180
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aattcaggca tgaancncca t 741

<210> 727
<211> 751
<212> DNA
<213> Homo sapiens

<400> 727
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gaacaccaga ggctacacag tagctattcc tgctactcgg ttaatgagct tggcaggttc 420
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anggtaanca cncntttaat ttangcnctg gancattaac tttctttgca aaggctactt 660
atngccngnc acaantgcag cctcggacan ancnnangnn atatcctgtt ggccatggct 720
ntgatgtttg acanccgata ngccttctnc g 751

<210> 728
<211> 765
<212> DNA
<213> Homo sapiens

<400> 728
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cctgcagatt gcagagcggc gagagcccat aggcagcatg tcatccatgg aagtgaacgt 120
ggacatgctg gagcagatgg acctgatgga catatcggac cangaggccc tggacgtctt 180
cctgaactct ggaggagaag agaacactgt gctgtccccc gccttagggc ctgaatccag 240
tacctgtcac aatganatta ccctccaggt tccaaatncc tcagaattaa gagccaancc 300
nccttcttnt tcctncacct gcaccgactn ggncacccng nacatcanng agggtgggga 360
gtnccncnnt gttcagtccg atgaggagga anttcangtg gacactgncc tgnccacatn 420
acacactnac agagangcca ctcnngatgg tgntnangac agcaactntt aaattgggac 480
atgggcgtng tntggccaca ctggaatcca nntttggctg tatgcggaat ttcacctgcn 540
aagccaggtt nnttnataga cgttcttgat tattacataa ttgccaatca tgtggtgagn 600
aacttgtgng aacantttaa caattaantg tgaagaccgt acaangaatt agttaaangc 660
natnnagggc taaacaagct attacttntg annnaantta angnatntaa nntttnctgn 720
ttctnaaaat nttcaatntn nngggaacan ttgtaanttt nncnt 765

<210> 729
<211> 743
<212> DNA
<213> Homo sapiens

<400> 729
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acgaggagat ctctgggatg tcagtgaggc tggttgaaga ccagaggtaa actgcagagg 120
tcaccacccc caccatgtcc caggtgatgt ccagcccact gctggcagga ggccatgctg 180
tcagcttggc gccttgtgat gagcccagga ggaccctgca cccagcaccc agccccagcc 240
tgccacccca gtgttcttac tacaccacgg aaggctgggg agcccaggcc ctgatggccc 300
ccgtgccctg catggggccc cctggccgac tccagcaagc cccacaggtg gaggccaaag 360
ccacctgctt cctgccgtcc cctggtgaga aggccttggg gaccccagag gaccttgact 420
cctacattga cttctcactg gagagcctca atcagatgat cctggaactg gaccccacct 480
tccaactgct tcccccangg actggggct cccangctga nctggcccag agcaccatgt 540
caatgagaaa gaaggaggaa tctgaacctt gggtaaggat ttggggcaca gtaccaggaa 600
gggggcttgg tgccagacct tatgaggaag aaggattttc ctatgtacag agaangggac 660
cctgtnctgt tgggaagtgc ttgtgcaaac ctaaccaagt tactaacccc tctgntttct 720
gtgctacaca aaggggataa att 743

<210> 730
<211> 744
<212> DNA
<213> Homo sapiens

<400> 730
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gcacgagggg tcctccaaga gtttggggcg cggacnnnag taccttgcgt gcagttatgt 120
cggcgtntgt agtgtntgtc atttcgcggt tcttacaaca gtacttgagc tccactccgc 180
agcgtctgaa gttgctggac gcgtacctgc tgtatatact gctgaccggg gcgctgcagc 240
acggttactg tctcctcgtg gggaccttcc ccttcaactn ttttctctng ggcttnatct 300
cttgtgtggn tgagtttnat cctagcggtt tgcctgataa tacngatcaa cccacngaac 360
aaagcngatt tccaaggcnt ctgcccagag cnagcctttg ntganntttct ctttgccagc 420
accatcctgc accttgttgt natnancnta ggtgnctgaa tcattctcan ttncntaatt 480
gangagtang anactaaaag aatgttgact ctttgaatct gctggataag agactngaga 540
tggcagctta ttggacacat ggattttctt cngatntgca cttactgcta gctntgctan 600

ctatgcagga gaaaagccca tagttactgc gtgtnacaac aactntctaa cnaacattca 660
ttaatccann ngannccttt caangaatgg taancctatg ccnttcaana tactgaactt 720
nntgccactt ntggcaaaaa aaat 744

<210> 731
<211> 746
<212> DNA
<213> Homo sapiens

<400> 731
cttattccct ttgnaactna ctctttntca tccctttgtg caggatccca tcgattcgaa 60
ttcggcacga gtgtccttat ctgaaattca gcgatcttnt tgaataagca tttctctgat 120
tgtggtatat gcctttaatt ttatttctag agtgacaaat ttttggtttt gacagttttt 180
ttctagcttt atagtttctt cttggggaga gaatatgtca acctcactcc atcatgctga 240
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ctgataagta attgcagtat ctggtttcta tggttggatg attcaggatt ccaggaataa 360
tagttacttt ttagacctct aaagaagaag taacaaccac gtaaatgaaa agatgcttct 420
taaatcatgg agaatcaggg cttagtatca ctgtattttc aaactgtttc agccttactt 480
tataactgat ttagtatatt tttcttttaa tttcagactt cagtgaagtt ccttatgact 540
tcccctgaaa ttgcttcctt atcatggggg caaatgaaag taaaaggctc taatacaacc 600
tataaggact gcaaagtatg gccagggggt agtcngactt gggattggag agaaacagga 660
actgagcatt ctcctggtgt gcacctgcag atgtgaagga agttgttgag aanggtgtcc 720
agactcttgt gattggncna nggata 746

<210> 732
<211> 756
<212> DNA
<213> Homo sapiens

<400> 732
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cgattcgaat tcggcacgag gtggcccata agttttacct tttaaacatc cggctgcctg 120
tgaatgagaa gaagaaaatc aatgtgggaa ttggggagat aaaggatatc cggttggtgg 180
ggatccacca aaatggaggc ttcaccaagg tgtggtttgc catgaagacc ttccttacgc 240
ccagcatctt catcattatg gtgtggtatt ggaggaggat caccatgatg tcccgacccc 300
cagtgcttct ggaaaaagtc atctttgccc ttgggatttc catgaccttt atcaatatcc 360
cagtggaatg gttttccatc gggtttgact ggacctggat gctgctgttt ggtgacatcc 420
gacagggcat cttctatgcg atgcttctgt ccttctggat catcttctgt ggcgagcaca 480
tgatggatca ncacgagcgg aaccacatcg canggtattg gaagcaagtc ggacccattg 540
ccgntggctc cttctgcctc ttcatatttg acatgtgtga gaaaggggta caactnacga 600
atcccttcta cagtatctgg actacagaca ttggaacana gctggccatg gncttcatca 660
tcgtggctgg aatctgcctc tgcctctact tcctgtttct atgcttnatg gnatttcaag 720
tgtttcngac atcantggga agcaatccac ctgccn 756

<210> 733
<211> 742
<212> DNA
<213> Homo sapiens

<400> 733
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cacgagctca cacctgcttt ggatgcttca agcacctcag ccctctgaac tacaaaacag 120
aagagcctgc aagtgacaaa ggaagtgagg cagaggccca catgccccca ccgttcacac 180
cctacgtgcc tcggattctg aacggcttgg cctcggagag gacagcactg tctccgcagc 240
agcagcagca gcagacctat ggtgccatcc acaacatcag cgggactatc cctggacagt 300
gcttggcgca gagcgccacg ggcagtgtgg ctgctgcccc ccaggaggcc tgaggctggg 360
tctcactgct ctgaaaagac acaaccagaa tggcctgggg ctcaggccct tggctgagtg 420
ggaatgcgtt gggactgccc agctgagcta tcaggtgccc atcttttctg gtcccagcag 480
tggtgaggag agcacaggca ggcctcgccc ctcccttgct cacccagttt cccctncggc 540
acaagcttcc agctctgcag ctggggtgac atccccagtg gtttgtcgcc aagacatgtg 600
gtggactttt cgcccccaa actgatgagt nccggagaat atatggagag agagatgtaa 660
aaaaaaaaaa nnnnnnnnnt nntnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnna annnnananc tc 742

<210> 734
<211> 749
<212> DNA
<213> Homo sapiens

<400> 734
nntanaatcc ntttnnctnt aatccctcta ncaaatccct tgggcaggat cccatcgatt 60
cgaaaattta tagtaatgac aaatgactta tcagtgttca tcatctgaaa gctaagtggt 120
tcgttcaatc actttttcaa agttgatagt agattgcatg gtttcatgtt tcctcatatt 180
ggtttattaa ttctatttaa tcaaggaaaa taacttcaga ttccataaag tttcagttta 240
tttttagttt actactaggt gagatagcac attacatact tttactatca aatattattt 300
tagcagcttc ccatagtacc aaatgatttg attccctact ctcatttttt aaagcatata 360
aatatttatg ggcttaaaaa gggggttttt aaaaactgag gatatcagta ataaattgca 420
gaatattttg caaagctttc ttttggaaag caaacttttg tgcctgccta tatgcaaagt 480
attttatcag ggacttgaac aaagacctca ctctttttca cttgtcttat gtcgagagaa 540
aagggtattg gcagccacat tcctaagact ggggaatggt gtgtcccttt aaatttgaag 600
ataactttan gtaattatng gaactcctca aagaggagaa agtaattttt tncagacatt 660
ttctcaatct gggnctttca cacactantt tncatagtcg agaatctggt tttacccatt 720
gggctgngaa tgtccaatat cagtcctgg 749

<210> 735
<211> 770
<212> DNA
<213> Homo sapiens

<400> 735
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catcgattcg aattcggcac gagggtgccc atcaccacac ccagctaact tttgtatttt 120
tagtagagac ggggtttcac catgttggcc aggctggtct tgaactcctg acctcgtgat 180
ccgcccgcct tggccccgca aagtgctggg attacaagca tgagcccagc gcctggctgt 240
atctttcatt ttacccaagt cactttaccc aagtaagtaa ttaggggaaa gcctgagtct 300
tgtaccacct gttcatttgg ggaactgtgg gaaacggagc caacggacct aagtgccctt 360
tgacagtgag tttcatacca tttcagtagt gtatttcttt cttaatctga ataaaccaga 420
atgatactct cagcacagaa gaataaaggg agcgagtcat taacgttntc tttttaaacc 480
tttatgatga cttncttatg aattactgaa cgaacactgg aatgggactc acgtatcctg 540
aggacatctc tcaactctgg ccttantttc ccctctgtaa aattagggtg ccaactaaat 600
gatctacaag gtccctttnc aagcgcccgn cattctgtaa ttacatcatg tggaactgna 660
ttaaacatac accagtgaac tggcangcat tgggaatgta actttcccag taaaatgctt 720

tnggtttggt tcaaaataca ctntgaactt cttttcaaag acnggttnng 770

<210> 736
<211> 746
<212> DNA
<213> Homo sapiens

<400> 736
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catcgatgct natcnggcac gaggtgatgn cagcttgcaa actggtctac atnncaaact 120
gatagtacat tgccatctnc aggaagactt gacggctttg ggattttgtt taaactttta 180
taataaggat cctaagactg ttgcctttaa atagcaaanc agcctacctg gaggctaagt 240
ctgggcagtg ggctggcccc tggtgtgagc attagaccan ccacagtgcc tgattggtat 300
agccttatgt gctttcctac aaaatggaat tggaggccgg gcgcagtggc tcacgcctgt 360
aatcccagca ctttgggagg ccaaggtggg tggatcacct gaggtcagga nctcgagacc 420
agcctggcca acatggtgaa accccatctc tactaaaaat acaaaaatta gccangtgtg 480
atggtgcatg cctgtaatcc cagctcctca gtaggctgag acaggagcat cacttgaacg 540
tgggangcag angttgcagt gagcccgaga ttgcaccacc gtactnnaac ctgggtgaca 600
gagcgagact tatcttatan ataaatagat ngatcttcac ctgggtgaca naacgagact 660
tatagataga tagatagata gatggataga tngatngatn gatagataga ttgataaacg 720
gaattgggcc ttttgcttta atgaaa 746

<210> 737
<211> 751
<212> DNA
<213> Homo sapiens

<400> 737
ntnnnncttt ttgatcantc ctttnttgga tcccnttgct acttgttctt tttgcaggat 60
cccatcgatt cgaattcggc acgaggctga cctacagcag aagctgctgg atgcagaaag 120
tgaagacaga ccaaaacaac gctgggagaa tattgccacc attctggaag ccaagtgtgc 180
cctgaaatat ttgattggag agctggtctc ctccaaaata caggtcagca aacttgaaag 240
cagcctgaaa cagagcaaga ccagctgtgc tgacatgcag aagatgctgt ttgaggaacg 300
aaatcatttt gccgagatag agacagagtt acaagctgag ctggtcagaa tggagcaaca 360
gcaccaagag aaggtgctgt accttctcag ccagctgcag caaagccaaa tggcagagaa 420
gcagttagag gaatcagtca gtgaaaagga acagcagctg ctgagcacac tgaagtgtca 480
ggatgaagaa cttgagaaaa tgcgagaagt gtgtgagcaa aatcagcagc ttctccgaga 540
gaatgaaatc atcaagcaga aactgaccct tcttcaggta gccagcagac agaaacatct 600
tcctaaggat acccttctat ctncagactc ttcttttgaa tatgtcccac ctaagccaaa 660
accttntcgt gttaaagaaa agttnctgga caaaacatgg acatngagga tctaaaattt 720
ggtcanagca tctgtgaatg agcatganga t 751

<210> 738
<211> 795
<212> DNA
<213> Homo sapiens

<400> 738
aatccctttg ctttaancct tgtttgaacc cctttggaac tncctctntn tgnaggatcc 60
catcgattcg aagagcncan gcaggaagag agagaccctn actgctgggg anttnctgcc 120
acactcaagt ccccaaccca ctggaatctc ccctactaca agtgccatgt anaccccttg 180

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aaaaggggag gggcctaggg agccgacctt gtcatgtacc atcaataaag taccctgtgc     240
tcaaccaaaa aganaantan anaaaactcn agcctctaga actatagtga gtcttattac     300
gtagatccag acatgattng anacattgat gagtntngac aaaccacanc tcgaatgcng     360
tgaaaaaaat gcnttatntn tgaaanntga natgctatat nnntcattnn ttaccattnt     420
antctgcagt aaacaaantt tacagcancn nttgnntnga tttcatgtnt caagttcaag     480
gnganntgtt tggcgttnat ntaattcggc ccnacncgng accctttgc attgggcccn     540
nnacccanct ntagttccct nttagngagg ggnaattgcg cnctttggcg taataatngg     600
gcanangctg nttttcccnn tgtnnaaatt ggtttatcca gtttannaat ttcaacacga     660
tnaatatcaa acccggtaag cnattaaatg gtnaaaaacn ntgnggggng cccttaanga     720
gttgaactta accnganatt aaattgcnnt tncgcnttna atntcccncn ttttaaatcc     780
nggaaaacct tcccc                                                     795
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<210> 739
<211> 763
<212> DNA
<213> Homo sapiens

<400> 739

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ttnnnnncct catnaatccc ttctttgatc cctcnccnca aaacccttgg cnactcgctc      60
tttntgcagg atcccatcga ttcgaattcg gcacgaggca nccttcgcct cctgggttca     120
agtgattctc ctccctcaca tcccaagtag ctgggactac aggcacgtgc caccacaccc     180
agctaattnt tgcattttta gtacaggcag ggcttcatca tgttggccag gctggtctca     240
aactcctgat ctcaagtnat ctgcccactt tggcctccca aagtgctggc attacaggaa     300
tggagccacc gcgcccagcc tgatttcttt anntangtct tgtcangaaa natattgant     360
ctnttgattc ntnaacatgg cnttnggtcg tctttaatnn gnctcatcan tgcctccatg     420
tgttnttgat gccttngaac tggtattttt aaaatnncaa tttctaattg nnnattatnn     480
aaacacaatt gggntnnata tattggcatt gtattaatgc aactttccta aactcactag     540
taattctagt agcntnantt ggtanattct taaggatttn ctgngtnaat agncatgtca     600
tctgtgaatn aagccattct ttganccttt tcaaattttg agccttgtat ttcttattct     660
taccatatca cattggcaaa gacctccagt atganattga ataaangtgg tganagaaaa     720
caccctncta aaantgctng aattacaggc atgaaccacc ntn                      763
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<210> 740
<211> 765
<212> DNA
<213> Homo sapiens

<400> 740

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tnnnnnnnnn tttttnaacc ntttnttgna tncntctntc aaatcgcttg gctacttgtt      60
ctttttgcag gatcccatcg attcgctagc ctgggcaata tagtacgacc ctgtctttac     120
taaaaatgca aaaattaacc acgtatggtg gctcacacct gtagtcctgg ctactgagga     180
ggctgatgca ggagaatcat ttgaacccag gaggtcaagg ctgcagtgag ctatgattgc     240
accactgcaa tccagcctgg acaacacagt gagaccctgc ctcacaaaaa ttatattctg     300
attttctgag tccatgaaca cattgtccaa atggattttt ctagctcctc caagttacag     360
atagttccac gcacacacag aactcaccac tctcaaatat tttccccact agtattacta     420
ttaaattttt caaacatgca aaagatgaaa gaattgctca gtgaacacca tgtacccacc     480
acctagattc tacaattaac atttaccct actttcttta tcacatatat gtacctatcc     540
atctatccat tcttccatga atccatcaat tcatctaatt ttttatatat ttcaagttaa     600
gttgcagata tgtagcttat gtttcacctt aaatgtttct gcctggctat tattaactgg     660
agtgcaatat gtttttggnt cttctttatg gtaaaatcta tgttcagtga aatgcacaag     720
acttangtat gccattaata gggtttgacg aatagacaaa ccttn                    765
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<210> 741
<211> 753
<212> DNA
<213> Homo sapiens

<400> 741
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cccatcgatt cgaggaaggt ggaggggcag gnaacaggac ggacaggccc cgggctctgg 120
cacatcctgg ggaacaaggg accacaagga cgggggcagt ctccagactt cccctgggcg 180
cttgacccca ggccttgcag gggagagagc cagggcctcc ctcaggtctt tgttcatgct 240
gttttccctg ccgtggacac cctttcccgc tctccgattc tctaaatcct gccccatctc 300
ccagatcttg ttcatgtcca agcttttcca ggaagtctta gcagctccca caccgcagag 360
ctcgagatgt ctccctgact tggtcccaga ccccaactat gtgcaagcat ccacttatgt 420
gcagagagcc cacctgtact ccctgcgctg tgctgcggag gagaagtgtc tggccagcac 480
agcctatgcc cctgaggcca ccgactacga tgtgcgggtg ctactgcgct tccccancgc 540
gtgaagaacc agggcacagc agacttctnc ccaaccggca cggcacacct gggagtggca 600
caactgccac cagcattacc acagcatgga cgagttcanc cactacgacc tactggatgc 660
aaccacaggc aaanaangtg gcccanggcc acaaaggcca atttctgnct ggaggacanc 720
acctgtgact tnggcaacct naaacgctat gcn 753

<210> 742
<211> 767
<212> DNA
<213> Homo sapiens

<400> 742
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tcgattcgca ggacatggag cagtacctgt ccactggcta cctgcagatt gcagagcggc 120
gagagcccat aggcagcatg tcatccatgg aagtgaacgt ggacatgctg gagcagatgg 180
acctgatgga catatcggac caggaggccc tggacgtctt cctgaactct ggaggagaag 240
agaacactgt gctgtccccc gccttanggc ctgaatccag tacctgtcag aatgagatta 300
ccctccaggt tccaaatccc tcagaattaa gagccaagcc ancttcttct tcctncacct 360
gcaccgactc nggcacccgg gacatcagtn agggtgggga gtcccccgtt gttcaanccg 420
atnaggagga agttcaggtg gacactgccc tggccacatc acacactgac aganaggcca 480
ctccggatgg tggtgaggac agncactctt aaattgggac atgggcnttg nctggccaca 540
ctggaatcca ngtttggctg tatgcngaat tncacctgga aaagccaagg ttggtntata 600
ganggtcttg atttttacnt anttgncaat aatgggttga gnaaacttaa agaaccagtt 660
taacaataaa atngttaggg acccgttnan aaaatggang tctnccttcc atntnaacct 720
gganncсttn aaacntttnt gngtccnaat tttcgttnca tccannn 767

<210> 743
<211> 768
<212> DNA
<213> Homo sapiens

<400> 743
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gggcttcgcg agnnntggga natnacanag gctngttanc ataccngttt ttnactgcan 120
aggnnnccac angcagcatg gcccatgnna tgnccatgcc antgatggcn ggnggccatg 180
ctgtcagcgg anncgcactt gtgaggancc nntntggann cngtanncna canncacccc 240
cagtctggna cccnagtgtt cttactacac caantgaaac gctggnnagc caagagcccn 300

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gatggcccac gtnccctgca tgganccccc tgancngact ccaccagcct atacangngg     360
aagccanaag cagctgtttt cngccntgcc ctgctgataa tgccttgaag accccatacg     420
acctnnacgg nctacattga cantnngact gtgncancct ngatcagatn atcctggaac     480
tgggnccnng attccaggan cttnccntca atggacctgg gngcttgtaa tcngttntgg     540
accatacanc cnttgtanna gataaaagan ngaggaaatc tgaaaccntn gnaataagat     600
ctgnggcatt agtnnntcaa ggggaggntn ggtnncaaaa cnctatgagg aagaacgatg     660
gnactatgtc catgnaaggg gaacatntan tgttgganna tgcnatgcaa ncntnnccnt     720
gatntaacnc tttganaaac tnangcttna caaaggggga aaaanact                  768
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<210> 744
<211> 757
<212> DNA
<213> Homo sapiens

<400> 744

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gatcccatcg attcgcttga cctctgtact ttaaaggaaa tcactaacca aattttcaaa     120
gtttcctttt aaatgcgttt agctagaaat ctatgtattt atccctttcc tattttgcat     180
tcttctccca ctatttttaa aaactcattt acagtagaaa ccattcttct ttctcccaac     240
agtatccttt gccaagacca tgagaacagt aaggagcatg ttgttggtca gggtttcaga     300
atacgcgtga tgtcactgag aatgtttgct cacagtcaat aattgtcttt gtggatgtga     360
taattttgga gatacacttc tggtcagaac tcaggtgaga taatcttgca atactccaaa     420
tgcagatact ccagccaccc gcaaggttcc aggaaaggac aatgtcctgc gagaaaatca     480
ggaggcctcc acttcctggg ccacttgaga agttcctggg catgtcacta catgttggtt     540
gactcagcca tttctcatgc tgntttgttt cttgcggtgg ccacttaacc ccaaagaatg     600
aanggaggat ccacagtgaa agtgcctgag tttctctatg agaccagatg ctgtcgaaac     660
caaacatctt ttcctttgct ctatnggaac attttaaggg ttggtttgca caactggttt     720
tcagactngg aagattacca agtttgggtc ccccctn                              757
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<210> 745
<211> 751
<212> DNA
<213> Homo sapiens

<400> 745

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cttnttnnnt ttnntttgat ncctctacnc aaacccttgg ctactngctc tttntgcagg      60
atcccatcga ttcgaattcg gcacgaggaa naacagacag gtttcaacat ggatggatct     120
gaaatgctgt tgaagcatat catttgcata aaaatcaggg acagtttcca aagaattata     180
tattttttc agttggctct ctagttagtt tttttgggag taaggacaaa cctggaatag      240
atagcaaaac tgaaaatcan cagtgctgat ggtggtacat atgtctttcc tttagcttct     300
cccctgataa ttcccatctg cttttacttc gggtgagcag agggggatgt gtgtgtgcgt     360
gtgtgtcagt ctgtttgtga gtgtgttaaa ggctacagac cacagttggt ttaaaatgct     420
tggaacttcc caaactggct ttactttatg tttatacagt gctcagggtt aacgcagtac     480
atccatgcca ttgctgtggg aggtatcccc ggatgcatgt gttttgagtc tataaatata     540
gaaaatatat attggtttct ttttccaact taatangttt attaaagcat gaaatgaaag     600
ggtgcatatc atgcattcaa gntatntcct aatttttggt ctgacagtgc atgtctttgg     660
agcatgctga aacaanaatn acacaggaat tgantaaccn gaaagaaaca ttgttaaatg     720
tccaacattt gttatgcatt tntattgggg g                                    751
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<210> 746
<211> 760

<212> DNA
<213> Homo sapiens

<400> 746
tnnnnntntn nnnnntttnn nttcntnnnn ctttgaancc ctttgctact tgctcttttt 60
gcaggatccc atcgattcgc tgaaacaaaa gatgtatttc aattaaaaga cttggagaag 120
attgctccca aagagaaagg ctttactggn tntgtcangt aaaagaagtc cttcaangct 180
tagttgatga tggtatggtt gactgtgaga ggatcggaac ttctaattat tattgggctt 240
ttccaagtaa agctcttcat gcaaggaaac ataagttgga ggttctggaa tctnagttgt 300
ctgagggaag tcaaaagcat gcaagcctac agaaaagcat tgagaaagct aaaattggcc 360
gatgtgaaac ggaagagcga accangctag caaaagagct ttcttcactt cgagaccaaa 420
gggaacagct aaaggcagaa gtagaaaaat acaaagactg tgatccgcaa gttgtggaag 480
aaatacgcca agcaaataaa gtagccaaag aagctgctaa cagatggact gatnacatat 540
tccaataaaa tcttgggcca aaagaaaatt tgggtttgaa gaaaataaaa ttgatagaac 600
ttttggaatt ncagaagact ttgactacct ngactaaaat attccatggt ggtgaaagat 660
tttcaagctt gngaatttgt aaattttnaa ctattatcta actaatgtnc tgaattgccn 720
ttggctgtac tgggttatca ttttattaat ggtaaataaa 760

<210> 747
<211> 786
<212> DNA
<213> Homo sapiens

<400> 747
tnngncttta nnccntttnn attgnnnnnn nttgaaaccc ttggcnactn gctctttntg 60
caggatccca tcgattcgaa ttcggcacga ggaggctgtg tcaaagaatg aatggaacgc 120
ctactatgag gaggtgggtg tacgtnctag anggagatcg agtacatgat ccagaagctc 180
cctgagtggg ccncggatga gcccgtggag aagacgcccc anactcanca ggacgagctc 240
tacatccact cggagccact gggcgtggtc ctcgtcattg gcacctggaa ctaccccttc 300
aacctcacca tccagcccat ggtgggcgcc atcnctgcan ggaactcagt ggtcctcaag 360
ccctcggagc tgagtgagaa catggcgagc ctgctggcta ccatnatccc ccagtacctg 420
gacaaggatc tgtacccagt aatcaatggg ggtgtccctg agaccacgga gctgctnaag 480
ganaggttcg accatatcct gtncacgggc agcacggggg tggggaagat catcatgacc 540
gctgntgcca agcacctgac cctgtnacgc tggaactggg aaggaagagt ccctgctacg 600
tgggacaaat aactgtgaac tggaccttgg ncttnctaac attggncttg gggggaaatt 660
catnaacaag ttngccaana cctgcgtggg cccctgaaat acattctttt nggacccccct 720
tgnatccaga accccaattg nnngnngaaa acttnaaana aantnncttt naaaannntt 780
tttnct 786

<210> 748
<211> 722
<212> DNA
<213> Homo sapiens

<400> 748
tggaactngc tctttntgca ggatcccatc gattcgaatt cggcacgagg aggaagaggc 60
ctgctccact tgtctgggaa cctgggcagg aggcacagag gaagccaagg cctggagctg 120
caggtccccc ggcatctctc tctgtcccgg cagcccagga tggcctggtg cccccacctg 180
ctgcagcagg agccccaagg agtgctagct gagggtggtt gctggggtgg tcctcatgga 240
cagtgaggtg tgcaagggtg cactgagggt ggtgggaggg gatcacctgg gttccaggcc 300
atccttgctg agcatctttg agcctgcctt ccggtgggag canaaaaggc cagaccctgc 360

tgagttanag gctgctggga tccactgttt ccacacancn ggaaggctgc tgggaacagg 420
tggcanagaa gtgccatgtt tgcgtngaac cttgcantct tncanctggg gactggtnct 480
tgctgaaacc cacgagctgn acantnanga gctgtccanc ttgcttggct cactgngacc 540
aggaaagcct gtctttggtt agctcgtgtc ttctgcagga aaaaaaaaag gatgtgtcat 600
ttggccatga tatttgaaaa aggggaagga tngccnaant ttgtttncca tttattccag 660
tanttggaaa attttttgac cccctnngct taattctttt gcaanaacta ctggggggtn 720
tg 722

<210> 749
<211> 821
<212> DNA
<213> Homo sapiens

<400> 749
tttnaanncc cttgctactn gttctttttg caggatccca tcgattcgtn gacatagaaa 60
acatacagta agaatatggt attataatct tacggggacc actgtcaaat cgcggtctgt 120
ctttgaaaag ttgtnatggc ggcgcatgac tataaatacc ctagctggtt agcatttaca 180
ttccttgcca gggagtttga aatttatnct nggcgggctg nctttaggnt ttaggtagag 240
ttaaagaggt aaagcacatg tttgccacaa cccaggaaag tatttttaag aaagatttgg 300
attttcctac ctttagagat ctaaaaaaaa tttaatataa aaaatcattt tgagntggtg 360
tttattacta gttcagaatg agtggctgct gaagggggcc cccttgnnat tttcattata 420
acccaatttt ncactttatt ttgaactctt aagtcataaa tgtataatga ctttatgaat 480
tagcacaggn taagttgaca ctttgaaact ggccatttct gnattacact atcaaatagg 540
aaacattgga aagatnggga aaaaaaattc ttattttaaa atggcttaga aaagttttca 600
agattacttt ggaaaattct aaacnttnct ttctgngttc caaaactttg gaaaatatgg 660
tagatnggac ctcattgcca tttaagactg gttttcaaaa gctttccctc aacatttttt 720
aaaggtgtgg antttttccct ttttaaatat tccataattt aantttcctt ttnaaaggcc 780
nctnnttttc ccaaacccat ngnctttttgg ggnaaatccc c 821

<210> 750
<211> 770
<212> DNA
<213> Homo sapiens

<400> 750
gntttnnnnn nnctttnttn nntgnctntt tctaagagct tngcnnatgc tnggtcggca 60
cgaggcaaca tttgtctaca actctactgt aaaattggaa atgcttttcc acagaaaaac 120
ctctcaaaat gctgaatgca aaagttggga tcacagaaac attgtgccta tttttggtct 180
gctggaaact gtatttntac aaggtaatcc ctgttctcaa tatagttcct gtcttgccac 240
tggcggtttt cttgtagcat ttttctagtt ctgagattgc tactacccaa agtattcatt 300
tctttcttac tggggtgtcc tctgtcttca cagcctgctt ctggattgta ggttttttcc 360
tttctttctg ttgagatatt tatggcattt gatagagtca aaccagatgt attgcagccg 420
gacatactta tgtggcttca gatgtgtaaa ataagtaact tcctatcttt gtctgtctag 480
ctcaagagtt gactgtggac gaggaatgcc tgtattgatt cattaatgta ataactattt 540
actgactgcc taccatgtac aaccagaaac acagttccta acctcatgaa cttaccatgt 600
aacatgggaa gacaagccta agttcttatt tggntggnaa ttgcgataac gctcacagaa 660
caaattcccg attcctacga acccatgtat agggggggaaa tatttaaggt cccatttaat 720
actgacattn gcccnccccc ctnntatttt aagctgagaa tctgaaggnn 770

<210> 751
<211> 774

<212> DNA
<213> Homo sapiens

<400> 751
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cgttnnnttt ccnccttttga agccctttttt gcaggacttt cnaatncttg gtagacttta      60
tgtcagttct gtgtagactt tatgtcagtt tttgtcatta tttgaaaatc tattctgaca     120
actttttaat tcctttgatc ttataagtta aagctgtaac aactgaaatt gcatggatca     180
agtaagcata gttttatcca gggagacngc tcnnnggaag ccatagaatt gctctggtca     240
aaaccaagca caccatagcc ttaactgaat atttaggaaa tctgcctaat ctgcttatat     300
ttggtgtttg ttttttgact gttgggcttt gggaagatgt tatttatgac caatatctgc     360
cagtaacgct gtttatctca cttgctttga aagccaatgg gggaaaaaaa tccatgaaaa     420
aaaaaagatt gataaagtag atgattttgt ttgtatccct acccatctcc tggcagccct     480
actgagtgaa attgggatac atttggctgt cagaaattat accgagtcta ctgggtataa     540
catgtctcac ttggaaagct agtcctttta aatgggtgcc aaaggtcaac tgtnatgaga     600
taattatccc tgcctgntgt ccatgtcaga cttttgagct gatcctgaat aataaagcct     660
tttaccttat ctggaaaaaa aaaacattnt anancaaaaa aaaactnnga gccctttana     720
actnttagng agnccntttt ccgtagaatc ccngacntgg ntaaggaanc nnnc           774
```

<210> 752
<211> 778
<212> DNA
<213> Homo sapiens

<400> 752
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gntttgaann ccnttgtttc gnatcctttt tgnaggactc tgaagncctt tgttcggcnc      60
gagaagaaac tctgcctcag aaaatgttta cagcttccag tggaatcaaa cataccatga     120
ccncaattta tccaagttct aacacattag tagaaatgac tcttggtatg aagaaattaa     180
aggaagagat ggaaggggtg gttaaagacn ttgctgaaaa taaccacatt ttagaaaggt     240
ttggctcttt aaccatggat ggtggccttc gcaacgttga ctgtctttag ctttctaata     300
gaagtttaag aaaagtttcc gtttgcacaa gaaaataacg cttgggcatt aaatgaatgc     360
ctttatagat agtcacttgt ttctacaatt cagtatttga tgtggtcgtg taaatatgta     420
caatattgta aatacataaa aaatatacaa atttttggct gctgtgaaga tgtaatttta     480
tcttttaaca tttataatta tatgaggaaa tttgacctca gtgatcacga gaagaaagcc     540
atgaccgacc aatatgttga catactgatc ctctactctg agtggggcta aataagttat     600
tttctctgac cgcctactgg gaaatatttt taagtggaac caaaataggc atcccttacc     660
aaatcaagga agactgactt ggacaccgtt tggaaaatgg gtaaaaacgg tggnttactg     720
gtganttggg gagcnagaac cggacccact ggtatactgg ggantaacaa ttttttttc      778
```

<210> 753
<211> 775
<212> DNA
<213> Homo sapiens

<400> 753
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gcttttgaaa ccctttttgtt aacgcctttc tgcatgatct tctcgtcctt gaaagggccc      60
taaaagagat gaacaatacc gtatcatgtg gtttgaatta gaaacccttg tcagagccca     120
tatcaacaac tcagagaaac atcaaagagt cttggaatgt ctgatggcat gcaggagcaa     180
accccccagaa gaggaagaac gaaaganacg cggctgaaag agggaagaca aagaggacaa     240
gtcagagaaa gcagtgaaag attatgaaca ggaaaagtct tggcaagact cagagagatt     300
aaaaggaatc ttagaacgtg gaaaagaaga attggctgaa gctgagatta taaaagattc     360
gcctgattcc ccagaacctn caaacaaaaa accccttgtt gaaatggatg aaactccaca     420
```

```
agtggaaaaa tcaaaagggc cagtgtcgtt attatccttg tggagtaata gaatcaatac     480
tgccaattcc agaaaacatc aggaatttgc tggaccgttt gaactctgtt aataacagag     540
ctgaactata tcaacatctt aaagaggaaa atgggatgga gacaacagaa aatggaaaag     600
ccagccggca gtgaagagtg acttgangaa ctaaatttta gcatattgca aaaatatttt     660
gtgcgggaat tcgatatnag tacttttacc agcaagatgg natngttatg tttgcctgga     720
ctggntttta catttttnaa attttttcag tgnccttttt tggtcctaaa ttatc          775
```

<210> 754
<211> 1032
<212> DNA
<213> Homo sapiens

<400> 754

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ggnntttttc ccaaaaaaaa ggggcccccct nggggntttt tncncaanng gncccctttt     60
tctttgncca gggnaacntt ttttgngaaa agancccccct ttttggatnn accggggccc    120
cccggaaggt tccnaaattt tnagggttna aacccaaatc cttggggaaa aaaaaaaaac    180
ccagggccnt ntntggggnc cccctngggg gggtngggaa aaaaaaaaaa gggggaatgg    240
cccccaaaaa aaaatnnggg gcccctnggg ggaaaaaaaa gggaaagccc aggtngggaa    300
nggaaagggg gaaggntccc ccgggggggaa aggaaatggg tgggtnggna atggcccaat    360
ggttggaaaa ggcccaaacc aatttgggnt ntaaaacaat ttcaacctgg gggggtcctg    420
gcccanaaaa aatgcngggc acccncgngg ggtctggctt aagaattggt tacaagggca    480
aagggaaagg gaagagttct agagataaag aactatatgc ttggatgaag tgtgtgaagg    540
gacagcctca tgatcacaaa catttaatgc caacccaaat tatacctggt tctgttttga    600
cagatcttct agatgccatg cacactctta gggaaaaata tggtattaaa tcccattgnc    660
attggactaa caaacagaat ttacaagttg gaaattttcc tacaatgaat ggtgtatctc    720
aagttttaca gaatgntctt aatcacagna ataaaatttc tctgtgcatg cctgagtctt    780
cagcagcaaa aatactcctc cgaagtctga gaaaaatggn ggcagcagcc caagaagagt    840
gatgtaggca cagataacna aggntaacct cctccagaat ccccagtcac cactgcactg    900
gttaagcaga acttngcagg agcaaaaaag cccngangan ggaaaaaaaa aannaaaaaa    960
aactcggagc cctcttagaa ctatangggg ggccgnnnta ccgnangatc cccgacctga   1020
anaggaaccc cc                                                       1032
```

<210> 755
<211> 798
<212> DNA
<213> Homo sapiens

<400> 755

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ngnnnnnttt nncccnacna aatccctttt ttgaagcctt ctantgnctt catcgtnctg     60
gtaaattggn tgaattattg tattgaagct tgagctgtat tttnaagtaa tttnggttnc    120
ccctaagatg ttattatgtt agggacataa cacttttggg aggttgttgt gggagatggt    180
tgatttaggt tttcaaaagc tagaaataaa atttacatnn ccccggntnn cataaaattc    240
tgctctaatt gggtggaagg tgctgtatct aacttgtgtt cctnctaagg ttatgtccta    300
ataactattc ttttaggagt atacttctac tttatagaag gttgcttttt ctttttaatt    360
ttntctaaca aagaaaagaa tnaagtattt attaataaag aaccagaaag cacttgaaac    420
tgatgttttt aaatgggctc acttanggta gatttattta tctcattaac ttaaaaacag    480
ctatgtgnat tgaaataagt cacaacagaa cttgaacacc agggtgggtg tctgagcaat    540
cccctttctt atggggaaaa acaaatggtt cttgtttgaa cangaaggta tcattgcagt    600
cngcattcac ccgtgtataa ttgnnatata agntgnataa tatgctcgta aaggctnaag    660
gtnagctgga tctggatgcc ctttnaccaa ttangatttt aacttttaan aataaaattt    720
naaanctaat tgncnaaata aaaaaaatan naaacttcgg ncctctacaa nttntagatg    780
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ngtcgattnn cgnncanc 798

<210> 756
<211> 834
<212> DNA
<213> Homo sapiens

<400> 756
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tccttcagct ggtagcttnc attcgnantt nnanatanta tntgtgcatg cncnnttgaa 120
tttttgtgga agaacagant gcagaagaag gcnaggaaag ccgaagagan tnntncggca 180
ncagaagctt aaagnaggcc aaactggtgg tgcnctttcc tcggnacaga agctggatga 240
ctatggccaa tttggagaaa nagctccagg agatggaggc acggttcgag aaggagtttg 300
nagatggatc ggatgaaaat gaaantggaa gaacatganc tcaaagatga ngatggatgg 360
taangacagt gatgaggncc gaagacnctg agctctatga tgacctttta ctgnccanca 420
tgtgacaaat cgtnaanaac agtaaaggcc atgaanaatc acntagaagt caaangaaag 480
cnnttgggaa aaatggnggn nctttgntaa aaccacnagc tgganggang gaagaannna 540
aaatttttta agnacctcaa attgattgaa aaatncatta tgatgacaat tcctgnanga 600
ataaattggn agatgcncta naancaaaan gcntttttn antnnaaana nacaaannnt 660
nnagcctntt ngaacntata gtnnannctn cntttanctn tntatcccgg actttnttnt 720
ggataccntt gactnagctt ttggacaaaa ncncnacttt gtattncatt ngnnaaaaaa 780
atgcntttat ttttcgnaaa tttggtgaat ncntaattng ntnntattnn nnnc 834

<210> 757
<211> 1062
<212> DNA
<213> Homo sapiens

<400> 757
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gggccagggg aatncccccca atnccggaat tttccggggt ntttgggggg nttggaaagg 120
gccccttggg gaaagggncn tttccnaagn aaaggggtng gaaaattttn taaatggcct 180
tttngggggg aaaaagcccc ctnggaatnc ccccaaaaaa cccttgggaa aaaggggggga 240
aaaagggggg aacctttngg gnaatccttn cccnttnaat aatttggggn aattaaancc 300
ctggtttggg aaagggaaaa gggttggtct tggtcttggg ggaanggaat tgggggccaa 360
nttaaaatgg aaggtttggc canaatnggc cncttcgggg gcttnttcaa aagccaagcc 420
tttgggancc ctgcttcatt tttngggccc tttnctgcca aggaanccca acccttaact 480
tancaggaaa anggagatga aaggccttct tccaaggaag gtaaggtcct ttggctgccc 540
cnacttaaat gctttttgaa antctcttag atgtggnaaa tattttttcc gaaccttgaa 600
atcaactngg tagaatttca attggaagca taatccattg taaaatatat tttagttgat 660
atttggtaaa atgccttttt tggtggtgtg gttngaatcc tgggtttccc aagaatcttg 720
natttcaaat ggtttaacaa angggaagga aaggganctt ttcccttaac cttccctttt 780
tgaccaggaa agattttnaa aagtaccttt ctttttaagg aaaaaaaaaa attaaatttt 840
gaagaaaaat tgggatttgg attttanaaa aaangggaaa aaaaatatna ntattnatan 900
ntcnnannat nnttnatnnt ctanntantt nctntnnnta ntnctnntnt ntnnannnna 960
nannnannaa ataaatantc nnncatnctt anctacanat nccnntcttn nttntannac 1020
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<210> 758
<211> 845
<212> DNA

<213> Homo sapiens

<400> 758

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aanccccttn tttnaaatcc tttttanang attcatcgat tcgaattcgg nacgaggcgc     60
tagcgtcggn tccgcntggg cccttgcggt gcgctgnggg caggcggtga ggcttacgcn    120
tntgcttacg ggcaaaaacc tgcacacgca ccanttcccg tnnccgttgt ccaacaacca    180
gaaggtgatt gcctttgggg aancttctan gncaacnacn tgaacntatg gacagtgcgc    240
tgntttggac agaantggga acnttnaggn tgntgtgcgc ttcnagcatn tgggcacctt    300
tgtgttcctg tcantcacgg gtgagcanta tggaagcccc atccgtgggg cagcatgaag    360
gtccacggca tgcccaattg caacacgcac aaatacttgg aangccatgg aangcatntt    420
natcaagcct aatgtgggag ccctttttgca agtcacgaat taactctnaa nngtntggat    480
ggattgggtg ggantggang gttgcaagtt ngggccnttt tgaaaggcca ctttttggna    540
aaaaactttt gggtttttaa ngggttcntc aaaatgccct ttgnnaattn aaagaaatgt    600
tgggcctatt naaaaaaaan atnatacttt atntaatctn nataataata nttantaata    660
aaantcttnn agccttttta aaanttttta atgaanctct ttattttanc gttanantnc    720
ntaacnttta attaaaggaa taacaatttg ttgaantttt ggtataaana ncccccantt    780
tttaaaattc ntntngaaaa aaaatncntt tattttggta aaaatttgng gaatcnnttt    840
tgctn                                                                845
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<210> 759
<211> 947
<212> DNA
<213> Homo sapiens

<400> 759

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ttnccntttt gggggggaaa ngcccccccc caaangnaaa aacccntttt nnnnaatttn    120
ngggnanggg ntntggggnc ccnttaaccc caanggggggg gggttttnan cctgggggnn    180
naaaatnggg ggaanaantn nnnaatgggn antcccttna angggaaaaa naatttnncc    240
ttaaggnnat gggncattaa tnttnatccc tantggattn caatttcatt cgnattaaag    300
gcttttactg gnataatcct tnncggcccg cnctggtagt ttaaagtgcc canaanttga    360
atgggaaatn acgggttttg aaaatcgcac aaagcagtgc cnggcacnga ggngtcacgc    420
cngtaatncc agcattttgg gaggcctgag gcangcggat cacganggca anagagtcca    480
gaccattnct ggctaacacn gggaaacccc gggnctaata aaaaatcaaa aattaggntg    540
gacatggtgg cacgtgccng taatcncagc tacttangga agctggatgc aggaagaatt    600
gcgtgnnanc cnggccccng tggaangntg cattgatacg aagaaccgtg ccaaatgaan    660
ttanannctg ggcngaannn gagcggaaaa agccctnttt aaaaaaaaan gggantggaa    720
aaantggtgc canagncatn nggggaaaaa attttnnnnt tnnttnancg gttttnanct    780
tgnggaaggc cntctttaat nttggggaaa aggcactttt gggntnggtt ttggaaaacg    840
nntggctttt ccctttnaaa agggaaaaan ggnnttaanc ccctgaaaaa ngngcngnnt    900
tttaaanggg gnnnnaaaca nggggncttt ggaancccca nnaaacc                  947
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<210> 760
<211> 759
<212> DNA
<213> Homo sapiens

<400> 760

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agaagatatg cagagatatt ccaggatctt ttagctttgg tgcggtctcc tggagacagt    120
gttattcgcc aacagtgtgt tgaatatgtc acatccattt tgcagtctct ctgtgatcan    180
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gacattgcac ttatcttacc ggctcttctg aagggtctat ttctgaactg gagcagctct 240
ccaattctct accaaataaa gaattgatga cctcaatctg tgactgtctg ttggctacgc 300
tagctaactc tgagagcagt tacaactgtt tactgacatg tgtcagaaca atgatgtttc 360
ttgcanagca tgattatgga ttatttcatt taaaaagttc tttaaagaaa aacagtagtg 420
ctctgcatag tttactgaaa cgagtggtca gcacatttag taaggacaca ggagagcttg 480
catcttcatt tttagaattt atgagacaaa ttcttaactc tgacacaatt ggatgctgtg 540
gagatgataa tggtctcatg gaagtanaag gagctcatac atcacggacg atgagtatta 600
atgctgcaga gttaaaacag cttctacaaa gccaaagaag aaagtncaga aaaatttgtn 660
ccttgaacta gagaaacttg ntntggaaca tttcaaaaga tgaatgacaa tctggattcn 720
ttggtngaca gtgtaatttg gactttaacc ngatgctcg 759

<210> 761
<211> 752
<212> DNA
<213> Homo sapiens

<400> 761
cctnactaaa cctttgcnaa ngccnttnnt gctgatccca tcgattcgca ggcctggact 60
tcgcccccag gcctaggacc gcggtgggtn ttaaccctgc tnctgcccca acagggactc 120
caatcaatcg gagttctccc cttgccggag ctgcccttca cctttggggc ccgagacagt 180
cataagggat ggacttacnt ttcttgcagg gaaaaaggtg gacagccgtg tttcttaagg 240
atgctgaggg catggggcca ggaccagggg agaggcacag ctccttcctg agcagcctct 300
caccactgcc acaaggctcc ctaatgctgg tctctgctcc actccccggc ttcccgtgag 360
gcangaggca gagccacagc caaggccctg accacttctg tgccagttgt ctaagcagag 420
cgcctcaggg acgctggaaa tgccttaagg atagaggctg ggcatcacat caaatgggac 480
tgtggtgttt ggtgaaaacc ttcctgagga tctggattca ggaccctcca tgactggcct 540
atttactggt tacagctggc cagtgcanan ctgctgctct tttacctttt taggcccctg 600
taacttncca cctttaaact gcccaanaag catgcctntt ccacaggaag aagggagcag 660
acagggaaat ctgcctacca anaagggtgt tgtgtgtctt tgtgcccaca cgtggtggct 720
ggggaatgcc tggatggtgc cgtggntgat ct 752

<210> 762
<211> 1032
<212> DNA
<213> Homo sapiens

<400> 762
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aagtggtagt ggcgcttntc gggtgntgtg cttcacgttt tggtctaaag gncgagactg 120
ttgtggcnac ngngnaantn tacnggaang gnttaaantn tnnntgnagt nggaanaatt 180
cnatcngaan gaanttgggg gggntagnnn nggttanatn attgatgaat ggnttcaana 240
tngnaaantt tatnancgan atgnnatant tnnaaangan gaccaactgg gntnanatgg 300
agnannnatn aannggntaa ncnatanana tantncattt ggtanganaa tngangaagg 360
attntcaaat agncatgtng gangatgaac ntnnaggnnn nagaatattt ggataaaatt 420
ggtantatga agatntggnn taataatacc nanaaatnnn nnantttnat nanngangaa 480
ntaggganttn atgnctatgn ggatannntn nanntatnat agngataaan tatgatactg 540
tttannntat ntnganttag tnattnaatg ntcttgtnan aanttatttt ncgntagtta 600
gntagnnnta tnnactttgg naancanana tgtaattctc tctanacggg aatntttnta 660
tnntnnntat caagaggtnt ntnnattgna aatantatac nnttgnanaa antatatcna 720
tanaanaaan ggnnattatt ntatatganc aaanaaaaaa ntattgngga nntanattat 780
ctctcatnat ngattatncn gtantgtata atggnnnata antatgtnnn tntaanataa 840

atggatataa gtnttatant atgcncntna aggnggtcng anaantatgt aattatattn 900
angctanata cnatnnanat gtntnactaa atatngntgt gaaangtntg cgnggnaaaa 960
tntgttanta ntnaaacang gtataganat atanatgngn ngaatatcta ctatntgtan 1020
atacttatan ca 1032

<210> 763
<211> 817
<212> DNA
<213> Homo sapiens

<400> 763
aanncccttn tttctaatnc ttggctactc gtnctttctg caggatccca tcgattcgaa 60
tttcggcacg aggggaggga cccttggggn caggttgtgg gtagccagtt gcagtctgtg 120
gcctccctca gaggtttgga gtcgggcgtg gcatgctgct gttggcctct ttccgaggga 180
gtgccatcca ctccctgtcc caccgctnnc cctngtgagg acagtgaggg cagtgctacg 240
tggtggggag gtgtgtgtga agccacggaa gggcttcaca gggcaaatgc caaggccagt 300
gggccccgga cagagtnagg ctccctgggc ggncttgtgt cttggtggcc ctgatcatcc 360
tgccaatgca naaagccagc aggcaagaga cccctactcc ctttaaggac cattagcata 420
aacaaaccat tgngttgaat gcaatgatcc aggtgcactt tnagggtaca agctggactn 480
gttggaacag gattacatgg aaaannggaa angggggcan gctgtctctt gggacatnag 540
taatgtcttt ttacccantt gncactctng aanttcaaan ttggncatgt tttctggggc 600
ctnctngnaa aagcagtttt ttcaccncat natgaagaaa aaacttgttg gcttgganng 660
tannggbatt nttgntnana cttnccctaa anggntncct ttnggggcat ttntgaaggn 720
taaataatgg gggatacctt tttaannttc cttgcagatt taaaaatgtt ccttaaanga 780
nncctcaatg nttnggtctt nttccaaaaa acnattc 817

<210> 764
<211> 777
<212> DNA
<213> Homo sapiens

<400> 764
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cggtgctgaa catcatcatc tttgaagact gtaggaacca gtggtctatg tcccgaccac 120
tacttggctt gatattgctt aatgaaaagt atttttctga cctaagaaac agtattgtga 180
acagccagcc acccgcgaag cancnggcca tgcacctgtg ttttgagaac ctgatggaag 240
gcatcgagcg aaatcttctt acgaaaaaca gagacaggtt cacccagaac ctgtcagcat 300
tccgtcgaga agtcaacgac tcaatgaaga attccactta tggcgtgaat agcaatgaca 360
tgatgagctg acacctnctt ggactctacc tgtacagagc agcgtccctt tggtttggcc 420
cagaggggcg aacaattgca agggagaggg cctggctgat cctggctctt ttctccaggg 480
gtgtggggaa aaatggcaaa ggtcaactag ctgcttcccc aagggaatag gggtgtgagt 540
acactcacta nggggcaagg cgctgcttgg ttcctggggg gactgggtgg gaaagggtgg 600
tgnganggag ataaagagat tcaaactgag actccagtct ttccttctgg gggccaccca 660
aagttgggga gnaacccccct antggtncct gccaacaacc ttgccttggg attaaacatt 720
ntncattttt ttcantaana tttttgaaca aagggttant attgnctnaa gtttann 777

<210> 765
<211> 774
<212> DNA
<213> Homo sapiens

<400> 765
ntttctaatg cttggctctc gntttgatgc angatcccat cgattcggga aatgcaagtc 60
aaaacagctt tgtaggtctc agagtttgct tttaagaagt agtacaagaa ggaatagtta 120
tatcaataca ccagtggctg aaattatcat gaaaccaaat gttggacaag gcagcacaag 180
tgtgcaaaca gctatggann gtgaactcgg agagtctagt gccacaatca ataaaagact 240
ctgcaaaagt acaatagaac tttcagaaaa ttctttactt ccagcttctt ctatgttgac 300
tggcacacaa agcttgctgc aacctcattt agagagggtt gccatcgatg ctctacagtt 360
atgttgtttg ttacttcccc caccaaatcg tagaaagctt caacttttaa tgcgtatgat 420
ttcccgaatg agtcaaaatg ttgatatgcc caaacttcat gatgcaatgg gtacgaggtc 480
actgatgata catacctttt ctcgatgtgt gttatgctgt gctgaagaag tggatcttga 540
tgagcttctt gctggaagat tagtttcttt cttaatggat catcatcagg aaattcttca 600
agtaccctct tacttacaga ctgcagtgga aaaacatctt gactacttaa aaaaangga 660
catatttgaa aaatcctggg agaanggact atttggctnc ttttgccaac ttacttcata 720
ctggnaagcc agattantng ctcaaggaag ttttgatgag ccaaaaaagt tttn 774

<210> 766
<211> 779
<212> DNA
<213> Homo sapiens

<400> 766
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ccatcgattc gcgaaattcg gtggcgccac gtccgcccgt cttngccttc tgcatngcgg 120
cttcggcggc ttccacctag acacctaaca gtcgcggagc cggccgcgtc gtgagggggt 180
cggcacgggg agtcgggcgg tcttgtgcat cttggctacc tgcgggtcga agatgtcgga 240
catcggagac tggttcagga gcatcccggc gatcacgcgc tattggttcg ccgccaccgt 300
cgccgtgccc ttggtcggca aactcggcct catcagcccg gcctacctct tcctctggcc 360
cgaagccttc ctttatcgct ttcagatttg gaggccaatc actgccacct tttatttccc 420
tgtgggtcca ggaactggat ttctttattt ggtcaattta tatttcttat atcagtattc 480
tacgcgactt gaaacaggag cttttgatgg gaggccagca gactatttat tcatgctcct 540
ctttaactgg atttgcatcg tgattactgg cttagcaaat ggatatgcaa gttgctgatg 600
attcctctga tcatgtcagt actttatgtc tgggcccanc tgaacagaga catgattgna 660
tcatttttgg tttggaacac gaatttaagg cctgctattt accctggggt atccttggat 720
tcaactatat catcggangc tcngtaatca atgagctaat tggnaaattn ggtggacac 779

<210> 767
<211> 799
<212> DNA
<213> Homo sapiens

<400> 767
gnnnnnnttn cccgcctttn gaaanccccct tctttctaat gcttgttcaa cgcctttgct 60
gcaggatccc atcgattcgt ggatactgac aatggtggca ggcatttcaa gccttttaaa 120
ttagtacttt ttgtcgnctt gcttattaaa attttgttaa ttttagcaaa gaccaattgt 180
tgtgataaac tggtgttttt nggatgcttc aagcacacgt taaccaatcn gccaatnccc 240
ctttnggttc ctcccattgn tctaaaatag gactttcata ttattaaaac ctcaaaagat 300
gatccaccca ggatgaacaa agatcaccaa ggggaaagaa aacatttttt atctttacag 360
aaaacatgtt aagattatat atagatgtat tctttacatt ggatattgta ttagagtcct 420
ccttacaaga aatgaaatag gtttttagca ctcttagcat tagagttcct agattggtgt 480
tgatagctac agttttaaaa tgtataacct gaaaatgaag gttaatttg cattgtaaag 540
agcacatttg atctatgtaa aaagtgtcca tttggtgtat ttttttaaa aaagagaaag 600

cactttcata ttaagtagca tgtgtatgaa tttaagattt tcatatttgn tgngtctggt 660
attcagtgaa gtaaaattga gcattttaaa agtttggtgg atggcaacca ttaactatta 720
aattaaaagc caccttatac tctgctgctt aacttgcttg naaattgcac ctttggnacc 780
ctgcacattt tcatattnc 799

<210> 768
<211> 826
<212> DNA
<213> Homo sapiens

<400> 768
gnnnntnncn ccctttctaa tggcttgttt ctaaatgctt tttcnaatcc ttggtacatg 60
atcccatcgn ttcgcgctgt gcttgagacc aacctgacgg gtaccttcta catgtgcaaa 120
gcagtttaca gctcctggat gaaagagcat ggaggatcta tcgtcaatat cattgtccct 180
actaaagctg gatttccatt agctgtgcat tctggagctg caagacnggg tgtttacaac 240
ctcaccaaat ctttagcttt ggaatgggcc tgcagtggaa tacggatcaa ttgtgttgcc 300
cctggagtta tttattccca gactgctgtg gagaactatg gttcctgggg acaaagcttc 360
tttgaagggt cttttcagaa aatccccgct aaacgaattg gtgttcctga ggaggtctcc 420
tctgtggtct gcttcctact gtctcctgca gcttccttca tcactggaca agtnggtgga 480
tgtngatggg ggccnggagt ctctatactc actcgtatga ngtccagatc atgacaactg 540
gcccaaggga gcangggacc tttctggtgt caaaaaagat gaaaggagac ctttaaggag 600
aaagctaagc tcttgagctt gangaaaaca aggggtcctt ccatncccca aatgccttta 660
catttttgga ggatatgcct nnnggnacnt ttttaaaaaa gcttatnagt tngntatggg 720
naaaacaatt ttttccttan tttttaaagt ggntaataaa tnaaantcct aatggnaaaa 780
aaactantcc ttggnaanta ttttccaggn cttnantgtn cccncn 826

<210> 769
<211> 802
<212> DNA
<213> Homo sapiens

<400> 769
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caagcctgga gctgcaggtc cccggcatc tctctctgtc ccggcagccc aggatggcct 120
ggtgccccca cctgctgcag caggagcccc aaggagtgct agctgagggt ggttgctggg 180
gtggtcctca tggacagtga ggtgtgcccg ggtgcactga gggtggtggg aggggatcac 240
ctgggttcca ggccatcctt gctgagcatc tttgagcctg ccttccggtg ggagcagaaa 300
aggccagacc ctgctgagtt agaggctgct gggatccact gtttncacac agcgggaagg 360
ctgctgggaa caggtggcag agaagtgcca tgttngcntt gagccttgca gctcttcagc 420
tggggactgg tgcttgctga aacccaagag ctgaacagtg aggaggctgt ccaccttgct 480
tggctcactg ggaccaggaa agcctgtctt tggttaggct cgtgtacttc tgcaggaaaa 540
aaaaaaagga tgtgtcattg gtcatgatat ttgaaaaggg ggaaggangc cnaaanttgt 600
tcccatttta ttcaagtatt ggaaaatatt tggccccccct ttggctgaaa ttctttttgc 660
aanaactaac tgngtggctt gttcncttac cctttttcan gnttaattgg tttnaatttt 720
ttgcattgaa attaaagacg tttttaaatt tcntttncaa naacaaaggg cttanatncc 780
ngantcnana nattggnant tc 802

<210> 770
<211> 1157
<212> DNA
<213> Homo sapiens

<400> 770
ccctttttt tttttcccnn aaaaaaanat tggggncccn ttttttggg nttttttttc 60
ccnaaaaaaa aattgggncc ctttttgggg ggnntnaaaa aaannnnnnn nccccccntt 120
tttttggggn nnnnnaaann tnnnnnncnn nttnnnnnnn nnnnnnnnnn ggnnttnnng 180
gggnnnannc cnccccccaa tttcccggnn attnttccgg gcccaatttt tgggaccccc 240
cagggnnnag aataaggccc ggggnttttt tttncnaggg ncccaaaagg gcccttgggc 300
caaaggnaaa tccnttggga aattttggga atttggccct tggnanntcc caataccggn 360
aaaaatgggg aaangnaaaa aaggnttncn ccaaattggt tgggggggg ttccaaagat 420
tttcattggg ggtncntggg ctttcaaccc naaggnaang ggtttncttt caaaaaatta 480
cctttaattg ccattaagca attcccaang gttannaaag ggtgtttntt ctcanctatg 540
cttcganagn gaaaatcaac naatggaaaa tgtgttgtaa ttggtctgca ntctacanga 600
gaagctagaa cattagaagc tttggaanag ggcggnggag aattgaatga tntttgnttc 660
aactgccaaa gagtgttgtt gcagtcactc atttgaaaaa ctattttcct gctccagaca 720
ngaaaaaaac tttatangtt tactaggaat cgatttgaca agcnttcang taacaaacag 780
ttctnccaag agatatcctt gttnaagaan nattanaata ncnngaaagc ggaaanngtg 840
aataaatnnc ttcnagaagc ccaaaaannc acngaanaag tatggtgggn cttactggtt 900
agcacgttct tgacnacaga tggaaattga antctngatt ncctctgatt antgaatgaa 960
aaggtgacta ttnaanagct cttnanatac catgagtntt tggancattg attgaccaat 1020
ttcaannсca tttttangat ngaattntta tnaatgattn attnanaant gannncсttn 1080
gtttaaatta nnaaanaanc cntcnaaana cnanagggga tttataaaat ctaataanan 1140
ttttnnncnt ntnaann 1157

<210> 771
<211> 760
<212> DNA
<213> Homo sapiens

<400> 771
ngncctttna tnccttntga ancсntttgn aattnctcnn nnngttgatc ccatcgattc 60
gaattcggca cgaggtggaa gaaaattttt tgctgcttct ggttnccaga aaagggagcc 120
attttaacag acacatctgt caaaagaaat gacttgtcga ttatttctgg ctaatttttc 180
tttatagcag agtttctcac acctggcgag ctgtggcatg cttttaaaca gagttcattt 240
ccagtaccct ccatcagtgc accctgcttt aagaaaatga acttatgcaa atagacatcc 300
acagcgtcgg taaattaagg ggtgatcacc aagtttcata atattttccc tttataaaag 360
gatttgttgg ccaggtgcag tggttcatgc ctgtaatccc agcagtttgg gaggctgagg 420
tgggtggatc acctgaggtc aggagttcga gaccaacctg accaacatgg tgagaccccc 480
gtctctacta aaaataaaaa aaaaattagc tgggagtggn ggtgggcacc tgtaatccta 540
gctacttggg aggctgaacc aggagaatct cttgaacctg ggaggcanag gttgcaagtg 600
agcccgagat cgtgccattg cactccaacc agggcaacaa gagtgaaact ccatcttaaa 660
aaanaaaaan gaaaactcga gcctctagaa ctatagtgag tcgtattacg tagatccaga 720
catgataaga tacattgatg aattttggac aaaccccann 760

<210> 772
<211> 777
<212> DNA
<213> Homo sapiens

<400> 772
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ccatcgattc gaattcggca cgagctctac taaaaataca aaaattagct gggcgtggtg 120
gcacacacct gtaatcccag ttacttggga ggctgaggca caagaatcgc ttgaacccgg 180

gaggcggagg ttgcagttag ccaagatcgc cctgctgcnc tccagcctgg gcaacagagg 240
gagactctgt ctccaaaaac aaaaacaaaa actgttagtg aaggttccct gggacttttg 300
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ctacttttcc agtagtttgc cactttctcc gaggtanttt ggctgctctt tcagtaatgc 480
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tgtctccagc actatgcatc cctattttct atttattggg gtacactcac tttcagtaat 600
gngtttcaaa ctggtatttt ttaaaaaaca aatcaatgta aggactgaag ttgaaatanc 660
caatgtaata aagttaatta gggttatttt taaaaaaaan aaaaataana actcnagccc 720
tctagaaact atangtgagt cgnnttacct tgaatcccag accttgataa gatacnc 777

<210> 773
<211> 782
<212> DNA
<213> Homo sapiens

<400> 773
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aattcggcac gagacagtct cgggtttcat attttgctgt tttgatgga catggaggaa 120
ttcgagcctc aaaatttgct gcacagaatt tgcatcaaaa cttaatcaga aaatttccta 180
aaggagatgt aatcagtgta ncncccgccg tgaagagatg ccttttggac actttcaagc 240
atactgatga agagttcctt aaacaagctt ccagccagaa gcctgcctgg aaagatgggt 300
ccactgccac gtgtgttctg gctgtagaca acattcttta tattgccaac ctcggagata 360
gtcgggcaat cttgtgtcgt tataatgagg agagtnaaaa acatgcagcc ttaagcctna 420
gcaaagagca taatccaact cagtatgaag agcggatgaa gatacagaaa gctggaggaa 480
acgttaaggg atgggcgtgt tttgggcgtg ctagangtgt cacgctacat tggggacngn 540
cantacaagc gctgcngtgt nacctttgtg ccccgacatc agacgctgcc agctnacccc 600
caatgacagg ttcattttgn tggccttgtt atnggctctt naaaggnctt tnccccatna 660
aggaagccng tggaactttc atcttgncct gnantcgang atnaaaaagn atncagaacc 720
cggggaaggg gaaaatcctn aannctgact tcccggtttc caaaccagtn ttgnaacaaa 780
nc 782

<210> 774
<211> 793
<212> DNA
<213> Homo sapiens

<400> 774
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tgatcccatc cgattcgaat tcggcacgag atggcagttg cttttgaagt atatgatgnn 120
ttcctccact acaaaaaggg gatctaccac cacactggtc taagagaccc tttcaacccc 180
tttgagctga ctaatcatgc tgttctgctt gtgggctatc ngcactgact cagcctctgg 240
gatggattac tggattgtta aaaacagctg gggcaccggc tggggtgaga atggctactt 300
ccggatccgc agaggaactg atgagtgtgc aattgagagc atagcagtgg cagccacacc 360
aattcctaaa ttgtagggta tgccttccag tatttcataa tgatctgcat cagttgtaaa 420
ggggaattgg tatattcaca gactgtagac tttcagcagc aatctcagaa gcttacaaat 480
agatttccat gaagatattt gtcttcagaa ttaaaactgc ccttaatttt aatatacctt 540
tcaatcggcc actggccatt tttttctaag tattcaatta agtgggaatt ttctggaaga 600
tggtcagcta tgaaagtaat agagtnttgc ttaatcattn ggaattcaaa catgctatat 660
tttttttaaa aatcaatgtg aaaacataga cttattttta aattgntacc aattacaata 720
aaaataatgg gcaattaatt tttnaaaact ttttaaaata gnatgctcat atttttaaaa 780

ataaaanttt tnc 793

<210> 775
<211> 1009
<212> DNA
<213> Homo sapiens

<400> 775
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ccntntntna nngtttttnn gatncccaca tncngnaatn tncgggcncg ggnnactgnc 120
nannggcncc cttcgggggn ccngtgntaa gncnatnctt gtntntanaa agntggnnnt 180
nttttncgat ngngactatt gncnacnctc ttccntnttg gcagngngtc tgganggttg 240
nggtngctca tntggntaan ccnatcctgg ngaccaanng gccgnggtgn gcntgcaagc 300
tttgnccacn tgggaaancc gnnagtggtn gtctcanttg cntgntgggn ncntgncccc 360
atcttgnctg ctgnancctt ggggagcagg nnctnggtng tggtnctgcc tgcttgctgc 420
tngttccccg ggcatgcgtn nncannaagg gncatgcntn gggcaanaag gtgcgtggnc 480
ancgtnngna tnnnnaggac caccntgggt cgngaatcnn tgggttncct gataggaacc 540
ntnaannnct gcngntttta ttaaatggga nnananggt ncanttcaaa gccagtnnaa 600
tgcccttatg gaanggngtg natnacatan cnnnntatgt gtcntanann angaaatcgt 660
tnnncaaatt tnnacaanaa tntttntaan aaagggtatt tnantntngg tgaaanaaca 720
angntttaaa gtnaaatgnt tntancanaa ttaantaaac nggtnttnat gattncttac 780
naaantaacn atncnnaagc atttacngct tanangtccn cnngatactn ncanaatatg 840
gnnnnaattn tannanatng cgataatctn gnananactn tcatnnnnna tngtgtaatc 900
antanntacn tgatttnnnt naaatgaaaa catntgatnc aagattaatn cattanntat 960
acnaaaatnt tcanatanta natntacata taatggtttc naataaacn 1009

<210> 776
<211> 785
<212> DNA
<213> Homo sapiens

<400> 776
gnnnnnnntt cccctttcta atcncttgga nntcgctctn tntgnangat cccatngatt 60
cgaattcggc acgagagaaa cacaggtgtc gtgaaaacta cccctaaaag ccaanatggg 120
aaaggaaaag actcatatca acattgtcgt cattggacac gtanattcng gcaagtccac 180
cactactggc catctgatct ataaatnngg tggnntcgac aaaagaacca ttgaaaaatt 240
tganaaggag gctgctgaga tgggaaaggg ctccttcaag tntgcctggg tcttggataa 300
actgaaagct gagcgtgaac gtggtatcac cattgatatc tccttgtgga aatttgagac 360
cagcaagtac tatgtgacta tcattgatgc cccaggacac agagacttta tcaaaaacat 420
gattacaggg acatctcagg ctgactgtgc tgncctgatt gttgctgctg gtgtnggtga 480
atttgaagct ggtatctnca agaatgggca nacccnaaag catgcncttn tggcntacac 540
actgggtgtg aaacaactaa ttgtcggngt taacaaaatg gattcacttg accaccctan 600
aggccngaag agatattgan gaaattgtta aaggaagtca gcacttncat taagaaaatt 660
ggcctacaaa tccnnganac aataancatt tgtgccaatt tnngggttgg gaatgggtga 720
ccaacattgc ttggagccca agtgnttaac aatgccttng gttnaaaggg antggaaaag 780
ttacc 785

<210> 777
<211> 1366
<212> DNA
<213> Homo sapiens

<400> 777
ananaanann annnnnnnaa ggnnaanana nnnnnannnn naanangnaa anananannn 60
tnnanaannn aagnngnttc nannctttc aaagcttgga aaacgcannc aannnnnggg 120
aaagcaagaa agaacagcta aagnnngncn cagaganagc ttttangang tntangaaga 180
aggaatannn gnggncaata nnnnannnnc ngaaantatc atganacnca aatganggan 240
aaggcagcac aagctgngca aacagctatn gngacggggg ggccgggaga gnctaaangn 300
cananatnca atatataagg actgcatgcn aagggatacn aaacaagnan actnntctag 360
gaagaaataa ntnttgacnt ancnnacntt cataacgaat agcaccgtac atcgagncaa 420
ccaactaana ggnctaagga aatggcaaan nacnttaatn nntgagcnaa ggaagggngt 480
atngnccnan anngaaatgc ntcntaacca antttttaatn gtaacggnat nangatnaan 540
ncntnanccc acgcaactca aaaanattac attanntaaa aaaganctat ancaaaacta 600
gtnttcaaaa tngnacgagn aaatgggnaa nantttntnn ccgggaaaat tggnagagat 660
ccanaaacac tggntnaggg naatanatgn ccgcccnaaa aaaccntnac cataggnatn 720
ggctancata gangagatat ancnatnagg ggatcaanan cntaggnatt ngaaaantaa 780
ncgagttaaa acancnagat nnggnantac gaganatagc ttggacgngt atcaaatcgg 840
accctnggat gggcntangg aaaaanaaaa aggntngagn gaanttcctc anaggaanng 900
tganagagcn aaanaanatn aagggccttg gngaaaangg aaaaacagat agngtcatnc 960
natatatncn natgananan tggggnaatn taatctacnn tanatnnggg ggaaaaaaat 1020
cnnncatgac nnnaaaanga gntaatgnna nnatgagaga ttaaacnnat aaaacnagag 1080
aantttgngn aaanctgnga gataaaaaat aaataaattc tntntggaac atntanaccn 1140
tctatnnaaa aaaaagaggg gaaaccatct ngattatgca cananaaatn tnacntngng 1200
gaaataaatn gggnacaata acatatatgn ggatgtacan tnntggncng aaaaactata 1260
caacntgaga nnnnacnang atataaagcn nnaggnagtn tatangggca tcatcaangg 1320
gaagntataa agcaactgna nnctcatata naaaactgnn cnncaa 1366

<210> 778
<211> 775
<212> DNA
<213> Homo sapiens

<400> 778
gntttnnatn cctctttcta atnncttggc tactcgntct ntctgnanga tcccatcgat 60
tcgaattcgg cacgagagat tatgagcatg tagaagatga aacttttcct cctttcccac 120
ctccagcctc tccagagaga caagatggtg aaggaactga gcctgatgaa gagtcaggaa 180
atggagcacc tgttcctgta cctcccgccg ccgaacagtt aaaagaaata tacccaagct 240
ggatgctcag agattaattt cagagagagg acttccagcc ttaaggcatg tatttgataa 300
ggcaaaattc aaaggtaaag gtcatgaggc tgaagacttg aagatgctaa tcagacacat 360
ggagcactgg gcacataggc tattccctaa actgcagttt gaggatttta ttgacagagt 420
tgaatacctg ggaagtaaaa aggaagttca nacctgttta aaacgaattc gacttgatct 480
ccctatttta catgaagatt tttgttagca ataatgatga agttgcggag aataatgaac 540
atgatgtcnc ttctactgaa ttagatccct ttctgacaaa cttatctgaa agtgagatgt 600
ttgcttcttg agttaagtag aagcctaaca gaaggagcca accacaaaga attgagagaa 660
atnaacaact gggccttngg aaagaaangc nggccaagct gcttgagtaa tagtcaganc 720
ctanggaaat gatntggtta atgaattcac cccaggncac acccngttga agagc 775

<210> 779
<211> 781
<212> DNA
<213> Homo sapiens

<400> 779

gcttttnann nccctncttt cnaancctct tcaaatcctt ggntatcgtt ctntctgnng 60
gatcccatcg attcgaattc ggcacgagag acaaagaaaa aggtggcaat catagaagag 120
ttagtagtag gttatgaaac ctctctaaaa agctgccggt tatttaaccc caatgatgat 180
ggaaaggagg aaccaccaac cacattactt tgggtccnnt nctacttggc acaacattat 240
gacaaaattg gtcagccatc tattgctttg gagtacataa atactgctat tgaaagtaca 300
cctacattaa tagaactctt tctcgtgaaa gctaaaatct ataagcatgc tggaaatatt 360
aaagaagctg caaggtggat ggatgaggcc caggccttgg acacagcaga cagatttatc 420
aactccaaat gtgcaaaata catgctaaaa gccaacctga ttaaagaagc tgaagaaatg 480
tgctcaaagt ttacaaggga aggaacatca gcggtagaga atttgaatga aatgcagtgc 540
atgtggttcc aaacagaatg tgcccaggct tataaagcaa tgaataaatt tggtgaagca 600
cttaagaaat gtcatgagat tgagagacat tttataggaa atcactgatg accagtttga 660
ctttcataca tactggatga aggaagatta cccttagatc atatgtggac ttattnaaac 720
tatgaagatg tactttnaca gcatncattt tacttcaagg cagcaagaat tgcttttaga 780
c 781

<210> 780
<211> 783
<212> DNA
<213> Homo sapiens

<400> 780
gnntttnnan nnccngnttt ctaatnctnt tcnaatnctt tgnnancgtt ctntatgcan 60
gacccatcga ttcgggaatc tcctagaaaa gttgtgattt tcgagccata tccttctgtg 120
gtagatccta atgatcctca natgttggcc ttcaacccca ggaaaaagaa ctatgatcga 180
gtaatgaaag cactggatag cataacttct atcagcnaaa tgacacaagc accatatctg 240
gaaatcaaga agcaaatgga taaacaggac ccccttgctc atcccttact gcaatgggtt 300
atatcaagta atagatcaca tattgtgaaa ctgccagtta acaggcaatt gaagtttatg 360
catactccac atcagttcct tcttctcagc agtccaccag ccaaagaatc caattttaga 420
gctgctaaaa aactctttgg aagcaccttt gcatttcatg gctcacacat tgaaaactgg 480
cactccatcc tgaggaatgg tctggttgtt gcttctaata cacgattgca gctccatggt 540
gcaatgtatg gaagtggaat ctatcttagt ccaatgtcaa gcatatcatt tggtactcag 600
ggatgaacaa gaaacagaag gtgtcagcca aggacgagcc agcttcaagc agtaaaagca 660
gcaaatacat cacagtcacn ggaaaaaagg acagcaatcc caattcctgc caaagccgta 720
acttaaaatg catagncctt atgtgaaagg gatcaccttc atctggacct gcacaaacat 780
ggc 783

<210> 781
<211> 796
<212> DNA
<213> Homo sapiens

<400> 781
gnnntncgcc ttcaatnctn ttcantctnt tcaatctttg aatcntcttt gttgtccatc 60
gttcaattcg gacgagaccc ttatggcaga tccccacagt ctggggcaga agaggcgtcg 120
aggngccaga agtgncggca gcagcagccg cagcagccca aagagaggca agagaaagag 180
aaagcggccg gtggaggggt nnncggaaga gctggtcccc gtggttgagc tgggtccccg 240
tggttgaatt ggaagaggcc atagccccag gctcagaggc ccagggcgct tgggtctggt 300
ggggacgcgg gggttgcccc caatggtgca gctgcagcag tcaccactag ggggtgatgg 360
agaggaaggg ggccacccca gggccattaa caaccagtac tccttcgtgt gagccaaccc 420
caccccgctcc accctttta aaccccccag cccttgctcg tgagattggg cttgggtagg 480
gacagaagag gcccgaaatc cctccccat gcttnctgac ccttgtttgg ccaaagggca 540

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tctttgatgg tacaaagcag angcttcggg anaagcttcc gtcacaacac tncaaggtcc    600
cttcccaagg gcaaggggat ttnggcttca tgagctnctt tgaggggctt ttttttggtc    660
anncccccacc ttnggggcca tttttcccaa ttaacttacc cccaacccca agncanggtt   720
naggggggnaa agggctttcn anttccatta aagggggttt gtttgttgnt gttttaaacc   780
aaaatgggga aancnn                                                    796
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<210> 782
<211> 886
<212> DNA
<213> Homo sapiens

<400> 782

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cggnnnnnnn gnagcccntt tggnaaangc ctctaaggga aangcctttt tgaaaacnan     60
angaaaacct ntgggaaaag nccncannna ttttngngaa annggcnnga gcnnanantn    120
ggacacngtt ntaannnnan nagngnnngt tttnnganan agggnnnnna gnggnannna    180
ngngnnggag ggaannaagg nanagnannn ggnagnnaag gnnnnaaaga agnagnnang    240
gaganggnnn gnggnggggc atgangnggg nncagaggca cgaggagccc aagaccatca    300
cngangagna ngagcagggn accnacatnn acnnggacna cgagaagngg ggccagcgga    360
agaaggaagg nagnacctng agnaccgnta ccaggaggan cgggaccnac agngacanag    420
gnccnnnncn anacggannn nanaaacgng aagcaggann nnnanggacc aagggaaggg    480
nncngnncnn ggaaaganng ggagggaggn ncgaaggcaa aggggggann cgnnannncc    540
aggaagnang gaagggggn cgggaggnna annganaaga ngaaccnngg gggnncaggg     600
gggcgagggn agcanaannn nnccnnagnc aanngaaggg gananaagag ngggaaaann    660
aannagaaag agggaaaana agnnaaggaa anaaaagang ngnnaannng gganaaaana    720
nggnganann gnnggganaaa ngngnannan aaaanngagg aggncanngg gnaaanaana   780
nggggagggn ngananaanag ngaannagac aaggaanagn gaannagngn anagnanngn   840
gnannaaagg nanngggna anaagnanna nannnnnagn gaagan                    886
```

<210> 783
<211> 805
<212> DNA
<213> Homo sapiens

<400> 783

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cnaatncttg ctcttgncct ntttcnaatn cttggcnact cgctttctnt gcggatccct     60
cnnganncna tcgttcgaat tcggcacgag cacaaggaga agaaagttaa ttaacattga    120
aagatgagaa gacatcttgg aagacttgaa ttgggccttg gaagaagaac agccattcaa    180
atagatagaa ttgtggtagc aaaggcatac ngntcggaaa gtatagatct ccagggacag    240
tagtcatggg gttggggcac tgttggaatt taaggttgga aggatatatt ggagcccctt    300
gaatacggta acaaggcaca ccttgggcag tggagagtta tcagagtgtt tgaaaggag     360
ggttattgag taaataaata gactggtact ttaggaattt taaaatgtgg atcattgtac    420
tactaataac tatntatttt atatttacta tctactaagt aatttacatg tattttcttg    480
tactgactgt aaaccttctg ggtgtgggtg ttttaagtgc cattttactg ataaagaaac    540
tgangcttaa atagntgaaa tanntcaccc tgttagtgag tggcacaatg acaagtcann    600
atcttanggt tgccnanntc caaaanncat ttaaanttnn agnatnattg annnttttnc    660
cttatggcnt nnnaaatttg gggagccatt attgaaatcc nttacnacnt angaattgnc    720
caaaaaaaat actttttggg gaaaactgga tttattaatt atccaaaata atttnantgg    780
cttgnttggc ttntttccac tntnc                                          805
```

<210> 784
<211> 776

<212> DNA
<213> Homo sapiens

<400> 784
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taatgctggt tactgccctt caaatccttg caatcccttg gnaancggnc cngcngaccc      60
atcgattcga attcggcacg aggttatatt aaattattct ttgntnttct ttgtctttta     120
ataaagcctg caagttacta aattgnagtt ncataaattc tgtagtnaag tatcatcttg     180
gcagngtgcc aaaggtgaaa angntgcttn ctctaacaga gaaattctta gngactccag     240
tcgtanaaaa acgtctttac aacctgaata agatnganga attgngaaca taccatggcc     300
tattggatga atcatttgcc ggnggctana ncagactgta gggtttgtga tggatntatg     360
gagtatgtgg gtatagaaat catgaatntn ccatttgnnn ncagagattc aagcntanac     420
ttaatgggta gatcataaat gacagaatga attcaaaacc tagcacgtgc attgtaaatg     480
tgtgcccaga tatgtnttgg aaatggcagn tccttggggt catgtntcta ctggcaaaat     540
ttgctatagn gnnactattg nantgtaatt ataaaattna tcannattat ncaccgattn     600
gccaagtaaa ctgtactgtn cataggaatt ttgggaattg tgcanaaatt ggatcaattg     660
aanttnagaa cngatgtctg ggcttaaaaa tttatcnggg accacnnatt angaaactna     720
catntttcgg ngctgaggtt cattgnccaa ggccangaag gtntttnccg aaaanc         776
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<210> 785
<211> 778
<212> DNA
<213> Homo sapiens

<400> 785
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ttngaaaacn ccttngcttn gttnccccta cngaaaccct tttgaaaacc ntttgcnann      60
tcctctttnt gnaggatccc atcgattcgt gaaagaggag atcggtgacc tgggctcctt     120
atgtgcctga atgagtttga gtttcctgtt aactccaaat caacagtatt ttcaacaaga     180
aatgtgcaat tgaaatcaag tgctgtttaa gtgcagctag gantccacag gaagacactt     240
gcagtgaaca gagttatgga gcagcaaaaa cacagatcta tttggaaaaa gagaaaacat     300
atgcgttgta ttttgcttca attataaaat accatcctct caaaggtggt tctaaattac     360
aaaggacttt gatttctagg tagattctgg gtagagactt cctttcatat tgaggcatta     420
atgacacctt ttaacctggg aagcaatatg actggagttg tactttgaga agattaatca     480
ggtttggttg cagaatgaaa gagaagatga agtcaagaga ttggtttaga ggctctagca     540
gaagcttagt catatttcaa aatgatcaaa tatcaagaaa aattctgagc tgcataactt     600
gtataaagta attttcagtg attttttca tggttatgat aaaagaactg gattagcaga      660
aacttttacc ctgaatcaag atttaatttt tctttgagct catcttaagg atatcggaac     720
atagggagca aacgatggtg tggctgcctc antgcttgaa ttttaacngt tttgaaan       778
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<210> 786
<211> 805
<212> DNA
<213> Homo sapiens

<400> 786
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ngccccccct ttccccccctn ttgaaanccc ctttggnana nnccnntttc aaatcncttg     60
naaatccttg gcnactcgtn ctntctgcag gatcccatcg attcgaattc ggacgaggag     120
aggatcactt gagcttagga gttcaaatcc agcctgagcc aacataacaa gactttgtct     180
ctaaacaaaa cagttattgt ttaaagaatc tgaaatcttc atctttaatt caggtagccg     240
tgaatcgagc ccaagtttgt ttgatatcca gttccaagtc tggagagagg catctttatc     300
ttattaaagt atcgagagac aaaatatcag acagcaatga ccaagagtca gcaaattgtg     360
atgcaaaagg gctatcaaag ggaggctttt tacagagaac taaggaagag aaggaggttg     420
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ttaaagagac ttgagatcag aaaaagatca agaacaactt gaatctcaaa gtatgaattt 480
gaagtatttt gctgagcaaa catttgaatg cctgtatgta ccgtaatcct ctatcactgg 540
ggtccccaac cccggtacca gcccgtggcc tgctagggac tgggccgcac agcaggaggt 600
gagcagtggg tgggcaagcg accattccca cctgagcttc ccctcctgtc agatcagcag 660
cagcgttaga ttctcatagg agtgcaaaac cctattgtaa actgcccatg ccaagggatc 720
tangttgcaa cgcttcctta tgagaanttg aatgcctgan ngaactgtca ctgncttcca 780
tnaaccccca gatgggtact ngttc 805

<210> 787
<211> 775
<212> DNA
<213> Homo sapiens

<400> 787
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gatcccatcg attcgaattc ggacgaggag aggatcactt gagcttagga gttcaaatcc 120
agcctgagcc aacataacaa gactttgtct ctaaacaaaa cagttattgt ttaaagaatc 180
tgaaatcttc atctttaatt caggtagcac cgactcgagc ccaagtttgt ttgatatcca 240
gttccaagtc tggagagagg catctntatc ttattaaagt atcgagagac aaaatatcag 300
acagcaatga ccaagagtca gcaaattgtg atgcaaaagg gctatcaaag ggaggctttt 360
tacagagaac taaggaagag aaggaggttg ttaaagagac ttgagatcag aaaaagatca 420
agaacaactt gaatctcaaa gtatgaattt gaagtatttt gctgagcaaa catttgaatg 480
cctgtatgta ccgtaatcct ctatcactgg ggtccccaac cccggtacca gcccgtggcc 540
tgctagggac tgggcccgca cagcaggagg tgagcagngg gtgggcaagc cgaccattcc 600
cacctgagct tncccctcct gtcagatcag cancagcgtt agattctcat aggagtgcaa 660
ccctattgta aactgccatg cnagggatct aggttgcacg ctccttatga ggaattgaat 720
gccctgatga acttgncact gncttccatc acccccagaa ngganctggc taacc 775

<210> 788
<211> 774
<212> DNA
<213> Homo sapiens

<400> 788
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cangacccat cgattcgaat tcggcacnag attatttcca aagcagccta cagtagaaaa 120
tagtcattat ggcagcagct tctgatgttt ttgtttggta ggttttctga tttcaatata 180
tagaatcata ttcatagagt atcttctntn ccgcctngca caaagtaccc atttaaaatt 240
tacatgcaca gttcattgcc acctttctta ggcctatgca tagttaataa ggttataatc 300
tactcaacat ggaaaatgga gcctatttgc aaacacacaa gtaattaaag taccaattct 360
ctcttagttt cttttttat agttggttta ttttgcaatt ataaatgtta aacatcccta 420
gagatgaaag ttaaaatggt tgatcacaga tcagtagcaa aatacaaatt gacaattcaa 480
aattataaat aaaactctgt tgaggatgtt taactttgag tctccaaatt taagagctaa 540
gcttggaaga aacaaattta taggttatat ttccctctta aattaaanaa acaaacttcc 600
tctggcagta gtttggtgaa ttcctttcat tgnaatgata ccatgattac aggatcaaaa 660
atgcttaact tacttgccat tctgctcaca tcatcacagg ttgttntttt tttaaagcac 720
tcnatgtagg cattttaaac cttcnggata accagagtat cttttgagaa annc 774

<210> 789
<211> 773
<212> DNA

<213> Homo sapiens

<400> 789
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attcgaattc ggcacgagag cagatttgng ataaacntnn tgnaggttna accnaagggg 120
aactnntggt gcaactatgn ngnttggaag atgctgcnta tgtttattga ggattgcann 180
anananatcc tgaatnctcg ccntttncaa aggcttggat aaagcactca agccagctac 240
atatgtatag aacggnttaa aatcnatgag gaagcctgga ctaaatatnc catnggactg 300
gngccnanaa ngctgncgat gaactttgna tctggnnaga agtntaaaga atggcaggat 360
nantnnctaa ngatgaattt cannacnggn nnnccaccan tcttnaatnc tttaagatca 420
ttatacgaag ncnangaaaa ggtggcaatc atngaanaat gngnatnatg ttangaaacc 480
tctctaaaaa gntgacggca ctttaacccc natgatgatg ggaaggaggn accaccaacc 540
acattantttt ngggtccagt actacttggc acanccttat nacgaaactg gncngtncnt 600
ctattgcttt gggagtaccn taaaatacng ccntngngag tncacctnca atgaatnnaa 660
nctctttntc anganagctn nngatccata ngacntgctg ganatnttta aggaancttc 720
nanggnggan tggattaggc ncaggccntt ggacacancc ntncttnatt tnc 773

<210> 790
<211> 953
<212> DNA
<213> Homo sapiens

<400> 790
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aannngncnnt ncngcttnaa accttggnaa ncnccgcccn nttgcannaa angngaannn 120
atgcttngtg aagcctgann ccaaanctna aggnanggac ctggatcccc ttatatngaa 180
naancggtnt ggaggaanga gnntgtcngg gaggatgggg cagaaaatga ngnnggcaga 240
ntggncccgg gggctctgca naccagcctt ggagcctgct cattctgggc ccttgctgcc 300
aagganccca gcctnaccta gcangaaang anatgaaagc ccttctccca ngaggtaggg 360
tctaggctgc ccnaacttaa atgcattnag aaanctcnta gatgtggaaa natttttncg 420
aacctgaaaa tgcagctggt anaatntcaa tgggaagcat aaatncatgt aaaatataat 480
tnagntngaa tatnanngta aaaatgcact tttnngcggt gtgacngatc ctgggnnccc 540
annatctgnn attnaagngn tttacnaang gaanggaaag gacctttncc taaactacct 600
ttttgaacag ancattaaga angnncnttc ttttaagnaa aaaaaaatca aattttgang 660
aaaantggna ttngaatgtn nagaaaaang gatananaan aaaanccaat nntaannacc 720
nannctctct gganttcnac tatctccact acntacntnt acntatngcg ntaanatnna 780
ctnttacntc nnnntantcn cacanacntc ntcnaacnta atnangcncn canaatcctc 840
tatannatnt antgtnnntc acannncnna cnggntaant ntnnncaacg ccatatcacc 900
nctnnnatcg ncnagntana taacacntat atcgncactc ncacananac tcc 953

<210> 791
<211> 798
<212> DNA
<213> Homo sapiens

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tnncaaaagg tgttngatnc naattacttt aaaataaaac ctgtaattgn ataatgncat 660
aatgntgntc catgcctnan tcccсttcta gnnntanaaa cntnantaan aantatatca 720
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<212> DNA
<213> Homo sapiens

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caattggcan ttcattttta atggttttna aggttcaagg ggggaaggtt tttgggaagg 720
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nttttttt 788

<210> 793
<211> 806
<212> DNA
<213> Homo sapiens

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tataaagtcc ttcagccctt tgggactcta aattggnggg ggattaaaaa gaatttaaaa 240
taattttnga accgaattta ttttcccctc agtttttgag ggcattaaaa aggcattaaa 300
tcaagacaaa tcatgtgctt gagaaaaata aaattaatga aaacncagca ctttatgttg 360
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angaacccat agggtgtaca aaangttcta ttaaaatctg cnttatagag acaaagaggc 480
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atttaccgtt gcccttgccn ttggan 806

<210> 794
<211> 815
<212> DNA
<213> Homo sapiens

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aggcttgaag tgggtngatc accttgaggt canganttn tagaccagnc tggccaacac 540
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<210> 795
<211> 1050
<212> DNA
<213> Homo sapiens

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tacntcntan nnnnganttn tcangnnntn ttactaacnt ncnatngnnc ntnganatag 600
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<210> 796
<211> 884
<212> DNA
<213> Homo sapiens

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caggcacact gcatcggctt cccggacctg ggctgcctg tggtcctgca gntgaagtcg 180
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<210> 797
<211> 773
<212> DNA
<213> Homo sapiens

<400> 797
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<210> 798
<211> 812
<212> DNA
<213> Homo sapiens

<400> 798
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accagntttt tggggcttta aattggcctt gg 812

<210> 799
<211> 758
<212> DNA
<213> Homo sapiens

<400> 799
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<210> 800
<211> 770
<212> DNA
<213> Homo sapiens

<400> 800
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cagaagctta tgtttttggc acagaagcct gggccatttt catggacacc tggctggacc 180
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<210> 801
<211> 573
<212> DNA
<213> Homo sapiens

<400> 801
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<210> 802
<211> 1390
<212> DNA
<213> Homo sapiens

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<210> 803
<211> 947
<212> DNA
<213> Homo sapiens

<400> 803
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ngagagcagc ccagaacccc tggacaacat cttgttggca gcctttgagt ttgacatcca 180
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<210> 804
<211> 532
<212> DNA
<213> Homo sapiens

<400> 804
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ccatgttggc caggctggtn tcgaactcct ggccctcaag tgatccaccc acctcagcct 180
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<210> 805
<211> 552
<212> DNA
<213> Homo sapiens

<400> 805
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<210> 806
<211> 1646
<212> DNA

<213> Homo sapiens

<400> 806

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aaaaaatcct ggcaaatgag aggccaaatt gaattttcct tctggattac aatattctgg    180
caatggcaga ctttttaaaa gatcttcgta tcttgctggc atcatagtct tgaagtcttc    240
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atctttgcag ttcaggagat cagcttggtg gtctccaaaa tcaagactaa ttgattccgc    420
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<210> 807
<211> 1029
<212> DNA
<213> Homo sapiens

<400> 807

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<210> 808
<211> 836
<212> DNA
<213> Homo sapiens

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<210> 809
<211> 1844
<212> DNA
<213> Homo sapiens

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<210> 810
<211> 489
<212> DNA
<213> Homo sapiens

<400> 810
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aaaatarttc tgttgaattt caccctggcr atgtaaaytg akagcttatc ttcacagatg 180
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aatgtgtgg 489

<210> 811
<211> 471
<212> DNA
<213> Homo sapiens

<400> 811
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<210> 812
<211> 579
<212> DNA
<213> Homo sapiens

<400> 812

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<210> 813
<211> 562
<212> DNA
<213> Homo sapiens

<400> 813
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<210> 814
<211> 594
<212> DNA
<213> Homo sapiens

<400> 814
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<210> 815
<211> 812
<212> DNA
<213> Homo sapiens

<400> 815

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<210> 816
<211> 999
<212> DNA
<213> Homo sapiens

<400> 816

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<210> 817
<211> 653
<212> DNA
<213> Homo sapiens

<400> 817

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atgctttgca gtctccagac gtgaacaaat gcatcagctt ctccctcact ctatggtccc     360
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cttcattcat agtttcaaca gtckgcacag catgtcccat aattccggtc acagacatgc 420
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cccatccttt atactcattc ttctcactgg ctgtcactcg gacctctttg taaatgtaat 540
cttgccattc taagggggcct ttcttcatcc attcactcat gattgccacc tggctaaatc 600
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<210> 818
<211> 1225
<212> DNA
<213> Homo sapiens

<400> 818
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<210> 819
<211> 1024
<212> DNA
<213> Homo sapiens

<400> 819
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<210> 820
<211> 631
<212> DNA
<213> Homo sapiens

<400> 820
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agttaaaaaa ctcctcgcaa ctctgggtac t 631

<210> 821
<211> 635
<212> DNA
<213> Homo sapiens

<400> 821
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ctgaggccct gctcatggtc ctgcctttca tctgtaacct gctgcgccgg caccctgcct 480
gccgggtcct cgtgcaccgt ccacacggcc ctcgagttgg aacgccgacc cttacgaacc 540
ctgggagagg aggacccagc ccagagccgg gctttgggag agttccttgt tggatttttc 600
agggccttnc agcggcatta ccaacttgag gtttt 635

<210> 822
<211> 752
<212> DNA
<213> Homo sapiens

<400> 822
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actgttcgat ccacagttta cccacaatga tattatgcac acagcaggtg ggatttgtcc     180
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tgatcttgga tagttccatt ccaatacatt ttctgaggat gctccagata ctgaagtcat     660
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<210> 823
<211> 899
<212> DNA
<213> Homo sapiens

<400> 823

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tcatgatcac atgaggatcg tcacagctcc gtgtccatta gcacattacc ctccttgtcc     180
ttaactctta tccgaccgga tctgtacttc gtttcttgat gaccgtttgc atatacggtt     240
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ccattattaa actctatgag tttgttgcca tcacgttgta ctctgacaat tgtaccatct     360
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gtgatttctt ttcttccatc tgggtaatgt ttttctrttt aaaaagttgt tacagtaaat     480
attttttgaa ggaagggaag aatttaatga gagggtggag caagtttgta cctatttgtc     540
cacttgagaa atgtaagact tccagtcctc cgggtatgtc gtgtgagtgg tctgggcagc     600
tgcatagtag tagatctgta aagacacaca gtcagtctgc cttttctcca gagatggtta     660
aactatggag gagaacactt ctggaaacat accactcttt ggtctggcat gacctgcttc     720
acgtcaccat taaagaaagt gacagtgatg gtcttcccat ctgcactcac ttcctttcga     780
gttccattgg gaaacagtat aacacggcac ccattcttat aaaccttttc cacctttcca     840
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<210> 824
<211> 1980
<212> DNA
<213> Homo sapiens

<400> 824

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ctcksmwytc ysskwswskm tstgcccrga gctggtttcc gtctctcggc tcggggctgg     180
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aagccgccgg ggagccggga accccagcat gattcttggc ctttgttcgc ttctgatact     300
aagagcagca cggtacatta tttcacttgt cccgctcccc ttcataacag aaaaagggga     360
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cgagcgtcgc cgcgcggaga agccagctgt cccttggcag tgatttcgga aatgtgtcaa     480
ggcaattcca aaggtgaaaa cgcagccaac tggctcacgg caaagagtgg tcggaagaag     540
cgctgcccct acacgaagca ccagacactg gagctggaga aggagtttct gttcaatatg     600
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ctgtataaat gtctattatt atgaagaatt gccaatcttg ttttaagcaa atgcattcta     1860
tcgttattat aaatgttagt tctagctcta tttacttcta atcttaaatc agaataaatt     1920
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<210> 825
<211> 333
<212> DNA
<213> Homo sapiens

<400> 825

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agggcagatt ttccaaatgc tcatcaccac ttggcactgt gtggactata attttggcca      120
gttaggaaat ggcatctcat tgttttcatc ttaatttgcg tcagcctgat tactcattga      180
aacttgtgag gttgagaaac ttttcttaag cttattggcc attcaagttt cctcctttat      240
gaaatggttg ttcatgtcat ttkctcattt ttatattaga ttgkwtttmt wttttccagc      300
tgacttgtag gaactctaca tcttatcaat att                                   333
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<210> 826
<211> 658
<212> DNA
<213> Homo sapiens

<400> 826

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caatttgtac aactcagtgt tatggcattc ggcagcaata gtgtttgttc cttattctct      180
ttttgtcacg ttaaaaanaa agcaattgga ccatattaaa tgtcactgct aaacaacaac      240
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cagtaatgac gttacaattt gtagcttaaa ctcaataact ttaaggtcca catatccagt      360
ttactttgaa aactaaagat gttttaaaac ttcatgaata catcaacctg aggagtattt      420
taggkcccaa atccagtttt taaatttata ctccacnaaa aangaaaata catacataaa      480
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awtttaaacc mcngttytgg gcccattwaa acaccmaaaa agaccccccn aaaagttaag 540
anttccagct tanttctgga ngggtgggnc aaaatarraw kktwtawwma wwwymytwwt 600
ccnkmattca gacaaactaa aatcttaaga ggaaacccag accaaaatat cactcatg 658

<210> 827
<211> 453
<212> DNA
<213> Homo sapiens

<400> 827
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cataaaatta accatcacaa ccatgttcta ggcactgttc ctcactgcct gagaagacac 180
cgttatgttt attagggttt ttgagtttta tccacagctt ttggttatct gcaaccatgt 240
ctcccaccat taacatagtt cacactgaga tgaggattcc ctatttaaca cttggtccca 300
acttcttcac agtccatctg gttttgtaga gggaacataa ctggacattc tggtcaggtt 360
aggtgaggtc aggccttcag gacgctattt tcactgagtt gctttataag gcacattatg 420
caaaattcca tcagctcttc tgttcactac att 453

<210> 828
<211> 657
<212> DNA
<213> Homo sapiens

<400> 828
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cacatcgcac agtcacaggg gcaaagcccc tgaaaaaggc tgtggtgatg cccctacagc 180
taattcagga gcaggcagca tccccaaatg ccgagatcca catcctgaag aataaaggcc 240
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gcgtggaggg cataacgggg aaacagatgg agtccttcct gaaggcaaac atcctgggtc 540
tcgccgccgg ccagcgctgt ggcgcctcct gaccgtcgtc tcctcactcc gccttttcaa 600
atttttgtat aaccccgtgt tgtgtaaata cagtttttgc tccggtaaaa aaaaaaa 657

<210> 829
<211> 775
<212> DNA
<213> Homo sapiens

<400> 829
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gtaagacacc aaacacacac ctcatttcct gaactgtgac ttccaagctg acatttttct 180
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cagtagcaat aggagtacta caaggaatct ggggtgcaca ctctctgttg ggctttcctg 660
aggcttctcc actttgttcc atttcttcag aagtttcttg ctttgcttta aacaatctat 720
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<210> 830
<211> 413
<212> DNA
<213> Homo sapiens

<400> 830
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gcagcagcag cagacctatg gtgccatcca caacatcagc gggactatcc ctggacagtg 180
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ggaatgcgtt gggactgccc agctgagcta tcaggtgccc atcttttctg gtmccagcag 360
tggtgaggag agcacaggca ggcctcgccc ctccccttgct canccagttt ccc 413

<210> 831
<211> 876
<212> DNA
<213> Homo sapiens

<400> 831
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ctgtgacccc cacaaagttt ncggaaccgc ccacca 876

<210> 832
<211> 768
<212> DNA
<213> Homo sapiens

<400> 832
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mrywtwwmma tycctksccm gggagtttga aatttnatac tatagaaata actttaggtt 180

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gaaagattgg attttcctac ctttagagat ctaaaaaaaa tttaatataa aaaatcattt     300
tgtgttggtg tttattacta gttcagatga gtggctgctg aaggggcccc cttgtcattt     360
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tcatgcatta agactgtttt caaagctttc ctcacatttt taaagtgtga ttttcctttt     660
aatatacata tttattttcy ttaaagcagc tatatcccaa cccatgactt tgggrgatat     720
acccataaaa ccmatataac agcaggggta ttggagcagc tttctcaa                  768
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<210> 833
<211> 1604
<212> DNA
<213> Homo sapiens

<400> 833

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aaaaaatcct ggcaaatgag aggccaaatt gaattttcct tctggattac aatattctgg     180
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<210> 834
<211> 617
<212> DNA
<213> Homo sapiens

<400> 834

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tgaaaatcca ttagatgaca attctgagga agaaatggaa gatgcaccaa aacaaaagct 540
ttctaaaaaa cagargaaaa agaaacagaa accagcacag gatgtacctg gcaaagattc 600
atatctgcct gcagctc 617

<210> 835
<211> 542
<212> DNA
<213> Homo sapiens

<400> 835
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gc 542

<210> 836
<211> 542
<212> DNA
<213> Homo sapiens

<400> 836
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ccacatgctn grarsgcaca gcagcctcac gctcccagnn gctgntccag agcagcgcac 360
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gc 542

<210> 837
<211> 719
<212> DNA
<213> Homo sapiens

<400> 837
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<210> 838
<211> 579
<212> DNA
<213> Homo sapiens

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gagatgataa tgggtctcat gggaagtagg aggggagctc atacatcacg gacgatgagt 540
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<210> 839
<211> 1172
<212> DNA
<213> Homo sapiens

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nacaaataga tttaactaaa gtgacaagca taattataaa taaataccag attatcagat 180
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 844
<211> 702
<212> DNA
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ggaatcgcaa atgcattgca atgtgcagtg aagagacgcg ag 702